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Listing first 45 summaries
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 BH133989 ENTWH17TF
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ALZ63436 Tetracdon
AZ685166 ENTLG11TF
ALZ54753 TETRACON
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AL075720 Drosophi1
AL05940 Drosophi1
BH164851 ENTQT04TF
AU052962 AU052962
AU052962 AU052962
AU052961 BT17605.9
B1471035 Sah92106.
ALZ55341 Tetracdon
B1176637 EST517582
AZ753057 RPCI-24-8
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ENTNW17TF
                                                                                                                Class: shotgun
High quality sequence start: 17
High quality sequence stop: 490
                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                        genomic, DNA sequence.
BH133989
BH133989.1 GI:15093050
GSS.
                                                                                                                                                DNA library
Seq primer: M13-Forward
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Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444441
                                                                                                                                                                      Clones are derived from the
                                                                                                                                                                                                                                             Unpublished (2001)
Contact: Brendan J Loftus
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Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Organism="Entamoeba histolytica"
/Strain="HM1:IMSS"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="pntamoeba histolytica Sheared DNA"
/clone_lib="pntamoeba histolytica Sheared DNA"
/clone_lib="pntamoeba histolytica Sheared DNA"
/note="Yector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), RockFville, MD
Institute for Genomic Research (TIGR), RockFville, MD
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
                                                                                                      Socation/Qualifiers
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BG790034
B1784659
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CNS04RW2
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BE603900
CNS0075A
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AL15931 Anopheles
AU060898 AU060898
AL060867 Drosophil
AI437626 sa33906 y
BG552395 sac03d01.
AI443457 sa33h07 y
AI442486 sa27f06.y
BE55599 sp96d11.y
BE805704 ss48f09.y
BE805704 ss48f09.y
AW734942 sk93b01.y
BE805704 ss495001.
BG790034 sae52c03.
BI784659 saf57f12.
BI7901733 sai19e04.
AL304427 Tetraodon
BH483310 BOGTE35TF
BE603900 GS104 GS
AL066834 Drosophil
BM159224 EST561747
AU060486 AU060486
AU033804 AU033804
AZ304119 IM0004404
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                                                                                                                                                                                                                                    y/12 Medical Center Dr., Rockville, Fax: 301 838 0208
Fax: 301 838 0208
Email: bjloftus@tigr.org
Clones are derived from the Fntamon.
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Seq primer: Ml3-Forward
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Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Entamoebidae; Entamoeba
1 (bases 1 to 868)
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Entamoeba histolytica
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/Clone_lib="Entamoeba histolytica Sheared DNA"
/Rote="Vector: pHoS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockyille, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica:
method for isolate identification. Exp. Parasitol.
                                                                                                         /db_xref="taxon:5759"
                                                                                                                /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
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52.4%;
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Pred. No. 0.00054;
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0; Mismatches 107;
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                                                   Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
This sequence is a single read and was generated as part of a lar
scale clone-end sequencing project of the Tetraodon nigroviridis
http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                              Bernot,A., Fizames,C., Wincker,F., Biourin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 AGAAGTCGGAGCTGCGACTGGGGCTGTTGTTGGCGGGTGTTGCTGGCCAGCTGTTTGGTAA 143
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                                                                                                                                                                                                                                                   2 (bases 1 to 279)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Boune
Bernot,A., Fizames,C., Wincker,P., Brottier,P.,
                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the treshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                        Tetraodontidae; Tetraodon.

1 (bases 1 to 279)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C.,
Billault, A., Quetier, F., Saurin, W., Bernot,
                                                                                                                                                                                                                                                                                                                                                                                                                 Elkaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostemi; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clo
063D14 of library G from Tetraodon nigroviridis, genomic survey
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="063D14"
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54.7%;
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Best Local :
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High quality sequence start: 26
High quality sequence stop: 726.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bjloftus@tigr.org
Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences HM1: IMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13-Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
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                   324
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301 838 0208
301 838 3543
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                         /db_xref="tax.n:5759"
/db_xref="tax.n:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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                   Barell, Oxford University
1 161 c 95 g 265
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/note="Genoscope sequence ID : C0BG063DB07SP1~end PUC-Ori"
155 c 2 g 13 t 3 others
                                                                                                                                                                                                                                                                                                                        /organism="Entamoeba histolytica"
/strain="HM1:IMSS"
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Pred. No. 0.0052;
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Query Match 9.5%;
Best Local Similarity 52.6%;
Matches 101; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 TAATTGGTTCTAAAATCGGTCAATCGATGGATCAGCAGGATAAAATAAAGCTAAACCAGA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 TGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGAT 193
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                                                                                                                                                                                                                                             Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis Unpublished
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Tetraodon nigroviridis.
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045118 of library G from Tetraodon nigroviridis, genomic survey
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot
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                                                                                    /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="045118"
/clone_11b="G"
/note="Genoscope sequence ID : C0BG0
PUC-Ori"
a 157 c 10 g 0 t 1 c
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                Score 46.4; DB
Pred. No. 0.04;
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194 TAATTGGTTCTAAAATCGGT 213
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                                                                                                               74 TTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTGTTGCTGGCCAGC 133
                                            TAGACGGTGGTTTTGGTGGTGCTGTAGACGGTGGTTTTGGTGATACTGTAGACGGTGGTG
                                                           TGTTTGGTAAAGGTAGTGGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGAT 193
                                                                                                 TTGGTGGTGCTGTAGACTGTGGTGCTAATGGTGCTGTAGACGATGGTTTTGGTGGTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medaka EST Project in Takeda's lab Unpublished (2001)
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BJ001798 MF018SA cDNA Oryzias
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                                                                                                                                                                                                                                                                                     /Clone_lib="MF01SSA_CDNA"
/Sex="mixture_of_female_and_male"
/tissue_type="whole_embryo"
/dev_stage="segmentation_stage_20
1 248 c 64 g 104 t
                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:8090"
/clone="MF01SSA027D02"
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryzias latipes"
/strain="Hd-rk"
                                                                                                                                                                                                                                         9.5%;
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                                                                                                                                                                                                                                 Score 46.4; DB 10;
Pred. No. 0.049;
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                                                                                                                                                                                                                     TGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGCTGTTTTGGGTGGAT 193
                                                                                                                                                                                                                                                                                                            GTTTCGATGGTTTTGGTGGTACTGTAGACGATGGTTTTGGTGGTGCTGTAGACGATGGTT 703
                                                     CNS00JTL 909 bp
Drosophila melanogaster genome sur
BACR39608 of RPCI-98 library from
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                                 fly), genomic survey sequence.
AL076720
fruit fly
                           AL076720.1
                                                                                                                                                                                                                                                                                                                                                                                           104;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGTGGTACTATAGACGGT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOhara,Y., Shin-i,T., Kimura,T., Narita,T., Medaka EST Project in Takeda's lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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BJ009355 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA131D04 5',
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                        GI:4956298
                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="segmentation stage 20 - 318 c 130 g 169 t 5 c
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/Sex="mixture of female and male"
/tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:8090"
/clone="MF01SSA131D04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryzias latipes"
/strain="Hd-rR"
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Pred. No. 0.054;
0; Mismatches 96;
                                          P DNA linear GSS 03-JUN-1999
survey sequence TET3 end of BAC:
rom Drosophila melanogaster (fruit
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; Neoteleostei;
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333 134 393 ORIGIN BASE COUNT

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Matches

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Similarity

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source

REFERENCE AUTHORS

TITLE

SOURCE ORGANISM

Japanese medaka. Oryzias latipes

KEYWORDS VERSION ACCESSION DEFINITION

sequence.

RESULT 6 BJ001798/c

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GTTGTTGTTGGT 46

202 TCTAAAATCGGT 213

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 GGATGTTTGCAAGGTAGTAGTCTAATTATTATCAGTGTGTTTTTAGTTGGCTGTGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                          GGATTAATTGGTTCT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGT 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence BACR26H16 of RPCI-98 library from Drosophila fly), genomic survey sequence.
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                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                 Drosophila melanogaster
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/clone="BACR39G08"
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55 c 175 g
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/db_xref="taxon:7227"
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                                                   Unpublished (2002, Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
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14; Conserv
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                9712 Medical Center Dr.,
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                            1 (bases 1 to 890)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Ent
HM1:IMSS sheared DNA library (2001)
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BH164851
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                                                                                                                                                                                                                                                                       Eukaryota; Entamoebidae; Entamoeba
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bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RRCI-98"
/clone="BACR26H16"
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s; Pred. No. 0.07;
133; Mismatches
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Clones are derived

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the

Entamoeba histolytica HM1:IMSS sheared

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AU052962/c
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                                                                                                                                                                3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project
                                                                                                                                                                                                                                                                 1 (bases 1 to 427)
Morio,T., Urushihara.H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,H., Developmental cona in Dictyostelium discoideum
                                                                                                                                                                                                                                  University of Tsukuba
                                                                                                                                                                                                                                                               Unpublished (1998)
Contact: Hideko Urushihara
                                                                                                                                                                                                                                           Institute of Biological Sciences
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Dictyostelium discoideum
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discoideum cDNA clone SLF389, mRNA sequence.
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Seg primer: M13-Forward
Class: shotgun
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_Xref="taxon:44689"
/clone="ELF389"
/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
/dev_stage="slug"
a 105 c 25 g 66 t
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/Clone_"Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville; MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
morthod for inclara identification
From Parasitol
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65.7%;
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/strain="HM1:IMSS"
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Pred. No. 0.17;
0; Mismatches
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191 GATTAATTGGTT 202
   131 AGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTG
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9; Conservative
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Morio, T. Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Oohiai, H. and Tanaka, Y., Unpublished (1998)
                                                                                                                                                                                                                                                                                       Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.
                                                                                                                                                                                                                                                                                                               University of Tsukūba
3-3-10 Ten-nodai, Tsukūba, Ibaraki 305, Japan
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1 (bases 1 to 440)
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Dictyostelium discoideum
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99; Conservative
                                                                                                                                                                                             /Clone_lib="Dictyostelium discoideum
/dev_stage="slug"
110 c 26 g 70 t
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/clone="SLF355"
                                                                                                                                                                                                                                                         /organism="Dictyostelium discoideum
/strain="AX4"
                                                                                                                                                   0,
                                                                                                                                          Score 43.2; DB 9;
Pred. No. 0.33;
0; Mismatches 93
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Pred. No. 0.32;
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442 bp mRNA linear EST 06-DEC-2001 srllg06.yl Gm-c1050 Glycine max cDNA clone GENOME SYSTEMS CLONE ID Gm-c1050-83 5', similar to TR:Q40786 Q40786 ARABINOGALACTAN-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         call: (800)-533-4363 or contact via email: ccu@resgen.com Insert Length: 893 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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                         Similarity
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Location/Qualifiers
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195 c
                                                                                                                                                                                                               of 3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a xhoir restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XhoI; The Clark NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1955). The cDNA library was constructed from mRNA isolated from leaf tissue at various developmental stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1050-83"
/clone_lib="Gm-c1050"
/tissue_type="leaf tissue at various developmental stages
of greenhouse grown plants"
/dev_stage="3 week old"
                                                                                                                                                                                  with Dr. Paul Keim's laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
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/db_xref="taxon:3847"
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                         53.38;
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                         Score 42.6; DB Pred. No. 0.48;
                                                                                                                                    71 g
                                                                                                                                          69
                                                      DB 10;
                                                   Length 442;
  Indels
                                                                                                                                                                                              Northern Arizona
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., I Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI471035 452 bp mRNA linear EST 29-sah92f06.yl Gm-c1050 Glycine max cDNA clone GENOME SYSTEMS ID: Gm-c1050-3707 5' similar to TR:Q40786 Q40786 ARABINOGALACTAN-PROTEIN PRECURSOR. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae;
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Glycine max
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314 286 1810
                                                                                                              /note-"vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The Clark NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from leaf tissue at various developmental stages of 3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments were directionally cloned into the EcoRI-XhoI fragments were directionally cloned into the EcoRI-XhoI
cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="leaf tissue at various developmental stages of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
                                                                                         restriction . site of the pBluescript vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
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/clone="GENOME SYSTEMS CLONE ID:
/clone_Lib="Gm-c1050"
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Qy., 77 GTCGTCAAGAAGTCGGAGCTGCGACTGGGGCTGTTGTTGGCGGTGTTGCTGGCCAGCTGT 136
                                                                                                                    BASE COUNT
ORIGIN
                                      Query Match
Best Local Similarity 56.9
78; Conservative
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Best Local
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                                                                                                                                                                                           Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis http://www.genoscope.cns.fr/Tetracdon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 TTATTATCAGTETETTTTAGTTGGCTGTGCCCAGAACTTTAGTCGTCAAGAAGTCGGAG 94
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                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 536)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                     Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the reshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodontidae; Tetraodon.

1 (bases 1 to 536)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J.

Weissenbach, J.

Weissenbach, J.

Meissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Tetraodon nigroviridis genome survey sequence T7 end of clone
046624 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                           (bases 1 to 536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 53.3%; 90; Conservative
                                                                                            /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="046624"
/clone_1ib="G"
/clone_1ib="G"
/note="Genoscope sequence ID : C0BG046BD12LP1~end : T7"
a 236 c 79 g 43 t 15 others
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56.9%;
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193 c
                                       ; Score 42.6; DE; Pred. No. 0.5; 0; Mismatches
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Minimum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-825-781-2

US-09-243-920-2

US-09-243-920-2

US-08-332-766A-1

US-08-276-452A-24

US-08-798-740-25

US-08-298-687A-25

US-08-298-829-25

US-08-298-829-25

US-08-298-829-25

US-08-298-829-25

US-08-298-829-25

US-08-298-829-203A-4

US-08-469-203A-4

US-08-469-203A-4

US-08-469-203A-4

US-08-470-204A-44
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US-08-476-110A-2
US-08-556-978B-80
US-08-556-978B-81
US-08-556-978B-82
PCT-US95-10668-3
PCT-US95-10688-4
US-08-361-467B-4
PCT-US95-10668-2
PCT-US95-10668-2
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US-08-232-463-14/c
 Query Match
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ALIGNMENTS

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US-08-232-463-14
                                                                                                                                                       APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELERAS: (89914)
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                      STRANDEDNESS: s
TOPOLOGY: linea
IMMEDIATE SOURCE:
CLONE: pTZgpt-F
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-005/MS-DOS SOTTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: V
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                                                                                                                                          LENGTH:
                                                                                                                   nucleic acid
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Score 47.8;

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Length 7218;

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Best Local Similarity 2.0%; Pro Matches 7; Conservative 206;

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136 TTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGGTGTTTTTGGGTGGATTA 195

Pred. No. 2.5e-05; 06; Mismatches 138;

Indels

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/476,102A
APPLICATION NUMBER: US/08/476,102A
CLASSIFICATION CHARATION:
NAME: Marks, Michelle S.
REFERENCE/DOCKET NUMBER: 41,971
TELECOMMUNICATION INFORMATION:
TELEX: 301-399-8504
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 465 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                                            MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                  Query Match
Best Local Similarity
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US-08-476-102A-2
; Sequence 2, Application US/08476102A
; Patent NO. 6355450
; GENERAL IMFORMATION:
; APPLICANT: Fleischmann, et al.
; Patent NO. 6355450
; Patent NO. 6355450

***Fluinnian Patent No. 6355450

****TITLE OF INVENTION: Nucleotide Sequence of the Haemphilus
; Patent NO. 6355450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 TATAGTGTTGAGCCAGTGCGTACTTACCAGCGTTACAATAAGCAAGAGCGTCGCCAGCAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 TTGGAAAAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGGATACAGGCAATAGT 315
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                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Rockville
STATE: MD
               8.8%;
54.9%;
     Score 42.6; DB 4;
Pred. No. 0.00027;
              Length 465;
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ON TS PARTICIPADAMANICATION OF HISMATCHES 69; Indels 0; Gaps 6) DO 171 TANTAMAGRITIANTOGRACTTOGGACT		Thereof	0;
··	ry Match t Local Similarity 56.3%; Pred. No. 0.032; thes 67; Conservative 0; Mismatches 52; Indels 0; Gaps 84 AGAAGTCGGAGCTGGGACTGGGGCTGTTTGGGGGTTTTGGCTGGC	B-80 APPLICATION: PINTENTION: NOVEL RECOMBINANTLY P. SEQUENCES: 107 INVENTION: SPIDER SILK ANALOGS DENCE ADDRESS: EE: E. I. DU PONT DE NEMOURS AND WILMINITON BELLANARE 107 MARKET STREET 108 MERCA WILMINITON WILTED STATES OF AMERICA READABLE FORM: SYPE: DISKETTE, 3.50 INCH G SYSTEM: MICROSOFT WINDOWS 95 PLICATION DATA: CON NUMBER: US/08/556,978B MICROSOFT WORD FOR WINDOWS 95 ATION: 435 CON NUMBER: 08/077,600 MINDER: 108/077,600 MINDER: 33.692 ADOCKET NUMBER: CR-9389-A SOLON INFORMATION: 302-892-8112 303-892-8112 303-892-8112 303-892-8112 303-892-8112 303-892-8112 1303-892-8112 1303-892-8112 1303-892-8112 1303-892-8112 1303-892-8112 1303-892-8112 1303-892-8112 1303-892-8112 1303-892-8112 1303-892-8112 1303-892-8112 1303-893-812 1303-893-8	Matches 84; Conservative 0; Mismatches 69; Indels 0; G. 75 TAGTCGTCAAGAAGTCGGAGGTGCGACTGGGGCTGTTGTTGGGGGTGTTTGCTGCCACCT 1 1 1 1 1 1 1 1 1 1

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RESULT 5
US-08-556-978B-82
; Sequence 82, Application US/08556978B
; Patent No. 6268169
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL RECOMBINANTLY PROTECTION:
TITLE OF INVENTION: SPIDER SILK ANALOGS
TITLE OF SERUENCES: 107
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Patent No. 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 302-892-811
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,60
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9389-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED TITLE OF INVENTION: SPIDER SILK ANALOGS
                                                                                                                    NUMBER OF SEQUENCES: 1
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COMPUTER READABLE FORM:
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Local Similarity 56.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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                                 COUNTRY:
                                                     STATE:
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                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                      AGGCGCTGGTGCAGCAGCAGCTGCCGCTGGCGGTGCAGGCCAAGGTGGATATGGTGGCT 201
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                                                                    MILMINTON
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                                                                                    E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: E. I. DU PONT DE NEMOURS AND CÓMPANY 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                 UNITED STATES OF AMERICA
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302-773-0164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application PC/TUS9510668 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.3%;
Best Local Similarity 53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                      OPERATING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/0 FILING DATE: JUNE 15, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MICROSOFT WINDOWS SOFTWARE: MICROSOFT WORD FOR WINDOWS CURRENT APPLICATION DATA:
                                                   CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112
APPLICATION NUMBER: 08/294,133 FILING DATE: August 22, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 GTCAAGGTGGCTACGGCGGTT 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 TTGCTGGCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 TTTTGGGTGGATTAATTGGTT 202
                                                                                         APPLICATION NUMBER: FILING DATE: Herew
                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                     STREET: 210 Lake
CITY: Cherry Hill
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 GTGGCCAGGGTGCAGGTGCTGCTGCTGCTGCTGGCTGGTGGTGCAGGTCAGGGTGGTC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GTGCCCAGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9389-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGATCTCAGGGCGCAGGTCAAGGTGCTGGTGCAGCTGCGGCGGCAGCTGGTGGCGCGG
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                                                                                                                                                                                                                                                                                                      E: Jane Massey
210 Lake Drive
                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                             James Eberwine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302-773-0164
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                                                                                                                                                                            IBM 486
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                                                                                                                                                                                               DISKETTE,
                                                                                         Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                              A Method of Sequencing Proteins by
                                                                                                                                                                                                                                                                                                                                                                                            Epitope Ordering and
                                                                                                                                                                                                                                                                                                                                                                             Restriction Mapping
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                                                                                                         PCT/US95/10668
                                                                                                                                                                                               3.5 INCH, 1.44 Mb
                                                                                                                                                                                                                                                                                                      Licata, Esq
East, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.50 INCH
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                                                                                                                                                                                                                                                                                                          201
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                                                                                                                                                                                                  STORAGE
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; TOPOLOGY:
; ANTI-SENSE:
PCT-US95-10668-3

STRANDEDNESS: LENGTH:

Nucleic Acid DEDNESS: Single

Linear

TELEFAX: (609) 779-848
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

779-8488

Query Match
Best Local Sim
Matches 91;

Similarity

7.2%; 49.5%;

Conservative

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0;

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APPLICATION NUMBER: PCT/US95/106, ETLING DATE: Herewith CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/294,133 ATTORNEY/AGENT INFORMATION: 1994 NAME: TRANSPORT TO THE PRIOR DATE: AUGUST 22, 1994 NAME: TRANSPORTATION:
                                                                                   NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: PENN-0137
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A Method of Sequencing Proteins by TITLE OF INVENTION: Epitope Ordering and Protein restriction Mapping
                                                                                                                                                                                                                                  COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jane Massey Licata, Esq. STREET: 210 Lake Drive East, Suite 201 STATE: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 TGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGGTGTTTTTGGGTGGATTAAT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 TGTTGTTGTTGTTGTTGTTGGAATTCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PENN-0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GCAAGGTAGTAGTCTAATTATTATCAGTGTGTTTTTAGTTGGCTGTGCCCAGAACTTTAG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application PC/TUS9510668
                                                                                                                                                                                                                                                                       DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                          PCT/US95/10668
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                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: US 07/681,492
PILING DATE: 04-APR-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: WO PCT/EP90/01275
FILING DATE: 01-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION UNMBER: EP 89 402 224.3
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US-08-361-467B-4/c
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REGISTRATION NUMBER: 31,196
REFERENCE/DOCKET NUMBER: 010830-027
TELECOMMUNICATION INFORMATION:
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                                                        APPLICATION NUMBER: ED 8
FILING DATE: 04-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Schulman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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TOPOLOGY: Linear
ANTI-SENSE: No
PCT-US95-10668-4
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box J
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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Best Local :
                                                                                                                                                                                                          APPLICATION NUMBER: US/08/361,467B FILING DATE: 22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 TGGT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 TGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGATTAAT 197
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                                                     Schulman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTGTTGTTGTTGTTGTTGGAATTCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT
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5. 5633441
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                                                                                                                                                                                                                                                                                                                                                                      E: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                        United States
                                                                                                                                                                                                                                                            PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                       Van Montagu, Marc
VENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Emmelo, John
De Oliveria, Dulce E.
De Souza, Maria-Helena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
                                             Robert M.
                                                                                                                                                                                                                                             Release #1.0, Version #1.30
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Pred. No. 0.04;
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PCT-US95-10668-4/c

equence 4, Application PC/TUS GENERAL INFORMATION: APPLICANT: James Eberwine

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

δÃ B δÃ Ъ Qγ Ъ δÃ

198

5 TGTT 2

INFORMATION FOR

TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400

(609)

9) 7/ 1779-8488 NO: 4:

CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT

COUNTRY:

.08002

USA

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US-08-484-332C-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                         APPLICATION NUMBER: WO PCT/EP90/01275
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                 APPLICATION NUMBER: EP 89
FILING DATE: 04-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Schulman, Robert M.
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE: CLONE: 3C9
                                                                                                                                                                                                 FILING DATE: 22-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/361,467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 TTTTGATGGGCTATAAGTGGGAGCCTTAGTTGGTGGTTTAACCGGTGGTTTAACTGGTGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 AGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGATTAATTGGTTC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 AGGAGCAGGATAAGGTGATGGTGTTGGTGGTGGTTTAACTGGTGGCTTAGCTGGTGG 270
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0: FILING DATE: 7-JUNE-1995 CLASSIFICATION: 800
                                                                                                                APPLICATION NUMBER: WO POFILING DATE: 01-AUG-1990
                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 04-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 AGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTGTTGCTAA 143
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: P.O. Box
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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REFERENCE/DOCKET NUMBER:
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                               Schulman, Robert M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.O. Box 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Montagu, Marc
VENTION: PLANTS WITH MODIFIED FLOWERS, SEEDS OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Van Emmelo, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Souza, Maria-Helena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Oliveria, Dulce E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De Greef, Willy
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                                                                                                                                                                                 US 07/681,492
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                                                                                 402 224.3
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                                                                         TELEFAX: (609) 779-84 (NFORMATION FOR SEQ ID NO:
                                                                                                                                                                           APPLICATION NUMBER: 08/2 FILING DATE: August 22, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                  SOFTWARE: WORDPERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TITLE OF INVENTION:
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                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204
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                                                                                                                                                                                                                                        FILING DATE: H
                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: WINDOWS FOR WORKGROUPS SOFTWARE: WORDPERFECT 5.1
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                                                                                                                                 REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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   TOPOLOGY:
                                TYPE:
                                                                                                     TELEPHONE:
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               STRANDEDNESS:
                                                                                                                                                                  NAME:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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74; Conservative
                                                                                                                                                                                                                                                                                                                                                                            08002
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                          Nucleic Acid
                                                                                                                                                              Jane Massey Licata
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                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Jane Massey Licata, Esq.
210 Lake Drive East, Suite 201
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              Single
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52.9%;
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                                                                                                      779-2400
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                                                                                                                                                                                              08/294,133
22, 1994
                                                                                                                                               32,257
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Pred. No. 0.18;
0; Mismatches 66;
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Query Match

Best Local Similarity 48.ys

Matches 90; Conservative

6.9%; 48.9%;

Score 33.6; DB Pred. No. 0.13; Mismatches

DB 5; Length 198;

94;

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18 GCAAGGTAGTCTAATTATTATCAGTGTGTTTTTAGTTGGCTGTGCCCAGAACTTTAG 77

78 TCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTGTTGCTGGCCAGCTGTT 137

PCT-US95-10668-1

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                                                                                                 , ANTI-SENSE:
PCT-US95-10668-2
                                                        Matches
                                                           Query Match
Best Local Similarity
                                                                                                                                                              TELEFAX: (609) 7/9-84
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-10668-2/c
Sequence 2, Application PC/TUS9510668
GENERAL INFORMATION:
APPLICANT: James Eberwine
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LENGTH: 198
18 GCAAGGTAGTAGTCTAATTAATCAGTGTGTTTTTTAGTTGGCTGTGCCCAGAACTTTAG 77
                                                                                                                                                                                       TELEPHONE: (609) 779-2400
                                                Local S.
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey L
STREET: 210 Lake Drive E
CITY: Cherry Hill
                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/2: FILING DATE: August 22, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                       TOPOLOGY:
                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                       NAME: Jane Massey Licata
REGISTRATION NUMBER: 32/
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: Herew: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM 486
OPERATING SYSTEM:
SOFTWARE: WORDPER
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                                                           48.98;
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PENN-0137
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                                       ; Score 33.6; DB
; Pred. No. 0.13;
0; Mismatches
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East, Suite 201
                                                             DB 5;
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US-08-825-781-2
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US-08-825-781-2
269 ATTCCACTGTCAGTTGCATTATCCTGTTTTGGTGGCCTCAATGCCTCCATTGTGGCTGCT
                  157 GTTGCAATGGCCATTGGTGGTGGTGTTTTGGGTGGATTAATTGGTTCTAAAATCGGTCAA 216
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                                         209 GCCAGTGATGCTGTTGCGGGCTTTTTGCAGATCAGATATTTTGGAATATTTAACTGGATA 268
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IMMEDIATE SOURCE:
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FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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                                                            97 GCGACTGGGGCTGTTGTTGGCGGTGTTGCTGGCCAGCTGTTTGGTAAAGGTAGTGGTCGA 156
                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08825781
                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                        Local
                                                                                                                                                            LIBRARY: PANCTUT02
CLONE: 2236771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
US/08/825,781
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
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CITY: Palo Alto
CTATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hillman,
APPLICANT: Shah, Put
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                     68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 TGGT 201
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                                                                                                                                                                                                                          1011 base pairs
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                                                                                                     0;
                                                                                             Score 33.2; DB 2;
Pred. No. 0.42;
0; Mismatches 58
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                                                                                                                Length 1011;
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; LIBRARY: ESOGTUT02
; CLONE: 2667831
US-09-073-362-2
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RESULT 14
US-09-243-920-2
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US-09-073-362-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                   1015
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APPLICATION NUMBER: US/09/073,362
                                                                                                                                   1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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APPLICANT: Yue, Henry
APPLICANT: Corley, Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: COTICY, Neil C.
TITLE OF INVENTION: AMINO ACID PERMEASE HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                              157 GTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGATTAATTGGTTCTAAAATCGGTCAA 216
                                                                                                                                                                                                                                97 GCGACTGGGGCTGTTGGTGGCGGTGTTGCTGGCCAGCTGTTTGGTAAAGGTAGTGGTCGA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                    TCGATG 222
                                                                                                                                                                                                   GCCAGTGATGCTGTTGCTGTGACTTTTGCAGATCAGATATTTGGAATATTTAACTGGATA 1074
                                                               TCTAGG
                                                                                                                                 ATTCCACTGTCAGTTGCATTATCCTGTTTTGGTGGCCTCAATGCCTCCATTGTGGCTGCT 1134
                                                                                                                                                                                                                                                                    68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                 1140
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54.0%;
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                            Sequence 1, Application US/08332766A Patent No. 5843647 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09243920 Patent No. 5981242 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: ESOGTUT02
CLONE: 2667831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
APPLICANT: JEFFREYS, Alec J. APPLICANT: ARMOUR, John
                                                                                                                                               1135 TCTAGG 1140
                                                                                                                                                                                                            1075 ATTCCACTGTCAGTTGCATTATCCTGTTTTGGTGGCCTCAATGCCTCCATTGTGGCTGCT 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pair
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APPLICATION NUMBER:
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APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: AMINO
                                                                                                                                                                             217 TCGATG 222
                                                                                                                                                                                                                                          157 GTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGATTAATTGGTTCTAAAATCGGTCAA 216
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SOFTWARE: FastSE(
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CITY: Palo Alto
STATE: CA
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54.0%;
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for Windows Version
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FR: PF-0514 US
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TITLE OF INVENTION: SIMPLE TANDEM REPEATS NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS

```
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COUNTRY: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 01-NOV-1994
PRIOR APPLICATION NUMBER: 25,323
FILING DATE: 21-DEC-1993
ANAME: BIRD, Donald J.
REFERENCE/DOCKET NUMBER: 25,323
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELEPHONE: (202) 861-3000
TELEPAX: (202) 861-3000
TELEPAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 1:
LENGTH: 377 base pairs
TYPE: NUCLeic acid
TOPOLOGY: linear
US-08-332-766A-1

COMPUTER STORED

COMPUTER READABLE FORM
COUNTRY SINGLE

COMPUTER READABLE FORM
COUNTRY SINGLE

COMPUTER: US.A.

REPERENCE OF CREATER STICS: TYPE: DNA (genomic)
                                                                                                                                                                                   Query Match
Best Local Similarity 53.5%; Pred. No. 0.29;
Matches 69; Conservative 0; Mismatches 60; Indels
186 TGGTGGTGA 194
                       198 TGGTTCTAA 206
                                   138 TGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGATTAAT 197
                                                                                                       ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P. STREET: 1100 New York Avenue, N.W. STATE: D.C.
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Search completed: October 27, 2002, 18:37:15 Job time : **44**.5337 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                               Score
                                                                486
295
295
73.2
71.6
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1: /SIDS1/gcgdata/g
2: /SIDS1/gcgdata/g
3: /SIDS1/gcgdata/g
4: /SIDS1/gcgdata/g
6: /SIDS1/gcgdata/g
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9: /SIDS1/gcgdata/g
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 1.0
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100.0
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15.1
14.7
14.2
12.8
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SIDSI/gcgdata/geneseq/geneseqn-embl/NA199.DAT: *
SIDSI/gcgdata/geneseq/geneseqn-embl/NA2000.DAT: *
SIDSI/gcgdata/geneseq/geneseqn-embl/NA2000.DAT: *
SIDSI/gcgdata/geneseq/geneseqn-embl/NA2000.DAT: *
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    486
489
483
768
110
118
102
454
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AAH79040
AAF86247
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(without alignments)
6762.541 Million cell updates
OspA 17kD antigen
Piscirickettsia sa
DNA sequence of E.
DNA sequence of cl
PCR primer #2 used
PCR primer #4 used
PCR primer #5 used
PCR primer #5 used
PCR primer #5 used
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                       99CA-2281913
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Human brain expres	AAK17542	22	887		8	45
Probe #14630 for g	Ð	22	887			44
	ABA69248	22	887		8	43
Human breast cell	ABA51240	22	887		38.8	42
Neurospora crassa	AAA65171	21	8045			41
DNA encoding novel	AAS67681	23	801		39	40
Probe #8238 used t	AAI39552	22	600	٠		39
Probe #6480 for ge	AAI16547	22	600			38
bone m	382	22	600	8.0		37
	AAK07956	22	600		39	36
-	822	22	600			35
foetal	968	22	600			34
used	AAI52634	22	350			<u>ω</u>
	AAI25744	22	350			32
=	AAK46795	22	350			31
m.	AAK20651	22	350			30
Probe #16570 for g	ABA38104	22	350			29
Human foetal liver	ABA72229	22	350	8.0		28
DNA encoding novel	AAS89524	23	1395		9	
#8101 u	AAI08110	22	522	•	39.6	
#16401 used	AAI47715	22	522		9	
#1235	AAI22424	22	522		9	
Human bone marrow	AAK41670	22	522		9.	
Human brain expres	AAK15928	22	522	8.1	9	22
	ABA34580	22	522	8.1	9.	21
foetal	0	22	522	8.1	9	
•	ABA49593	22	522		9.	
Arabidopsis thalia	588	21	2292		9	18
3	AAS78586	23	2226	٠	9	17
melano	27	23	5162		٥.	16
	ABL20279	23	1509		•	15
Sequence of Haemop	AAN80227	9	850	٠		14
Ω	387	11	790		42.6	13
	329	23	2309	9.1	44	12
sophila melar	1329	23	309	9.1	4	11
PCR primer #6 used	AAF86256	22	110	9.6	46.8	10

ALIGNMENTS

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AAF86246

ID AAF86246;

XX

AC AAF86246;

XX

T1-JUL-2001 (first entry)

XX

DT 11-JUL-2001 (first entry)

XX

Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen;

KW Poikilothermic fish; Piscirickettsial septicaemia; rickettsial disease;

XX

Vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease;

XX

SRS; ds.

XX

Location/Qualifiers

FT CDS

Piscirickettsia salmonis.

XX

Index a pathogen;

KW Poikilothermic fish; Piscirickettsial septicaemia; rickettsial disease;

XX

Piscirickettsia salmonis.

XX

Location/Qualifiers

FT CDS

Product= "OspA"

/partial

FT /product= "OspA"

FT /note= "Genus specific 17kDa antigen, the sequence does

XX

PN

CA2281913-A1.

XX

PN

CA2281913-A1.

XX

PF 17-SEP-1999; 99CA-2281913.

XX

17-SEP-1999; 99CA-2281913.
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RESULT 2
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ID *\AAH79040 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a particularly pointiothermic fish, against the mound of a particularly pointiothermic fish, against the bacterial pathogen animals. The method is also useful for protecting animals, sequence represents DNA encoding the P. salmonis that septicaemia (SRS) and other rickettsial diseases. The present protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 486 BP; 137 A; 79 C; 144 G; 126 T; 0 other;
                                                                          CAAGAGATTTACGGCACTGCATGCCGGCAACCGGATGGTCGTTGGCAAGTCATTTCAACA
                                                                                     61
                                                        GAAAAA
                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                    Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2B;
                                                                                                                                                        GATACAGGCAATAGTTATAGTGTTGAGCCAGTGCGTACTTACCAGCGTTACAATAAGCAA
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                                                                                                                                                                                                                                                                            Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KAYW/)
(BURI/)
                                                                                                                                                                                                                                                                                                                  TGTGCCCAGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGT
                                                                                                                                                                                                                                                                                                                           TGTGCCCAGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGCTGTTGTTGGCGGT 120
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DB; AAB81126.
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KUZYK M A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 100.0%;
Conservative 0
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Mismatches
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                                                                                                                                                                                                                  Sequence 489 BP; 139 A; 79 C; 144 G; 127 T; 0 other;
                                                                                                                                                                                                                            The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia protect fish against P. salmonis which causes piscirickettsia known as salmonid rickettsial septicaemia.
                                                                                                                           61
                                                                                                                                                                                                                                                                                          Claim 3; Fig 4; 25pp; English.
                                                                                                                                            61
                                                                                                                                                                                                                                                                                                     New nucleic acids encoding an amino acid sequence homologous to surface antigen present on Piscirickettsia salmonis are useful to
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01-JUL-2000; 2
01-JUL-2000; 2
29-JUL-2000; 2
1 ATGAACAGAGGATGTTTGCAAGGTAGTAGTCTAATTATTATCAGTGTGTTTTTAGTTGGC 60
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Burzio
                                 GTTTTGGGTGGATTAATTGGTTCTAAAATCGGTCAATCGATGGATCAGCAGGATAAAATA
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                                                                    GTTGCTGGCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATTGGCCATTGGTGGTGCT
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                                                                             GTTGCTGGCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piscirickettsia salmonis polynucleotide
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DB; AAG78025.
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; 2000GB-0016080.
; 2000GB-0016082.
; 2000GB-0018599.
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This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animal particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid
                                                                                                                                                                                                         17-SEP-1999;
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                                                                                 vaccine
                                                                                          septicaemia
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                                                                                                                                                        (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
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                                                                                                                                                                                                                                                                                                                                 salmonis
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/product= "ospA"
/note= "Genus specific 17kDa antigen,
/note= not include a stop codon"
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SRS; 17E2;
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 misc_feature
                                             misc_feature
                                                                                                                                                                   Synthetic.
                                                                                                                                                                                   Piscirickettsia
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                                                                                                                                                                                                                                                                                                                                                                   standard;
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/product=
/note= "No
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/note=
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No. 2.
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                 undefined N-terminal
                                                           with N-terminal is given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
?.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                             rickettsial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                            fusion
                 fusion
                                                                                                                                                                                                                                                                         partner.
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                                                                           partner"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                 partner'
                                                                                                                                                                                                                                                                                                                                                                                                                                              483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
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428
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Best Local
                                                                                                                                                                                                                                                                                                                                                         This invention relates to a method for the protection against infection of a polikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a perticular period of a vaccine. The method is used for protecting animals, polikilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial diseases. The present P. salmonis. The method is also useful for protecting against salmonid sequence represents P. salmonis Ospa DNA termed C17E2 optimised for expression in Escherichia coli fused to DNA encoding an undefined is used in a vaccine to create an anti-Ospa antibody response.
                                                                                                                   530
                                                                                                                                      248
                                                                                                                                                          470
                                                                                                                                                                             188
                                                                                                                                                                                                 410
                                                                                                                                                                                                                    128
                                                                                                                                                                                                                      350 AGAACTTCAGCCGCCAGGAAGTTGGCGCGGCCACCGGTGGGGGTTGTGGGCGGTGTTGCCG
                                                                                                                                                                                                                                                                                                                                                        Sequence 768 BP;
                                                                                                                                                                                                                                                                               290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
TTTACGGCACTGCATGCCGGCAACCGGATGGTCGTTGGCAAGTCATTTCAACAGAAAAA 486
                    GTCAGCAGTACTGCCGCGAATTTCAGCAGAAAGCCATGATCGCAGGTCAGAAACAGGAAA
                                œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1999;
                                                                     GCAATAGTTATAGTGTTGAGCCAGTGCGTGACTTACCAGCGTTACAATAAGCAAGAGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA2281913-A1.
                                                           GTAACAGCTACTCTGTGGAACCGGTTCGCCACCTACCAGGGTTACAACAACAGGAACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-MAR-2001.
                                                                                                   ACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGTAATCCGGACACCG
                                                                                                                ACCAGAGTTTGGAAAAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGATACAG
                                                                                                                                         GCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGATAAAATCAAACTGA
                                                                                                                                                     GTGGATTAATTGGTTCTAAAATCGGTCAATCGATGGATCAGCAGGATAAAATAAAGCTAA 247
                                                                                                                                                                                            GCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGG
                                                                                                                                                                                GCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGTCGATGGCCATCGGCCGGTGCGGTTCTGG
                                                                                                                                                                                                                                  AGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTGTTGCTG
                                                                                                                                                                                                                                                                           GAGGATGTTTGCAAGGTAGTAGTCTAATTATTATCAGTGTGTTTTTAGTTGGCTGTGCCC
                                                                                                                                                                                                                                                            2001-316844/34
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB81128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burian J,
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                             220 A; 183 C; 190 G; 175 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99CA-2281913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                     60.7%;
76.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuzyk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Optimised OspA construct c17E2"
                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΜĀ
                                                                                                                                                                                                                                                                                                                   Score 295; DB 22;
Pred. No. 2.8e-79;
                                                                                                                                                                                                                                                                                                          Pred. No. 2.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                          115;
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                           Length 768;
                                                                                                                                                                                                                                                                                                      0;
                                                           649
                                                                               367
                                                                                                   589
                                                                                                                      307
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                                                                                                                                                                                                                         409
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δÃ Вр Qγ D Qγ Вb οy DЬ δÃ Дb Qy DЬ Qγ Дb QΥ

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RESULT 6
RAF86254/C
ID AAF86254 standard; DNA; 118
XX
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Best Local
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AAF86252
ID AAF8
                                                                                                                                                                                                                                                                                   This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an Immunogenic amount of a post in the form of a vaccine, The method is used for protecting animals, Particularly poikilothermic fish, against the bacterial pathogen particularly poikilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial diseases. The present the P. salmonis Osph gene. The Osph gene is used in the method of the invention
                                                                                                                                                                                                                                                              Sequence 110 BP; 13 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 4B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAYW/)
(BURI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA2281913-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poikilothermic vaccine; OspA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer #2 used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF86252 standard;
                                                                                GCGGTGTTGCCTGGCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATG
                                                                GCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGGCGATG
                                                                                                                        TGGGTTGCGCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGGCCACCGGTGCGGTTGTGG
                                                                                                                                          TIGGCTGTGCCCAGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGCTGTTGTTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                710
                                                                                                                                                                                                    1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-316844/34.
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) BURIAN J.
) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burian J,
                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fish; Piscirickettsia salmonis; rickettsial salmonid rickettsial septicaemia; rickettsia ion construct; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99CA-2281913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              salmonis
                                                                                                                                                                                                                15.1%;
79.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in cloning an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                            28 C;
 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MA;
                                                                                                                                                                                                 0;
                                                                                                                                                                                                              Score 73.2;
Pred. No. 1
                                                                                                                                                                                       Pred. No. 1.96
0; Mismatches
                                                                                                                                                                                                                                                    45 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               optimisation
                                                                                                                                                                                                           DB 22;
..9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of OspA gene
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rickettsial
                                                                                               165
                                                                                                                                                                                                                     110;
                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogen;
al disease;
                                                                                                                                                                                  Gaps
                                                                                                                           60
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AAF8625/c
ID AAF862
XX AAF862
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Best Local 9
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vaccine; OspA; s
SRS; 17E2; fusic
                                                                                                                                                                                                                                                                                                                                                                                                                                salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen p. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of the p. salmonis OspA gene. The OspA gene is used in the method of the
Polkilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
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(BURI/)
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                                                                                                                                    AAF86255 standard; DNA; 102
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kay WW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piscirickettsia
                                             PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer #4 used in cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF86254;
                                                                                                                                                                                                                                          271
                                                                                                                                                                                                                                                                                                    211 GGTCAATCGATGGATCAGCAGGATAAAATAAAGCTAAACCAGAGTTTGGAAAAGGTAAAA 270
                                                                                                                                                                                                                58
                                                                                                                                                                                                                            GCAGGGCAAGTGACACGTTGGCGTAATCCAGATACAGGCAATAGTTATAGTGTTGAGC 328
                                                                                                                                                                                                                                                                      GGTCAGAGCATGGACCAGCATAAAATCAAACTGAACCAGTCTCTGGAAAAAGTGAAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-316844/34.
                                                                                                                                                                                                              GCCGGCCAGGTTACTCGTTGGCGTAATCCGGACACCGGTAACAGCTACTCTGTGGAAC
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BURIAN J.
KUZYK M A
                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burian J,
                                           #5 used in cloning an optimisation of OspA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 4B; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion construct;
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                           ВP;
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                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fish; Piscirickettsia salmonis; rickettsial pathogen;
salmonid rickettsial septicaemia; rickettsial disease;
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                                                                                                                                                                                                                                                                                                                                               14.7%;
75.4%;
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                                                                                                                                                                                                                                                                                                                                                                                         32 C;
                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                              Score 71.6; DB
Pred. No. 5.9e-1
                                                                                                                                                                                                                                                                                                                                                                                             28 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                             37
                                                                                                                                                                                                                                                                                                                                                                                           Τ,
                                                                                                                                                                                                                                                                                                                                                 DB 22;
.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                             0 other;
                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of OspA gene
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                             Length 118;
                                                                                                                                                                                                                                                                                                                                 0
   disease;
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RESULT 8
AAF86253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                           Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease SRS; 17E2; fusion construct; PCR primer; ss.
                                                                                                                                                                                      11-JUL-2001
                                                                                                                                                                                                                                                                             AAF86253 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 102 BP; 14
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(BURI/)
Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              кау ww,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRS; 17E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                    397 AAGGCGATGATTGCAGGGCAGAAGCAAGAGATTTACGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 ACTTACCAGCGTTACAATAAGCAAGAGCGTCGCCAGCAATATTGTCGAGAATTTCAGCAA 396
                                                                                                                                                                                                                                                                                                                                                                                              42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                         primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-316844/34
                                                                                                                                                                                                                                                                                                                                                                                                AAAGCCATGATCGCAGGTCAGAAACAGGAAATCTACGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTACCAGCGTTACAACAACAGGAACGCCGTCAGCAGTACTGCCGCGAATTTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAY W W.
BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KUZYK M A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burian J,
                                                                                                                                         #
W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 4B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                  (first entry)
                                                                                                                                         used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99CA-2281913
                                                                                                                                    in cloning an optimisation
                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 23 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.2%;
                                                                                                                                                                                                                                                                               94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a method for the protection against infection
                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 69; DB 22; L
Pred. No. 3.4e-11;
""smatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 G; 35 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer;
                                                                                                                                         of OspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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17-SEP-1999;

99WO-SE00230

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RESULT 9
AAZ06832
                                                            W09942479-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                  Rickettsia helvetica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                  diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                       Rickettsia 17 kD outer membrane protein DNA.
                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                       09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                   AAZ06832;
                                                                                                                                                                                                                                                                                                                                                                                AAZ06832 standard; DNA; 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 TCTAAAATCGGTCAATCGATGGATCAGCAGGATA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed Ospa, or an immunogenic amount of a particularly polkilothermic fish, against the bacterial pathogen animals, rickettsial septicaemia (SRS) and other rickettsial septicaemia (SRS) and other rickettsial diseases. The presents a PCR primer used in the cloning and optimisation of the P. salmonis Ospa gene. The Ospa gene is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 AAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGATTAATTGGT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 94 BP; 18 A; 20 C; 35 G; 21 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TCTAAAATCGGTCAGAGCATGGACCAGCAGGATA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 4B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-316844/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGGCTCTGGTGTGGGGGATGGGCCATCGGCGGTGCGGTTCTGGGGGGGTCTGATTGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1999;
                                                                                                                                                                                                                             intracellular; parasite; outer membrane protein; OMP; vaccine;
; immune response; antigen; peptide; tick; spotted fever; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burian J, Kuzyk MA;
                                                                                                               /partial
/product= "17 kD out
/note= "Stop codon n
277..360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                           /product=
                                                                                                                                                                            /*tag=
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99CA-2281913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.8%;
78.7%;
                                                                                                                                                                             ۵
                                                       "28 amino acid antigenic peptide from
17 kD OMP"
                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                              outer membrane protein on not given in specification on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.3e
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..3e-09;
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                         DЬ
                                                                 QУ
                                                                                              Ъ
                                                                                                                       Qy
                                                                                                                                                    Ъ
                                                                                                                                                                             Qγ
                                                                                                                                                                                                         DЬ
                                                                                                                                                                                                                                   Qy
                                                                                                                                                                                                                                                              DЬ
                                                                                                                                                                                                                                                                                       Qγ
                                                                                                                                                                                                                                                                                                                    DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a major portion of the coding sequence CC Rickettsia helvetica 17 kD outer membrane protein (OMP) and includes the Sequence was isolated from total pNA from the tick ixodes ricinus using CC amember of the spotted fever group (SFG) of the Rickettsia helvetica is CC amember of the spotted fever group (SFG) of the Rickettsia helvetica is CC amem negative bacteria. SFG Rickettsiae conditions and are transmitted to humans via ticks and conditions. The Rickettsiae found in Ixodes ricinus ticks and conditions of CC humans. The Rickettsiae found in Ixodes ricinus ticks are pathogen specific symptoms. However, the symptoms of rickettsiaes are obligate intracellular parasites in both ticks and CC similar to some other bacterial and viral infections. The immunogenic CC properties of Rickettsia bacteria are associated with structures exposed CC as the basis for a serological assay, the Weil-Felix reaction, but is sufficiently used in the surface of the Organism. Lipopolysacharides (LPS) have been used The peptide can be used in immunoassays to detect infection, but is CC amples. It can also be used in vaccines to protect against, or treat, or rickettsiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                      Matches
382 CGTGÁGTACACTCAAACAGTTGTAATAGGCGGAAAACAACAAAAAGCATACGGTAATGCA
                                                                                322 GTTGAGCCAGTGCGTACTTACCAGCGTTACAATAAGCAAGAGCGTCGCCAGCAATATTGT
                                                                                                                                      262 AAGGTAAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGATACAGGCAATAGTTATAGT
                                                                                                                                                               205 GGGCAAATCGTTGCAGGTATGGATGAGCAGGATAGAAGAGTTGCAGAGGCTTACCTCACAG 264
                                                                                                                                                                                  202 TCTAAAATCGGTCAATCGATGGATCAGCAGGATAAAATAAAGCTAAACCAGAGTTTGGAA 261
                                                                                                                                                                                                                       145 AAAGGTAAAGGGCAACTTGTCGGAGTAGGTGTAGGTGCATTACTTGGAGCAGTTCTTGGC
                                                                                                                                                                                                                                              142 AAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGGTGTTTTGGGTGGATTAATTGGT 201
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 454 BP; 138 A; 84 C; 117 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                   82 CAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGCTGTTGGCCAGCTGTTTGGT 141
                        CGAGAATTTCAGCAAAAGGCGATGATTGCAGGGCAGAAGCAAGAGATTTACGGCACTGCA 441
                                                      GGCAATTACGGTTACGTAACACCTAATAAAACTTATAGAAATAGCACTGGTCAATATTGC
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 182; Conserv
                                                                                                            AGAGCTTTAGAAGC---AGCTCCTAGCGGTAGTAACGTAGAGTGGCGTAATCCGGATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 16; 21pp; English.
                                                                                                                                                                                                                                                                          CAAGGTACAGGAACACTTCTTGGCGGTGCCGGGGGGGTGCATTACTTGGTTCTCAATTTGGT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide from outer membrane protein of Rickettsia helvetica.
used to diagnose rickettsiosis and in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527454/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nilsson K, Pahlson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NILS/) NILSSON K.
(PAHL/) PAHLSON C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-FEB-1998; 98SE-0000504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                         Conservative
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11.6%; 48.8%;

0;

Score 56.2; DB 20; Length , Pred. No. 5e-07; 0; Mismatches 188; Indels

454;

В

DЬ Ş

442 TGCCGGCAACCGG

В

442 TGCCGCCAACCTG

454

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RESULT 10
AAF86256/c
ID AAF862
XX AAF862
XX AAF862
XX AAF862
XX AAF862
XX DOT 11-JUL
XX POIkil
KW Vaccin
KW Vaccin
KW Vaccin
XX Piscir
XX Piscir
XX Piscir
XX Piscir
XX CA2281
XX I7-SEF
PR 17-SEF
XX I7-SEF
X
RESULT 11
ABL13299/c
ID ABL13299 s
XX
AC ABL13299;
                                                                                                                                   밁
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                                                                                                                                                                                                            망
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen p. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present
                                                                                                                                                                                                                                                                                                                                                                                                                      the P. salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                 Sequence 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-316844/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BURI/)
(KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA2281913-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF86256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF86256 standard; DNA; 110 BP
                                                                                                                                                                                                              110
                                                                                                                                                                                                                                                    413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KAYW/)
                                                                                                                                                                        473
                                                                                                                                     50
                                                                                                                                                                                                                                    GGCAGAAGCAAGAGATTTACGGCACTGCATGCCGGCAACCGGGATGGTCGTTGGCAAGTCA 472
                                                                                                                                                                                                              GTCAGAAACAGGAAATCTACGGCACCGCGTGCCGTCAGCCGGATGGCCGCTGGCAGGTGA 51
                                                                                                                                                                    TTTCAACAGAAAAA 486
                                                                                                                                     TTAGCACCGAAAAA
                                                                                                                                                                                                                                                                                     l Similarity
57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BURIAN J.
KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAY W
                                                                                                                                                                                                                                                                                                                                                                                                                   ial septicaemia (SRS) and other rickettsial diseases. The present represents a PCR primer used in the cloning and optimisation of almonis OspA gene. The OspA gene is used in the method of the
                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig 4B; 35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          salmonis
                                                                                                                                                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                       CDNA;
                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                               A; 34 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuzyk MA;
                                                                                                                                                                                                                                                                                                       9.6%;
77.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning an
                                       309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                   Score 46.8; DB 22;
Pred. No. 0.00019;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                 27 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         optimisation
                                                                                                                                                                                                                                                                                                                                                               32 T;
                                                                                                                                                                                                                                                                                                                                                               0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OspA
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                           110;
                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                   В
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RESULT 12
ABL13298
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The inventiuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1016176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
Drosophila; developmental biology; cell signalling; pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                   Drosophila
                                                                                                                        ABL13298;
                                                                                                                                                         ABL13298 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data 
specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster expressed
                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
P-PSDB; ABB69196.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                               148
                                                                                                                                                                                                                                                                                                                  196
                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                 AGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGATTAATTGGTTC
                                                                                                                                                                                                                                                                                                                                    GTCGGAGCTGCGACTGTGTTGTTGGCGGTGTTGCTGGCCAGCTGTTTGGTAAAGGT 147
                                                                                                                                                                                                                                             from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JC,
                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
71; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 34379; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 BP;
                                                   melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            htt for this patent did not form part of the printed
but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
                                                                                                                                                         CDNA; 2309
                                                                                                                                                                                                                                                                                                                                                                                                    9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid
a and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 113 C; 65 G; 23 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS.
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                                                   expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 23; 1
Pred. No. 0.0021;
0; Mismatches 45;
                                                                                                                                                         ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers
                                                 polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EW;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 309,
                                                   SEQ
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                                                                                                                                                                                                                                                                                                                                                                                        Indels
                  insecticide;
                                                    IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1000 or more and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                               203
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                    137
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is

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Drosophila melanogaster

Seid RC,

88US-0239572. 89US-0396572. 89WO-US03779.

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RESULT 13
AAQ03870
                         22-MAR-1990.
                                                                                                                                                                                                                                                                                                                                            WO9002557-A.
                                                                                Key
CDS
                                                                                                    outer membrane proteins; pBOMP-2; active immunisation; typable H influenzae; non-typable H influenzae; ss.
                                                                                                                            H.influenzae DNA fragment containing the PBOMP-2 gene.
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                            31-AUG-1990
                                                                                                                                                                                       AAQ03870 standard; DNA; 790
                                                                                                                                                                                                                 1174 Géragradracraccagracrararagracaracracracracracracracracrac 1229
                                                                                                                                                                                                                                                148 AGTGGTCGAGTTGCAATGGCCATTGGTGGTGGTGTTTTTGGGTGGATTAATTGGTTC 203
                                                                                                                                                                                                                                                                                                                      Sequence 2309 BP; 561 A; 405 C; 526 G; 817 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention inserticell indevelopmental biology and in elucidating cell signalling inserticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA engineers (ABB737-ABB72072).
                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                           88 GTCGGAGCTGCGACTGGGGGTGTTGGTTGGCGGGTGTTGCTGGCCAGCTGTTTGGTAAAGGT 147
                                                                                                                                                                                                                                                                                                        Local Similarity les 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 34376; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
genes from Drosophila and
interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
P-PSDB; ABB69195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY
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                                                                                                influenzae.
                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                 Conservative
                                    /product=PBOMP-2, outer membrane protein of H.influenzae.
                                                                     Location/Qualifiers
164..628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams M,
                                                                                                                                                                                                                                                                                                        9.18;
61.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                     Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                     DB 23; Length 2309;
0.0052;
ches 45; Indels
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RESULT 14
AAN80227
ID AAN80
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                                                  23-DEC-1987;
                                                                  14-JUL-1988.
                                                                                  W08804932-A
                                                                                                               Key
CDS
                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PRAX-) PRAXIS BIOLOGICS IN.
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11-DEC-1987;
02-MAR-1987;
31-DEC-1986;
(PRAX-) PRAXIS BIOLOGICS IN
                                                                                                                                                                            Haemophilus influenzae.
                                                                                                                                                                                               Vaccine; diagnosis; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                       Sequence of Haemophilus influenzae Praxis Biolgics Outer
Membrane Protein-2 (PBOMP-2) gene.
                                                                                                                                                                                                                                                             12-JAN-1991
                                                                                                                                                                                                                                                                                               AAN80227 standard; DNA; 850 BP,
                                                                                                                                                                                                                                                                                                                                               454 AGCTGGAAGTAAAATCGAAGAAAAAATGAGTCA 486
                                                                                                                                                                                                                                                                                                                                                                   195 AATTGGTTCTAAAATCGGTCAATCGATGGATGA
                                                                                                                                                                                                                                                                                                                                                                             394 AATTGGCGGTGGTCGTGGTCAAGCTATTGCAGCAGTAGTTGGTGCAATTGGCGGTGCAAT 453
                                                                                                                                                                                                                                                                                                                                                                                          135 GTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGGTGTTTTGGGTGGATT 194
                                                                                                                                                                                                                                                                                                                                                                                                                        334 TAATCAAGGTETAGTTGGTACGCTTGGTGGTGGAGCTTTAGGTGGTATTGCTGGTAGTAC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 790 BP; 240 A; 106 C; 176 G; 266 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is a 789bp BstEll-Xmnl fragment of paal30.The predicted see also AAQ03869,R03948 and AAR03949.
                                                                                                                                                                                                                                                                                                                                                                                                                                       75 TAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTGTTGCTGGCCAGCT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 14; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane protein epitopes of Haemophilus influenzae. used i diagnosis.
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P-PSDB; AAR05799.
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                     87US-0132073.
87US-0020849.
86US-0948364.
                                                             87WO-US03423
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                   /*tag=
                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.8%;
                                                                                                                                                                                    passive immunisation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deich RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42.6; DB 11,
Pred. No. 0.0085;
Thes 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2lotnick GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 790;
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RESULT 15
ABL20279/c
ID ABL20279;
XX
AC ABL20279;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic
XX
Drosophila developmental biolc
XX
Drosophila melanogaster.
XX
OS Drosophila melanogaster.
XX
V
PN W0200171042-A2.
XX
PD 27-SEP-2001.
XX
PP 23-MAR-2000; 2000W0-US09231.
XX
PF 23-MAR-2000; 2000US-0514150.
XX
PR 11-JUL-2000; 2000US-0514150.
XX
PA (PEKE) PE CORP NY.
XX
PA (PEKE) Adams M, Li PWD,
XX
PA (PEKE) PE CORP NY.
XX
Venter JC, Adams M, Li PWD,
XX
PR WPI; 2001-656860/75.
XX
New isolated nucleic acid detec
PT genes from Drosophila and for e
PT interactions -
XX
Claim 1; SEQ ID NO 12310; 21pp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A pure antigenic peptide or protein related to an epitope of Haemophilus influenzae is claimed. Also claimed is a recombinant vector comprising a DNA sequence coding for an antigenic determinant of an Haemophilus influenzae outer membrane protein, the transformed cell, a subunit vaccine in a pharmaceutical carrier, a method of immunising humans and an assay for Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pure peptide related to epitope of used as immunogens in vaccines and passive immunisation and assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 850 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTGGAAGTAAAATCGAAGAAAAAATGAGTCA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGGTGTTTTTGGGTGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTGGCGGTGGTCGAGCTATTGCAGCAGTAGTTGGTGCAATTTGGCGGTGCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster genomic polynucleotide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 A; 116 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8%;
54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    biology;
                                                       detection reagent for for elucidating cell s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42.6; DB 9
Pred. No. 0.0088;
0; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 G;
                                                                                                                                                Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                      cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus influenzae for producing antibodic
                                                                                                                                                띺
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          producing antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                         r detecting 
signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO 12310
                                                                                                                                                                                                                                                                                                                                                                                                                                      insecticide;
                                                         1000
and (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                           0 or more cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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ch completed: October time: 127.389 secs

21pp + Sequence Listing; English

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                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                 GGGGAAGTGTGGGTGGATAAGTAGGTGGATGTTGGT
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          Description
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AX252413
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Fish vaccine against piscirickettsia
Patent: WO 0168865-A 5 20-SEP-2001;
Aqua Health (Europe) Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                              Sequence 5
Ax252413
                                                                                                                                                              Piscirickettsia salmonis.
Piscirickettsia salmonis
Bacteria, Proteobacteria;
                                                                                                                          Simard, N., Brouwers, H., Jones, S.F.,
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from Patent WO0168865
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AL1602004
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RAU11013
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                                                                                                                                                                   gamma subdivision; Piscirickettsia group;
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                                                                                                    salmonis
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D16515 Rickettsia
M28480 R. conorii 1
AE008675 Rickettsi
M16486 R. rickettsi
M16486 R. rickettsi
AJ269516 Male-Kill
AJ269517 Male-Kill
AJ269518 Male-Kill
AF195118 Rickettsi
U11020 Rickettsia
AF027124 Rickettsia
AF060704 Rickettsia
M28482 R. prowazeki
AF060704 Rickettsia
M200706 Rickettsia
M200706 Rickettsia
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AF260571 Rickettsi
166494 Sequence 14
AC102004 Mus muscu
AL160412 Human DNA
AC027343 Homo sapi
AC103214 Rattus no
AL158162 Homo sapi
AL158162 Human DNA
AE003872 Xylella f
AC104133 Homo sapi
                                                                                                                                                                                                                                                                                                                                                                 072952 Plasmodium
AF104714 Plasmodium
L19047 Plasmodium
L19045 Plasmodium
AC018090 Drosophil
AC008362 Drosophil
AC020587 Homo sapi
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U11017 Rickettsia
U04162 Rickettsia
M74042 R.australis
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AJ235273 Rickettsi
AF031534 Rickettsi
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AC104133 Homo sapi
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AF184152 Piscirick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AAGCTAAACCAGAGTTTGGAAAAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCA 300
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                                                                                                                                                                                                                                  Direct Submission
Submitted (10-SEP-1999) Biochemistry &
Victoria, Petch Building, PO Box 3055,
                                                                                                                                                                                                                                                                                                        Unpublished
2 (bases 1 to 4983)
Kuzyk, M.A. and Kay, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGAGATTTACGGCACTGCATGCCGGCAACCGGATGGTCGTTGGCAAGTCATTTCAACA 480
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                                                                                                                                                                                                                                                                                                                                                  Kuzyk, M.A., Burian, J., Thornton, J.C. and Kay, W.W. Identification of a genus-common Rickettsial surface antigen in manufication pathogen Piscirickettsia salmonis
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Piscirickettsia salmonis
Bacteria, Proteobacteria; gamma subdivision; Piscirickettsia
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                                                                                                        /Organism="piscirickettsia
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<1. .501
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Pred. No. 4.7e-123;
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Victoria, BC V
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V8W 3P6, Canada
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                                                                                                      sequence-like element"
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repeat_region
BASE COUNT 1360
ORIGIN
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KEYWORDS
SOURCE
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DEFINITION
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RSU76907
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                                                 Rickettsiaceae; Rickettsiaee; Rickettsia.

1 (bases 1 to 448)
Davis,M.J., Ying,Z., Brunner,B.R., Pantoja,A.
Rickettsial relative associated with papaya b
Corr. Microbiol. 36 (2), 80-84 (1998)
                                                                                                                                 Rickettsia sp
Rickettsia sp
           2 (bases 1 to 448)
Ying, 2. and Davis, M.J.
                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
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 Direct Submission
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Pred. No. 6.3e-123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAATATTGTCGTGAATACACCCAAACAGTTGTAGTAGGTGGAAAAACAACAAAAAGCTTA
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 mitochondria
Nature 396 (
                              Rickettsiaceae; Rickettsiae; Rickettsia; typ 1 (bases 1 to 237523)
Andersson, S.G., Zomorodipour, A., Andersson, J. Sicheritz-Ponten, T., Alsmark, U.C., Podowski, R Eriksson, A.S., Winkler, H.H. and Kurland, C.G. The genome sequence of Rickettsia prowazekii
                                                                                                                                               Rickettsia prowazekii.
Rickettsia prowazekii
Bacteria; Proteobacteria;
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AJ235273.1 GI:3861237
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                                                                                                                                                                                                       complete genome.
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(6707), 133-140 (1998)
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51.6%;
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Pred. No. 5e-1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to
Andersson, S.G.
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ISGTEEVRROIEHHQEGGYVKSERNNLGGILDIRNNTYSELMTHRSNIIALNIDLPY
ELIIKTLLSGAHTRIPLMODNRNIIGILDIRNSLIKALIENNDDKVDINTLLTPPM
FIPDNALVVDOLHAFRENNHFACVVDEYGTILGIITLEDVIELTGAINTDLPY
EIIQESNTEFIIKGTTTIDJARELDMNLSGIAGAITHAGLIIHKIARIPNOGEVIKIF
NFKIIIKKIANKIDSVKITVLPMTEETISSE"
3341 5353
                                                                                                                                                                                      complement(7264. .12195)
/gene="RP704"
/product="CELL SURFACE ANTIGEN (sca5)"
                                                                                                                                                                                                                                                                                                        Complement(7264 . . 12195)
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                                                                                                                                                    codon_start=1
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/codon_start=1
/transl_table=11
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/strain="Madrid E"
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                                                                                                                                                                                                                  complement(15220. .15507)
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complement(12953. 13216)
/gene="RP705"
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RESULT 5
AF031534
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Best Local S
Matches 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172684 CAAGGTAAAGGACAACTTGTCGGAGTAGGTGTAGGCGCATTACTTGGGGGCAGTTCTTGGT 172743
                                                                                          172981
                                                                                                                                                                                                                                                                                                                                                                                                                                                  172744 GGACAAATCGGCGCAAGTATGGATGAGCAGGATAGAAGACTTCTAGAACTAACATCACAA 172803
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nes 197; Conserv
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                                                                                                                                                                                                                                                                                              GTTGAGCCAGTGCGTACTTACCAGCGTTACAATAAGCAAGAGCGTCGCCAGCAATATTGT
                                                                                        TGCCGTCAACCTGATGGGCAATGGCAAGT 173009
                                                                                                                                                                                                                                                                                                                                                                                                    AAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGATACAGGCAATAGTTATAGT
                                                                                                                                                                            CGTGAATACACTCAAACAGTTATAATAGGCGGAAAACAACAAAAAAACATATGGTAATGCA 172980
                                                                                                                                                                                                                     CCAGAATTTCAGCAAAAGGCGATGATTGCAGGGCAGAAGCAAGAGATTTACGGCACTGCA 441
                                                                                                                                                                                                                                                                                                                                                          AGAGCTTTAGAATCTGCACCTAGCGGTA---GTAACATAGAATGGCGCAATCCAGATAAC
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/gene="RP711"
complement(21112. .21608)
/gene="RP711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAVGRQYIEDHTEQLHKLCDNLVKYIELETKAITHEKAAEDTEV VIEVSLDLDNSSDDASIINKKAITVTSDDIANSNEDAARNTNKSHGDVLRCYYQ" complement(19685...20789) /gene="RP710" complement(19685...20789)
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LKNFGSFEVKQKTPRPGINFHTKSPVMIASKKNLRFTPSEKLKALINKSML"
18405. .18701
/gene="RP709"
18405. .18701
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/gene="RP712"
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authentic in-frame terminat
transposase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="unknown"
/protein_id="CAA15144.1"
/db_xref="GI:3861245"
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/protein_id="CAA15145.1"
/db_xref="GI:3861246"
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                                                                                                                                                                                                                                                                                                                                                                                                                          171 TGGTGGTGCTGTTTTGGGTGGATTAATTGGTTCTAAAATCGGTCAATCGATGGATCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 CGGCGGTGCATTACTTGGCTCTCAATTCGGTAAAAGGTAAAGGACAGCTTGTCGGAGTAGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 TTTAGTTGGCTGTGCCCAGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                       GCGTAATCCAGATACAGGCAATAGTTATAGTGTTGAGCCAGTGCGTACTTACCAGCGTTA
                                                                                                                  CGGAAAACAACAAAAAGCATACGGTAATGCATGCCGCCAACCTGACGAACAATG
                                                                                                                                                AGGGCAGAAGCAAGAGATTTACGGCACTGCATGCCGGCAACCGGATGGTCGTTG
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RIRANT17KB
R.typhi 17K
M28481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF031534 COOLEYI 17 kDa AF031534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Billings,A.N., Teltow,G.J. and Walker,D.H. Molecular characterization of a novel spotted rickettsial species from Ixodes scapularis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Billings, A.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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/trans1_table=11
/product="17 kDa antigen"
/protein_id="AAB95267.1"
/db_xref="GI:2654013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="GSYIGPRGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGVGLLGAVLGGQIGAGMDEQDRRLAELTSQRALEAAPSGSSTEWRNPDNGNYGYVTPNKTYRNSTGQYCREYTQTVYIGGKQQKAYGNACRQPDEQ"
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/db_xref="taxon:69410"
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Pred. No. 4.1e-08;
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Source
                                               497 TGCCGCCAACCTGACGGACAATGGCAAGT 525
                                                               442 TGCCGGCAACCGGATGGTCGTTGGCAAGT 470
                                                                              382 CGAGAATTTCAGCAAAAGGCGATGATTGCAGGGCAGAAGCAAGAGATTTACGGCACTGCA 441
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MEDLINE
COMMENT
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AUTHORS
                                                                                                                                                                           320 AGAGCTTTAGAATCT---GCTCCTAGCGGTAGTAACATAGAATGGCGCAATCCAGATAAT 376
                                                                                                                                                                                             262 AAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGATACAGGCAATAGTTATAGT 321
                                                                                                                                                                                                                         260 GGACAAATCGGTGCAAGTCTGGATGAGCAGGATAGAAAACTTCTAGAACTAACATCACAA 319
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                                                                                                                                                                                                                                                                                       142 AAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGATTAATTGGT 201
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-10_signal
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antigen.
R.typhi DNA.
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Comparative sequence analysis of a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="17 kD antigen signal peptide"
116. .532
/Product="17 kD antigen"
93 c 122 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /PICTEIN_Id="AAA26377.1"
/PICTEIN_Id="AAA26377.1"
/Gb_xref="GI:152460"
/Cranslation="MKLLSKVMILALAASMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGGHGKGQLYGVGYGALLGAYLGGQIGASLDEDDRKLLELTSQRALLSAPGGSNIEWRIPDMGNHGYYTPNKTYRNSTGQYCREYTQTVVIGGKQQTTYGNACRQPDGQWQVVW"
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/transl_table=11
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6. .535
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/db_xref="taxon:785"
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498	438 441	321 378 381	321		Gaps 1;	LLGGAGGALLG ETAPSGSNVEW OPDGOWOVVN"		clinical .	Prefectural ku, Yokohama, 3-1037)	siales; er group.	BCT 04-FEB-1999 Complete cds.

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                                                                                                                                                                                                                               GAGTTTGGAAAAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGGATACAGGCAA 311
                                                                                                                                                                                                                                                                                                    ATTAATTGGTTCTAAAATCGGTCAATCGATGGATGAGCAGGATAAAATAAAGCTAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                        CATGAATAAACAAGGTACAGGAACACTTCTTGGCGGTGCTGGCGGCGCGCATTACTTGGTTC 193
                CGGCACTGCATGCCGGCAACCGGATGGTCGTTGGCAAGT 470
                                                                                                                                                                        TAGTTATAGTGTTGAGCCAGTGCGTACTTACCAGCGTTACAATAAGCAAGAGCGTCGCCA
                                                                                                                                                                                                             TACCTCACAGAGAGCTTTAGAAAC---AGCTCCTAGTGGTAGTAACGTAGAATGGCGTAA
                                                                                                                                                                                                                                                                                                                                                      TCAATTCGGTAAGGGCAAAGGACAGCTTGTTGGAGTAGGTGTAGGTGCATTACTTGGAGC
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CGGTAATGCATGCCGCCAACCTGACGGACAATGGCAAGT
                                                                 TCAATATTGCCGTGAGTACACTCAAACAGTTGTAATAGGCGGAAAACAACAAAAAGCATA
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                                                                                                                                         TCCGGATAACGGCAATTACGGTTACGTAACACCTAATAAAACTTATAGAAATAGCACTGG
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Comparative sequence analysis of a genus-common rickettsial antigen
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1 (bases 1 to 539)
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120. .536
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93 c 125 g 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKLLSKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLG
SQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNPDNGNYGYVTPNKTYRNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN"
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/db_xref="taxon:781"
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3 (bases 1 to 10127)
0gata,H., Audic,S., Renesto-Audiffren,P., Fournier,P.-E., Barbe,V., Samson,D., Roux,V., Cossart,P., Weissenbach,J., Claverie,J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogata, H., Audic, S., Barbe, V.,
Raoult, D. and Claverie, J.M.
Selfish DNA in protein-coding
Science, 290 (5490), 347-350 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia conorii
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (26-APR-2001) Unite des Rickettsies, Faculte de Medeci CNRS UMR 6020, Universite de la Mediterranee, 27 boulevard Jean Moulin, Marseille Cedex 05 13385, Faculte is accessible at http://igs-server.cnrs-mrs.fr/. The database intends to provide updated data. Annotation of the genome is an ongoing task whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEUU8675 AE006914
AE008675.1 GI:156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           authors are appreciated
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Direct Submission
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Samson,D., Roux,V., Cossart,P., Weissenbach,J., Claverie,J.-M. and
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Ogata, H., Audic, S., R
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            /gene="RC1277"
1141. .1452
                                                                                                                                                                    /product="methionine aminopeptidase [EC:3.4.11.18]"
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CHNFITSHNAVPAPLNYKGFPKSICTSINHVVCHGIPNDKPLKNGDIGHAIQSYAEKHNY
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                                                   1141.
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                                                            /note="REP02, RS3-like
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                                                                                                      /note="REP03,
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                                                                                                                                                                                                                                                                                                               /gene="map"
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                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Malish
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                                                   .1452
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                                                                                                 repeated element"
                                                                                                                        .1011)
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(2000)
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107 of 114 of the complete
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27 boulevard Jean
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codon_start=]

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repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3509. .4258)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="REP02, RS3-like 3313. .3353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="RC1281"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="mraY2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKQKIINKNINASWSSWIDYLKVNMGNWRLEQFRILFLNKKNIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="RC1279"
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Best Local
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192 ATTAATTGGTTCTAAAATCGGTCAATCGATGGATCAGCAGGATAAAATAAAGCTAAACCA 251
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                                                                                                                                              GCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGGTGTTTTTGGGTGG
                                                                                                                                                                                                                                                     CTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTGTTGCTGGCCA 131
                                                                                                                                                                                                                 CATGAATAAACAAGGTACAGGAACACTTCTTGGCGGTGCTGGCGGCGCATTACTTGGTTC 8267
                                                                                                                                                                                                                                                                                                                                                                   al Similarity
197; Conserv
                                                                                                                                                                                                                                                                                                                                                                Conservative
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Pred. No. 6.9e-07;
0; Mismatches 199;
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RIRANT17KD
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Matches 193
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-10_signal
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                                                                                                                                                                                                                                                            sig_peptide
 204
                            142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 CGGCACTGCATGCCGGCAACCGGATGGTCGTTGGCAAGT 470
                                                         144 CAAGGTACAGGAACACTTCTTGGCGGTGCTGGCGGCGCATTACTTGGTTCTCAATTCGGT
                                                                                        82 CAAGAAGTCGGAGCTGCGACTGCGGCCTGTTGTTGGCGGTTGTTTGCTTGGT
                 AAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGGGTGGATTAATTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGTAATGCATGCCGCCAACCTGACGGACAATGGCAAGT 8603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAATATTGTCGAGAATTTCAGCAAAAGGCGATGATTGCAGGGCAGAAGCAAGAGATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCGGATAACGGCAATTACGGTTACGTAACACCTAATAAAACTTATAGAAATAGCACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACCTCACAGAGAGCTTTAGAAAC---AGCTCCTAGTGGTAGTAACGTAGAATGGCGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTTCTTGGTGGACAAATCGGTGCAGGTATGGATGAACAGGATAGAAGACTTGCAGAGCT
AAGGGCAAAGGACAGCTTGTTGGAGTAGGTGTAGGTGCATTACTTGGAGCAGTTCTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGTTATAGTGTTGAGCCAGTGCGTACTTACCAGCGTTACAATAAGCAAGAGCGTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGTTTGGAAAAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGATACAGGCAA
                                                                                                                     al Similarity
193; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comparative sequence analysis of a genus-common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 539)
Anderson, B.E. and Tzianabos, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia rickettsii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .rickettsia DNA.
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                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .Anderson, 27-OCT-1989.
                                                                                                                     Conservative
                                                                                                                                                                                                                                                          /translation="MKLLSKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLG
SQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEW
RNPDNGYYGYVTPNKTYRNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN"
60. .119
                                                                                                                                                                                                                                                                                                                                                                                                 /product="17 kD mRNA" 60. .539
                                                                                                                                                                                             /product="17 kD antigen"
92 c 125 g 14
                                                                                                                                                                                                                             /note="17 kD antigen signal peptide"
120. .536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rickettsia
/db_xref="taxon:783"
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                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA26379.1"
                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                   /note-"17 kD antigen
                                                                                                                                                                                                                                                                                                                                                                      codon_start-
                                                                                                                                  13.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obacteria; alpha subdivision; Rickettsiales; Rickettsieae; Rickettsia; spotted fever gro
                                                                                                                   Score 64.2; DB 1;
Pred. No. 6.1e-07;
0; Mismatches 193;
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263
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                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
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142 AAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGGTGTTTTGGGTGGATTAATTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324
                                                  154 CAAGGTACAGGAACACTTCTTGGCGGTGCTGGCGGCGCATTACTTGGTTCTCAATTCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 TCTAAAATCGGTCAATCGATGGATCAGCAGGATAAAATAAAGCTAAACCAGAGTTTGGAA
                                                                      82 CAAGAAGTCGGACCTGCGACTGGGGCTGTTTTTGGCGGGTGTTTGCTTGGT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCGGCAACCGGATGGTCGTTGGCAAGT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTGAGTACACTCAAACAGTTGTAATAGGCGGAAAACAACAAAAAGCATACGGTAATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCAATTACGGTTACGTAACACCTAATAAAACTTATAGAAATAGCACTGGTCAATATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGAGCCAGTGCGTACTTACCAGCGTTACAATAAGCAAGAGCGTCGCCAGCAATATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGATACAGGCAATAGTTATAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGACAAATCGGTGCAGGTATGGATGAACAGGATAGAAGACTTGCAGAGCTTACCTCACAG
                                                                                                                   193;
                                                                                                                                                                                  Unreported.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsiaceae: Rickettsieae; Rickettsia; spott 1 (bases 1 to 620)
Anderson, B.E., Regnery, R.L., Carlone, G.M., Tzia McDade, J.E., Fu.Z.Y. and Bellini, W.J. Sequence analysis of the 17-kilodalton-antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 169, 2385-2390 (1987) 87222152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.rickettsii (strain Sheila Smith) DNA, clone Rickettsia rickettsii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Draft entry and computer-readable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rickettsii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B.E.Anderson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B.E.Anderson, 23-OCT-1987. and -10 regions are located at positions 12-17 Location/Qualifiers
                                                                                                                                                                                                   206
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rickettsia rickettsii"
/db_xref="taxon:783"
70. .126
                                                                                                                                                                                                                                                /protein_id="AAA26381.1"
/db_xref="GI:152468"
/db_xref="GI:152468"
/translation-"MKLISKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLG
/translation-"MKLISKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLG
SQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELTSCRALETAPSGSNVEW
RNPDNGNYGYVTPNKTYRNSTGQYCREYTQTVVIGGKQQKAYGDACRQPDEQWQVVN"
                                                                                                                                                                                                 /product="17kd antigen"
105 c 142 g 1
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                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                    /note="17kd antigen
                                                                                                                                                                                                                                                                                                                                                                                                     /note="17kd antigen signal peptide"
                                                                                                                                                                                                                                                                                                                                                      'codon_start='
                                                                                                                                   13.2%;
                                                                                                                  0;
                                                                                                                                 Score 64.2; DB 1;
Pred. No. 6.2e-07;
                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and 33-38
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                                                                                                                                                                                                                                                                                                                                                      Schulenburg, H.
Direct Submission
Submitted (03-APR-2000) Schulenburg H., Department of Evolutionary
Biology, Institut fuer Spezielle Zoologie, Huefferstr. 1, 48149
Muenster, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ269516.1 GI:8920292
17 kDa antigen.
17 kDa antigen.
male-killing Rickettsia from Adalia decempunctata.
male-killing Rickettsia from Adalia decempunctata
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 434)

von Der Schulenburg, J.H., Habig, M., Sloggett, J.J., Webberley, K.M.,
Bertrand, D., Hurst, G.D. and Majerus, M.

Incidence of male-killing rickettsia spp. (alpha-proteobacteria) in
the ten-spot ladybird beetle adalia decempunctata L

Appl. Environ. Microbiol. 67 (1), 270-277 (2001)
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Male~killing Rickettsia
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                                                                            /db_xref="SPTREMBL:Q9K4W8"
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VGVGVGALLGAVLGGQ1GAGMDEQDRRLAELTSQRALEAAPSGSNVEWRNPDNGNHGY
VTPNKTYRNSTGQYCREYTQTVVIGGKQQKSYGNACRQPDEQ"
415. . 434
                                                                                                                                            /transl_table=11
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/protein_id="CAB96381.1"
/db_xref="CI:8920293"
                                                                                                                                                                                                                       /note="PCR primer <1. .>434
                                                                                                                                                                                                                                                                        decempunctata"
/specific_host="Adalia decempunctata"
/db_xref="taxon:120393"
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Best Local Similarity 50. 
Matches 182; Conservative
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Submitted (03-APR-2000)
Biology, Institut fuer S
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17 kDa antigen.
18 kDa antigen.
male-killing Rickettsia from Adalia bipunctata.
male-killing Rickettsia from Adalia bipunctata
Bacteria, Proteobacteria; alpha subdivision; Ri
Rickettsiaceae; Rickettsiaee; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                               Muenster,
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/db_xref="GI:8920295"
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                                                                                                                                                     /note="PCR primer
                                                                                                                                                                                         /country="United Kingdom: Cambridge"
/note="isolated from 2spot ladybird"
                                                                                                                                                                                                                                          /specific_host="Adalia
/db_xref="taxon:38028"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182;
                                                                                                                                                                                                                                                                                                                          AJ269518.1 GI:8920296
17 kDa antigen.
17 kDa antigen.
male-killing Rickettsia from Adalia bipunctata.
male-killing Rickettsia from Adalia bipunctata
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiaee; Rickettsia.
                                                                                                                               Submitted (03-APR-2000)
Biology, Institut fuer S
                                                                                                                                                                                                                               Bertrand, D., Hurst, G.D. and Majerus, M.E.
Incidence of male killing rickettsia spp. (alpha-proteobacteria) in
the ten-spot ladybird beetle adalia decempunctata L
Appl. Environ. Microbiol. 67 (1), 270-277 (2001)
                                                                                                                                                                                                                                                                                                  Yon
                                                                                                                                                                                                                                                                                                                                                                                                                                                Male-killing Rickettsia from antigen gene (Denmark: Ribe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRI269518
                                                                                                                                                                 Direct Submission
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Der Schulenburg, J.H., Habig, M.,
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                                                                                                                                                                                 lenburg,H.
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VGVGVGALLGAVLGGQIGAGMDEQDRRLAELTSQRALEAAPSGSNVEWRNPDNGNHGY
VTPNKTYRNSTCQYCREYTQTVVIGGKQQKAYGNACRQPDEQ"
415...434
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/note="PCR primer R2"
1 88 C 114 g
/country="Denmark: Ribe"
/note="isolated from 2spot ladybird"
                              /organism="male-killing Rickettsia
/specific_host="Adalia bipunctata"
/db_xref="taxon:38028"
                                                                                                  Location/Qualifiers
                                                                                                                   GERMANY
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50.1%;
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Pred. No. 2.1e-06;
                                                                                                                               Schulenburg H., Department of Evolutionary Spezielle Zoologie, Huefferstr. 1, 48149
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                                                                 Adalia
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                                                                 bipunctata"
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AUTHORS
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 TGGGGCTGTTGTTGGCGGTGTTGCTGGCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                 462 TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 TCCTAGTGGTAGTAACGTAGAATGGCGTAATCCCGATAACGGCAATCATGGCTACGTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 TGGCGGTGCCGGCGGTGCATTACTTGGTTCTCAATTCGGCAAAGGGTAAAGGGCAACTTGT
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mes 182; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCGTTACAATAAGCAAGAGCGTCGCCAGCAATATTGTCGAGAATTTCAGCAAAAGGC
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                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiaee; Rickettsia; spotted fever gro 1 (bases 1 to 546)
Bouyer,D.H., Stenos,J., Crocquet-Valdes,P., Moron,C.G., Pop. Zavala-Velazquez,J.E., Foil,L.D., Stothard,D.R., Azad,A.F.,
                                                                                                                                                                                                                                                                              AF195118
Rickettsia felis 17 kDa
AF195118
AF195118.1 GI:11066087
                                                                                                                                                                                                                              Rickettsia felis.
Rickettsia felis
 Walker, D.H.,
                                                                                                              Rickettsia felis: molecular
                                                                                            spotted fever
                                                                                                                                 Walker,D.H.
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            (bases 1 to 546) uyer,D.H., Stenos,J.,
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                                                                                Syst.
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87 c 114 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:Q9K2N6"
/translation="ALATSMLQACTGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL
VGVGVGALLGAVLGGQIGAGMDEQDRRLAELTSQRALEAAPSGSNVEWRNPDNGNHGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="17kDA antigen"
/protein_id="CAB96383.1"
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Pred. No. 2.1e-06;
                                                                                                                                             Crocquet-Valdes, P., Moron, C.G., Popov, V.L., Foil, L.D., Stothard, D.R., Azad, A.F. and
                                                                                                                                                                                                                                                                                                              genus-common
               Crocquet-Valdes,
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12.2%; Score 59.4; DB 1; Length 546;

Bast Local Similarity 48.8%; Pred, No. 1.3e-05;

Matches 190; Conservative 0; Mismatches 196; Indels 3; Gaps
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                                                            506 TGCCGCCAACCTGACGGACTATGGCAAGT 534
                                                                                    442 TGCCGGCAACCGGATGGTCGTTGGCAAGT 470
                                                                                                            446 CETGAGTACACTCAAACAGTTGTAATAGGCGGAAAAACAAAAAAGCATACGGTAATGCA 505
                                                                                                                                   382 CGAGAATTTCAGCAAAAGGCGATGATTGCAGGGCAGAAGCAAGAGATTTACGGCACTGCA 441
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JOURNAL
                                                                                                                                                                             386 GGTAATCATGGTTACGTAACACCTAATAAAACTTATAGAAATAGCACTGGTCAATATTGC 445
                                                                                                                                                                                                     322 GTTGAGCCAGTGCGTACCTTACCAGCGTTACAATAAGCAAGAGCGTCGCCAGCAATATTGT 381
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                                                                                                                                                                                                                                                                      262 AAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGGATACAGGCAATAGTTATAGT 321
                                                                                                                                                                                                                                                                                                              269 GGACAAATAGGTGCAGGTATGGATGAGCAGGATAGAAGACTTGCTGAACTCACTTCACAA 328
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                                                                                                                                                                                                                                                                                                                                                                                                       142 AAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGGTGTTTTGGGTGGATTAATTGGT 201
                                                                                                                                                                                                                                                                                                                                                                                 209 AAGGGCAAAGGACAGCTTGTCGGAGTAGGTGTAGGTGCATTACTTGGAGCAGTTCTTGGT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                               149 CAAGGTACGGGAACACTTCTTGGCGGTGCCGGCGGTGCATTACTTGGTTCTCAATTCGGC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 CAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTGTTGCTGGCCAGCTGTTTGGT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (14-OCT-1999) Pathology, University of Texas Medical
Branch at Galveston, 301 University Blvd., Galveston, TX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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/protein_id=*nags4452.1"
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SQFGGKGGQLYGVGVGGALLGAVIGGQLGAGKDEQDFRLAELTSORALEATPSGTSVEW
RNPDNGNHGYVTPNKTYRNSTGQYLGAGKDEQDFRLAELTSORALEATPSGTSVEW
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2 AZ952777
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                                                T59966 yb67e08.rl
AW151916 xf72906.x
AZ952777 2W0217C15
AI965711 sc77e04.y
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AJ003546 AJ003546
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BM082634 fu23h09.y
BM083068 fu28h07.y
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CORGANISM
Mus musculus
EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mus musculus
Intervention of capture of the first of t

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                         Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
; Triticeae; Triticum.
1 (bases 1 to 395)
            Anderson, O.A., Appels, R., Bailey, P.,
                                                                                                                                                          EST
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395 bp mRNA linear EST 26-JUL-2000 turgidum subsp. durum cDNA clone MTD008.G05, mRNA sequence.
                                                                                                                                durum wheat.
                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100.
21; Conservative
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001), K., Fukuda, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa Hawashi, J., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                             GI:9426436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="heart"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                        4.3%; ~
100.0%; Pr
... 0;
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Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                            Score 21;
Pred. No.
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Blake,T., Close,T., Cloutier
                                                  Embryophyta; Tracheophyta;
la; Poales; Poaceae; Pooideae
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                                                                                                                       Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7380
Fax: 580 221 7380
                                                               Contact: Dixon RA
                                                                                                                                                                                                                                        Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzale Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts (Center for Medicago Genomics Research
                                                                                                                                                                                                                                                                                                                 barrel medic.
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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NF026601EC1F1005 Elicited Cell culture Medicago truncatula
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INRA, Unite de Biochimie et Biologie Moleculaire des Cereales
2, place VIALA, 34060 Montpellier cedex 01 FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://wheat.pw.usda.gov/genome-
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2, place VIALA, 34060
Tel: 33 4 99 61 23 84
Fax: 33 4 99 61 23 48
Email: joudrier@ensam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: joudrier@ensam.inra.fr
International Triticeae EST Cooperative (ITEC)
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/organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone_lib="ITEC MTD Durum Wheat Root Library"
/clone_type="root"
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/note="Vector: pSpoRT1; T7 primers used. See pSpoRT1
polylinker site. 0.3-2.0 Kbp average insert size."
111 c 114 g 72 t
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| Cultivar="Siliana"
| /db_xref="taxon:4567"
| /clone="MTD008_G05"
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Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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RPCI-24-128C18.TJ RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tlgr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 128 row: C column: 18
Seq primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 689)
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days. Cells were induced six days after subculture"
/note="vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
a 151 c 127 g 220 t
                                                                                                     /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong.
library was cloned in the pTARBAC1 cloning vector at
library was cloned in the pTARBAC1 cloning vector at
BamH1 sites using MboI partially digested male C57BL/
                                                                                                                                                                                                                                     /db_xref="taxon:10090"
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/clone_11b="RPCI-24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="NF026G01EC"
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This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveriomyces marxianus var. marxianus, Pichia saccharomyces kluyveriomyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipplytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
de-Montigny, A., Neuveglise, C., Ozier-Kalogropolos, O., Potier, S.,
Annual Control of Co
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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/clone="ASOAA005E09"
/clone_lib="ASOAA"
/note="end: T3"
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/note="similar to Saccharomyces cerevisiae
PTP3; protein tyrosine phosphatase]"
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                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 380)

Chissoe; L. Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore Schellenberg, K., Saares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldman, P., Waterston, R., Wilson, R. and Marra, M. Genome Res. 5 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 AGAGTTTGGAAAAGGTAAAA
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                  ATTGCAGGGCAGAAGCAAG 55
                                                                                                                                                                                                                                                                    T59966
T59966
380 bp mRNA linear EST 09-FEB-1995
IMAGE:76262 5' similar to SP:TCPD_MOUSE P80315 T-COMPLEX PROTEIN 1,
                                                                                                                                                                                                              Homo sapiens
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Max Planck Institut fuer Molekulare Genetik
Ihnestrasse 73, D14195 Berlin-Dahlem, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .H. and Yaspo,M.L.H. An integrated transcript map for Unpublished (1997)
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Szulzewsky, I., Hunt
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Homo sapiens
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clone MPIP112-9KB, mRNA sequence.
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/clone="MPIp112-9K8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
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          source
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/clone_lib="NCI_CGAP_Gas4"

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BASE COUNT
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                                                         Seq primer: -400F ILOW Stop: 412.
High quality sequence stop: 412.
Location/Qualiflers
                                                                                                                                                                  Enmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                           Possible reversed clone: polyT not Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 436)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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AW151916
AW151916.1 GI:6199901
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xf72g06.xl NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623642 3',
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19; Conservative
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Seq primer: M13RP1

High quality sequence stops: 257 Source: IMAGE Consortium, LLNL The Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
Insert Size: 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104
/clone="IMAGE:2623642"
                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI;
Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; -5; adaptor sequence: 5;
GARTTCGGCACGAG 3; -3; adaptor sequence: 5;
CTCCAGTTTTTTTTTTTTTTTTTTTT 3;
a 68 c 93 g 111 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
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/db_xref="GDB:505991"
/db_xref="taxon:9606"
/clone="IMAGE:76262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="49 year old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Stratagene ovary (#937217)"
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100.0%; Pr
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University of Utah Genome
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0217 row: C column: 1
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Islam, H., Longacre, S.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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461 bp DNA linear GSS 27-APR-200200217C15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic Clone UUGC2M0217C15 R, DNA sequence.
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Location/Qualifiers
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801 585 7177
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n,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
ROSE,M., ROSE,R., Stokes,R., Tingey,A., von Niederhausern,A.
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
                                                                                                                                                                                                                                  /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0217C15"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                        /sex="Female"
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Pred. No.
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red. No. 25;
Mismatches
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REFERENCE

AUTHORS

TITLE

JOURNAL

SOURCE KEYWORDS

ORGANISM

VERSION ACCESSION

FEATURES

RESULT 9 AZ952777

DEFINITION LOCUS В δô BASE COUNT ORIGIN

Matches

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RESULT 10
AI965711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., I Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., I, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., I, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
19; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Possible reversed clone: similarity on wrong strand This clone is
available through: ResGen, Invitrogen Corp. 2130 South Memorial
Parkway Huntsville, AL 35801 For further information call: (800
)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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from 2-3 week old greenhouse grown plants. The CDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally
                                                                                                                                                                                  /tissue_type="leaves of greenhouse grown plants"
/dev_stage="2-3 weeks old"
/lab_host="DH10B (Gibco BRL)"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
/xhoI; This ODNA library was constructed from mRNA isolated
                                                                                                                                                                                                                                                                                                                         /clone="GENOME SYSTEMS CLONE ID: Gm-c1018-919"
/clone_lib="Gm-c1018"
                                                                                                                                                                                                                                                                                                                                                                         /organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
Other_GSSs: RPCI-24-166M15.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MI
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTTTGGGTGGATTAATTG 324
                                        l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Szhaoltigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 166 row: M column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                        Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorg Russell, D., de Jong, P. and Fraser, C.M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/Sea- max
/Cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
// RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-166M15"
                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-24"
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann, R., Waterston,R. and Wilson,R.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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Fax: 314 286 1810
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                                                                                         //note="Westor: pBluescript II SK+; Site_1: EcoRI; Site_2: XhOI; The cDNA library was constructed from mRNA isolated from very young seeds (less than 20mgs). The library was prepared using the Stratagene pBluescript II SK (+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an Xho I restriction site. Eco RI adaptors were ligated to the blunt-ended cDNA fragments followed by Xho I digestion. The cDNA insert is protected from Xho I digestion via methylation during first strand cDNA sythesis. The cDNA fragments were directionally cloned into the Eco RI-Xho Irestriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroWax DHIOB host cell. The library was constructed by Anu Khanna (Lila Vodkin lab, University of Illinois)."
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/db_xref="taxon:3847"
/clone="ceROME SYSTEMS CLONE ID: Gm-c1086-203"
/clone_1ib="Gm-c1086"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="young seeds (Williams 82)"
/lab_host="DH10B"
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                                                                               fu28h07.yl
5′ similar
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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                                                            sequence.
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                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="4-5 months, 1 year and 2 years"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary(pooled); Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Whole ovaries collected from zebrafish
aged 4-5 months, 1 year and 2 years. Oligo-dT primed,
directionally cloned. Average insert size 2 kb. Library
constructed by invitrogen and donated by R. Campbell
(Marine Biology Laboratory, Woods Hole, MA)."
a 145 c 137 g 133 t 1 others
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/clone="5306345"
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/sex="female"
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S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwoo
, S., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waterston, R.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
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Other_ESTs: fu28h07.x1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                                                                                     Cyprinidae; Danio.
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="4-5 months, 1 year and 2 years"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Campbell zebrafish ovary"
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zebrafish gridded kidney Danio rerio cDNA clone
to TR:Q9Y6R2 Q9Y6R2 EMBRYONIC LUNG PROTEIN. ;, n
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100.0%; Pred. No.
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Search completed: October 27, 2002, 22:36:36
Job time : 978.679 secs
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JOURNAL
COMMENT
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Sest Local Similarity 100.0%; Pred. No. 27;

Matches 19; Conservative 0; Mismatches 0; Indels
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                                                                                source
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Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fal: 314 286 1800
Fax: 314 286 1800
Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Genome Systems, St. Louis, Missouri (web address:
Research Genetics, Huntsville, Alabama (web address: www.resgen.com)
(email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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Location/Qualifiers
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WashU Zebrafish EST Project 1998
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                                                                                                                                                                                                                                                             /tissue_type="kidney pooled from 300 wild type adults"
/lab_host="XLOLR"
/note="forgan: kidney; Vector: pBK-CMV; Site_1: EcoRI;
site_2: XhoI; Oligo dT cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
a 140 c 136 g 146 t 2 others
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/db_xref="taxon:7955"
/clone="4745043"
/clone_tib="zebrafish gridded kidney"
/sex="mixed"
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-280-590A-36
US-08-339-353-700-2
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US-08-338-353-700-2
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NAME/KEY:
LOCATION:
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US-08-985-908-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/08985908
Patent NO. 6004773
GENERAL INFORMATION:
APPLICANT: MASAYUKI ARAKI, MASAK
 Query Match 3.7%; Sometimes Sent Local Similarity 100.0%; If Matches 18; Conservative 0;
                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                     ORGANISM: ESCI
STRAIN: JM109
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                   TOPOLOGY:
                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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ALIGNMENTS

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APPLICATION NUMBER: US/08/985,908
APPLICATION US-05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHOD NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
NVENTION: METHOD FOR PRODUCING L-LYSINE
                                                                                                                                                                               Escherichia coli
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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0; Mismatches
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RESULT 2 US-08-162-809-7

GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET: 4370 La CITY: San Diego STATE: Californi COUNTRY: UZIP: 92122

California

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM

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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 91.3 815
REGISTRATION NUMBER: 9-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-901
TELEFAX: (619) 535-8949
TNPORMATION FOR SECO ID NO: 7.
                         APPLICANT: Lamb et al., Christopher J.
TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANGER ELEMENT AND
TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 7, Application US/08162809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08669721
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4370 La Jolla Village Drive, Suite 700
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Pred. No.
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Patent No. 6191258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Lamb e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
       NAME: Ellison, Eldora L. REGISTRATION NUMBER: 39,967 REFERENCE/DOCKET NUMBER: 07. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Ellison, Eldora L.
REGISTRATION NUMBER: 39,967
REFERENCE/DOCKET NUMBER: 07251/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
                                                                        APPLICATION NUMBER: US 01
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/189,344
                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619/678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                               STREET: 4225 EXCITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0
FILING DATE: 27-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
ZIP: 920
                                                                                                                                                                                                                                                                                                       92037
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                                                                                                                                                                                                                                                                                                                      USA
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VENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND

VENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
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61..1698
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100.0%; Pr
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                       07251/014001
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RESULT 3
US-08-669-721-2/c

**Gardence 2, Appl

**Gardence 2, Appl

Patent No. 5834236

GENERAL INFORMATION:

APPLICANT:

В

165 GGCCATTGGTGGTGCTGT 182

271 GGCCATTGGTGGTGCTGT 288

US-08-162-809-7

FEATURE:
NAME/KEY:
LOCATION:

CDS 290..3208

TOPOLOGY:

linear

TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

LENGTH: 3776 base p TYPE: nucleic acid STRANDEDNESS: both

3776 base pairs

Query Match

Matches

Loca1

Similarity

Conservative

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

2

2165 base pairs

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                                                                                                               ; TOPOLOGY: 13; MOLECULE TYPE: US-08-742-877-3
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US-08-742-877-3/c
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US-09-189-344-2
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                                                                        Query Match
Best Local
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                                                        Matches
                                                                                                                                                                                                    TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 940871
FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: FLESHNER, RAZ E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 0623
TELECOMMUNICATION INFORMATION:
TELEPONE: 7202 371-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFO
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
1495 TTTGGAAAAGGTAAAAG 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                           255 TTTGGAAAAGGTAAAAG 271
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                                                                                                                                                                              TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                      Local
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Local Similarity 100.0%;
es 17; Conservative (
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                                                                                                                                                                                    LENGTH:
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                                                        1 Similarity
17; Conserv
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20005-3934
                                                                                                                                                                                      2340 base pairs
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61..1698
                                                        Conservative
                                                                                                                                             linear
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                                                                      Score 17;
Pred. No.
                                                                                                                                                                                                                                                                             0623.0470001/REF
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Pred. No.
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                                                                      DB
14;
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                                                       Gaps
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RESULT 6

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: NUMBER OF SEQ ID NOS: 22

: SOFTWARE: PatentIn Ver. 2.1

: SEQ ID NO 22

: ENGTH: 2775

: TYPE: DNA

: ORGANISM: Homo Sapien

US-09-053-871a-22
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Best Local Similarity 100.0%;
Matches 17; Conservative
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GENERAL INFORMATION: CLARK, Anthony J.
TOTAL CANT: CLARK, Anthony J.
DNA SEQUENCES
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CURRENT APPLICATION NUMBER: US/09/053,871A
CURRENT FILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
TITLE OF INVENTION: STROKE OUTCOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                     TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9408717.8
FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                      SEQUENCE CHARACTERISTICS:
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FEATURE
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                               STRANDEDNESS:
TOPOLOGY: 11
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                                                               nucleic acid
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Stern, David
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                                                                                 2802 base pairs
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Pred. No.
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US-08-947-823-1
                                 Matches
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                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO. SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1,
                                                                                                                                                                   TOPOLOGY: 11
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICATION NUMBER: PCT/
FILING DATE: 09-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bodeau, J
APPLICANT: Milligan,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Williamson, Valerie M. APPLICANT: Kaloshian, Isgouhi APPLICANT: Yaghoobi, Jafar
                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                     LENGTH:
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LOCATION:
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                                                      Similarity
                                                                                                                                                                                                                                           1: 51952 base pairs nucleic acid
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               3.5%; Score 17; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                 linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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168..1412
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30..1412
                                                                                                                                                                DNA (genomic)
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30..167
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Pest Resistance in Plants
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Pred. No.
               Mismatches
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                                             DB 3;
16;
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15;
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RESULT 10
US-07-959-941-1
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Best Local Similarity
Matches 17; Conserv
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SOFTWARE: PATENTIN Releas
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07
FILING DATE: 19921009
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 435
PRIOR APPLICATION NUMBER: US 79
FILING DATE: 18-NOV-1991
ATTORNEY/ACENT INFORMATION:
NAME: Chin Torios
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HUTCHINSON
APPLICANT: MADDURI, K
APPLICANT: TORTI, Fra
APPLICANT: COLOMBO, A
TITLE OF INVENTION: P
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                             COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM C COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 GGCGGTGTTGCTGGCCA 131
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CITY: Washington
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20005-5701
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                                                                                                                                                                                                                                                                                             E: Nikaido, Marmelstein, Murray & Oram 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                    COLOMBO, Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                          HUTCHINSON, Charles
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                                     US 793,873
                                                                                                                                      Release #1.0, Version #1.
                                                                                                          US/07/959,941
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%; Pred. No. 15;
0; Mismatches
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15;
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REGISTRATION NUMBER:

P-36,105

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US-07-959-941-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                        APPLICATION NUMBER: US 07/959,941
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 1615-4003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)638-481
INFORMATION FOR SEQ ID NO:
                                                                                             TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 7
FILING DATE: 18-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 1632 base pair
                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                            LENGTH: 1632 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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TORTI, Francesca
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204..1271
               linear
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DNA (genomic)
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; LENGTH: 2251
; TYPE: DNA
; ORGANISM: Pinus taeda
US-08-991-677-11
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US-08-991-677-11
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US-08-097-997A-10/c
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APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/097,997A

FILING DATE: 29-JULY-1994

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 APPLICANT: Ihle, James N.
APPLICANT: Silvennoinen, Ollie
APPLICANT: Withhuh, Bruce A.
APPLICANT: Quelle, Frederick W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal TITLE OF INVENTION: Transduction
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                                                                                                                                                                                              STREET: 1100 New CITY: Washington
                                                                                                                                                   COUNTRY: U.S.A. ZIP: 20005-3934
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Local Similarity 100.0%;
les 16; Conservative (
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5. 5728536
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204..1271
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00 New York Avenue, Suite 600
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Pred. No.
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Pred. No.
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Samuel

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CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/282,012
PRIOR APPLICATION NUMBER: 08/282,012
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/097,997
PRIOR APPLICATION DATA:
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APPLI
                                                                                                                                                                                  NAME: Bugaisky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/LBB
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SEQUENCE CHARACTERISTICS:
LENGTH: 3429 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FERRITES: 1inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Silvennoinen, Ollie
APPLICANT: Witthuhn, Bruce A.
TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine
TITLE OF INVENTION: Signal Transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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5. 6136595
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371-2540
NO: 10:
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100.0%; Pred. No.
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48;
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US-08-946-994-10
                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/665,57,
FILING DATE: 18-JUN-1996
APPLICATION NUMBER: 08/282,012
FILING DATE: 29-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/097,997
FILING DATE: 29-JUL-1993
PRIOR APPLICATION NUMBER: 08/097,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NESULA 10/C
US-08-946-994-10/C
Gequence 10, Application US/08946994
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Sequence 10, Application.
Patent No. 6210654
GENERAL INFORMATION:
TOANT: Ihle, James N.
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                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                  NAME: FOX, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                      AFFLICATION NUMBER: 08/118,968
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Silvennoinen, Ollie
APPLICANT: Witthuhn, Bruce A.
APPLICANT: Quelle, Frederick W.
TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 New 1
CITY: Washington
STATE: D.C.
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CORRESPONDENCE ADDRESS:
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LOCATION:
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Local Similarity 100.0%; Pred. No.
es 16; Conservative 0; Mismatc
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRY: U.S.A.
20005-3934
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RESULT 14 US-08-665-574C-10/c

GENERAL INFORMATION:

Ihle, James N.

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

CITY: Washington

STREET:

ADDRESSEE:

COUNTRY:

RY: U.S.A. 20005-3934 D.C.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

APPLICATION NUMBER: FILING DATE: 18-JUI

18-JUN-1996

В γ

Matches Query Match

Local Similarity

Conservative

US-08-097-997A-10

NAME/KEY: CDS LOCATION: 1..3

1..3426

FEATURE:

TELEFAX: (202) 371-25. INFORMATION FOR SEQ ID NO:

371-2540 ID NO: 10:

TELEPHONE:

(202)

371-2600

SEQUENCE CHARACTERISTICS:

ó; 0; Gaps Query Match 3.3%; Score 16; DB 4; Length 3429; Best Local Similarity 100.0%; Pred. No. 48; Matches 16; Conservative 0; Mismatches 0; Indels

Search completed: October 27, 2002, 22:53:59 Job time: 942.093 secs

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AAX13065 AAX13065 ABL110082 ABL21060 ABL21060 AAS13655 AAI90320 AAI90320 AAI85399 AAX05021 AAC404356 AAC403514 AAC44035 AAC56443 AAC56443 AAC56443 AAC56443 AAC56479 AAF54079 AAF54077 AAF54077 AAF54077 AAF54077 AAF54077 AAF54077

DNA encoding novel Genomic DNA sequen Human polynucleoti Human polynucleoti probe #5005 for ge Human brain expres

Drosophila melanog Drosophila melanog Enterococcus faeca Eph-related PTK

Zea mays DNA fragm
Zea mays DNA fragm
Pinus radiata tran
Pinus radiata tran
Human CDNA Clone (
Arabidopsis thalia
hFIX gene AE3' age

AAS90536 AAH68197 AAC93386

DNA encoding novel C glutamicum codin Human secreted pro Human Factor IX ge Human foetal liver

DNA encoding novel Tobacco PABF cDNA.

Drosophila melanog

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Result
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Perfect score:
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Maximum DB seq length: 2000000000
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| SIDS1/gcgdata/geneseq/geneseqn emb1/NA1982_DAT: *
| SIDS1/gcgdata/geneseq/geneseqn emb1/NA1983_DAT: *
| SIDS1/gcgdata/geneseq/geneseqn emb1/NA1984_DAT: *
| SIDS1/gcgdata/geneseq/geneseqn emb1/NA1985_DAT: *
| SIDS1/gcgdata/geneseq/geneseqn emb1/NA1985_DAT: *
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                                                                                                                                                                                    Length DB
 50000
1300
1302
401
932
   IJ
AAF86246
AAH79040
AAF86259
AAF86353
AAA96363
AAC48250
AAC47949
AAS26580
AAF16080
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                                Forward OspA PCR p
Reverse OspA PCR p
Polymorphic repeat
Arabidopsis thalia
Arabidopsis thalia
                                                                                                                                                                                  Description
                                                                                                                           OspA 17kD antigen
Piscirickettsia sa
cDNA encodin
prostate can
ARESULT 1
ARESULT 1
ARESULT 2
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                    17-SEP-1999;
                                                       17-SEP-1999;
                                                                                         17-MAR-2001
                                                                                                                             CA2281913-A1
                                                                                                                                                                                                                                                                                                                Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                        OspA 17kD antigen gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a ospA in the form of a vaccine of the method is used for protecting animals. The method is also useful for protecting animals, rickettsial septicaemia (SRS) and other ricketterial pathogen sequence represents DNA encoding the P. salmonis. The method is also useful for protecting against salmonid protectin with an N-terminal (SRS) and other rickettsial diseases. The present an anti-ospA antibody response.
                                                                                                                                                                                                                                                                                                                         121
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                                                   GAAAAA
                                                                       CAAGAGATTTACGGCACTGCATGCCGGCAACCGGATGGTCGTTGGCAAGTCATTTCAACA
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hes 486;
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                                                                                                                 GAGCGTCGCCAGCAATATTGTCGAGAATTTTCAGCAAAAGGCGATGATTGCAGGGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                              GATACAGGCAATAGTTATAGTGTTGAGCCAGTGCGTACTTACCAGCGTTACAATAAGCAA
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(BURI/)
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)B; AAB81126.
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) BURIAN J.
) KUZYK M A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 486; DB 22; Length Pred. No. 6.8e-237; Mismatches 0; Indels
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                                                                                                                                                                                                                            The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia stamonis for production of a vaccine with antibacterial activity to known as salmonid rickettsial septicaemia.
                                                                                                          121
                                                                                                                                                                                                                   Sequence 489 BP; 139 A; 79 C; 144 G; 127 T; 0 other;
                                                                                                      61 TGTGCCCAGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGT 120
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                                                                                                                                                                                                                                                                                            Claim 3; Fig 4; 25pp; English.
                                                                                                                                                                                                                                                                                                    New nucleic acids encoding an amino acid sequence homologous to surface antigen present on piscirickettsia salmonis are useful
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01-JUL-2000;
01-JUL-2000;
                                                                                                                                                   1 ATGAACAGAGGATGTTTGCAAGGTAGTAGTCTAATTATTATCAGTGTGTTTTTAGTTGGC 60
        Burzio
AAGCTAAACCAGAGTTTGGAAAAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCA
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                                                                    GTTGCTGGCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATTGGCCATTGGTGCTGCT
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                                                                                                               TGTGCCCAGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial; septicaemia; SRS; surface antigen; vaccine; antibacterial; fish; ATCC VR-1361; ss.
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486; Conserv
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2000GB-0018599.
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Pred. No. 6.8e-237;
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                              This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against aslmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence The primer is used in the construction of pTYBI-17kD, which is used to express optimised OspA antigen with a C-terminal fusion partner. The OspA fusion protein is used in a vaccine to create an anti-OspA antibody manufacture.
                                                                                                                                                                                                                       Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
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(BURI/)
(KUZY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; OspA; sa
SRS; 17E2; fusion
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BURIAN J.
KUZYK M A.
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                       response.
                                                                                                                                                                                                                                                                                                     Burian J,
                                                                                                                                                                                                  Page 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          486
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(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                     salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of ospA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used to amplify the P. salmonis OspA DNA sequence. The primer is used in the construction of pTyBI-17kD, which is used to express optimised OspA antigen with a C-terminal fusion partner. The OspA fusion protein is used in a vaccine to create an anti-OspA
                                                                                                                                                                                                                                                                                                                                           This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine
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SRS; 17E2; fusion construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poikilothermic fish; Piscirickettsia salmonis; vaccine; OspA; salmonid rickettsial septicaemi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for protecting poikilothermic fish against salmonid rickettsial aemia and other rickettsial diseases comprises administering a e containing the OspA protein of Piscirickettsia salmonis
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                                                    response
                                                                                                                                                                                                                                                                                                                                                                                                                           Page 21;
BP;
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C; 7 G; 15 T; 0 other;
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Pred. No.
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a; rickettsial disease
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AAA96363;

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CC and flanked the human CTLA-4 locus were cloned and sequenced. The CC sequence data was assembled into a contiguous sequence that is presented CC in AAA95363-68. AAA95363-68 comprise BAC clone 22700, and AAA96365-68 CC microsatellite repeat (PMR) sequences contain polymorphic method for determining the predisposition of a human subject to develop CC cD28, ICOS gene or CTLA4 gene of the human costimulatory receptor gene CC locus (hCGRL). PMR sequences vary in length among individuals and can be detected by rapid and convenient high resolution processes. The method is useful for determining the predisposition of a human subject to develop CC cD28, ICOS gene or CTLA4 gene of the human costimulatory receptor gene CC amplified to generate products that differ in size. These products can be detected by rapid and convenient high resolution processes. The CC method is useful for determining the predisposition of insulin-dependent CC diabetes mellitus (IDDM), Addison's disease, Graves disease, autoimmune
                                                                                                                                                                                                                                                                              Determining predisposition of humans to develop autoimmune disease involves detecting polymorphic microsatellite repeat sequence within human costimulatory receptor gene locus
                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY ) GENETICS INST INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CGRL; lupus; insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy; daves disease; autoimmune hypothyroidism; myasthenia gravis; thymoma; thyroiditis; postpartum thyroiditis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hashimoto's disease; coeliac disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Autoimmune disease; polymorphic microsatellite repeat; PMR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA96363 standard; DNA; 50000 BP
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                                                                                                                                                                                                                                                       Page 67-82; 160pp; English.
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23904..23957
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19911..19956
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6550..6597
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99US-0148319.
99US-0148341.
                                                        Score 19; DB
Pred. No. 12;
0; Mismatches
                                                                        DB
12;
                                                                                           21;
                                                        0;
                                                                                           Length 1302;
                                                        Indels
                                                       0,
                                                       Gaps
                                                       0
 RESULT 8

AAS26501

ID AAS26

XX AX AAS26

XX AX AAS2

XX AX Hume

XX AX Hume

XX AX Hume

XX AX Hume

XX AX Hope

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XX
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31-JAN-2000
04-FEB-2000
24-FEB-2000
16-MAR-2000
17-MAR-2000
11-MAR-2000
28-JUN-2000
28-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
14-JUL-2000
14-JUL-2000
14-AUG-2000
15-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
01-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular corneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA; 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding
2000US-0186350.
2000US-019874.
2000US-0199874.
2000US-0199076.
2000US-0199123.
2000US-0216886.
2000US-0216847.
2000US-0216847.
2000US-0216847.
2000US-0217487.
2000US-0217487.
2000US-0218290.
2000US-0218290.
2000US-0218518.
2000US-0228518.
2000US-0228518.
2000US-0228518.
2000US-0228518.
2000US-0228518.
2000US-0228517.
2000US-0228518.
2000US-0229348.
2000US-0229348.
2000US-0229348.
2000US-0229348.
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2000US-0184664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiac arrest;
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); 2000US-0230437 2000US-0231242 2000US-0231243 2000US-0231243 2000US-0231244 2000US-0231414 2000US-0231414 2000US-0231414 2000US-023280 2000US-023280

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The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to grevent, treat or ameliorate a medical condition in e.g. humans, mice, CC to a pathological condition. Antibodies to the proteins can also used in alleviating symptoms associated with the disorders and in CC immunosorbant assays (ELISA). Disorders which are disprosed or treated cardiovascular disorders e.g. reducionamnoassays or enzyme linked CC hyperproliferative disorders e.g. remanatoid arrhritis, CC and coular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cardiac arrest, cerebrovascular disorders e.g. 
                                           AAF16080
                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                           Matches
AAF16080 standard; cDNA; 932 BP
                                                                                                 Claim 1; SEQ ID No 759; 980pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 NOV 2000; 2
17 NOV 2000; 2
17 NOV 2000; 2
17 NOV 2000; 2
17 NOV 2000; 2
17 NOV 2000; 2
01 DEC 2000; 2
05 DEC 2000; 2
05 DEC 2000; 2
05 DEC 2000; 2
06 DEC 2000; 2
06 DEC 2000; 2
08 DEC 2000; 2
09 DEC 2000; 2
09 DEC 2000; 2
09 DEC 2000; 2
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P-PSDB; AAU16593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                           l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-2000;
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                                                                                                                                                                            Conservative
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2000US-0249244

12 2000US-0249264

12 2000US-0249265

2000US-0249295

2000US-0249297

2000US-0249299

2000US-0250391

2000US-0250391

2000US-0250391

2000US-0251888

2000US-0256719

2000US-0256719

2000US-0251868

                                                                                                                                                                                        3.7%; Score 18;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
                                                                                                                                                                            0;
                                                                                                                                                                    Mismatches
                                                                                                                                                                                     DB
37;
                                                                                                                                                                                                      22;
                                                                                                                                                               0;
                                                                                                                                                                                              Length 401;
                                                                                                                                                       0,
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); 2000US-023399;); 2000US-023299;); 2000US-0232399;); 2000US-0232399;); 2000US-0232401); 2000US-0233063; 2000US-0233063;); 2000US-0233065;); 2000US-0233065;); 2000US-0234997;); 2000US-0234997;); 2000US-0234998;); 2000US-0235834; 2000US-0235834; 2000US-0235836; 2000US-0235836; 2000US-0236367; 2000US-0236367; 2000US-0236369; 2000US-0236369; 2000US-0236369; 2000US-023637039; 2000US-0237039; 2000US-0239375; 2000US-0239375; 2000US-0239937; 2000US-0239937; 2000US-0239937; 2000US-0234125; 2000US-0234125;

08-SEP-2000; 2
08-SEP-2000; 2
08-SEP-2000; 2
108-SEP-2000; 2
12-SEP-2000; 2
14-SEP-2000; 2
25-SEP-2000; 2
25-SEP-2000; 2
27-SEP-2000; 2
27-SEP-2000; 2
29-SEP-2000; 2
20-OCT-2000; 2
20-OC

2000US-0241808 2000US-0241809 2000US-0241809 2000US-0244617 2000US-0246475 2000US-0246475 2000US-0246475 2000US-0246478 2000US-0246478 2000US-0246478 2000US-0246524 2000US-0246523 2000US-0246525 2000US-0246526 2000US-0246526 2000US-0246526 2000US-0246527 2000US-0246510 2000US-0246611 2000US-0246613 2000US-0249211
0;

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RESULT 10
AAN71108
ID AAN71
XX
AC AAN71
XX
DT 01-JA
XX
DE OPtim
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate cancer associated gene sequences, referred to
cancer antigens, useful for treatment, prevention, and
disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the preser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, The prostate, immunomodulatory, musue neuroprotective, cytostatic, cardioactive, immunomodulatory, musue neuroprotective, gastrointestinal, cardioactive, immunomodulatory, musue neuroprotective, cytostatic, cytostati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200055174-A1
                  Optimized Escherichia coli aspC
                                                      01-JAN-1980
                                                                                                                            AAN71108 standard; DNA; 1293
                                                                                                                                                                                                                                                                                                                                                                 Sequence 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF16080
                                                                                                                                                                                                                      692
                                                                                                                                                                                                                                   237 AATAAAGCTAAACCAGAG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-587513/55
DB; AAB56877.
                                                                                                                                                                                                                      AATAAAGCTAAACCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Page 979; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate
                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM;
                                                                                                                                                                                                                                                                                          Conservative
                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                 BP; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer antigen nucleotide sequence
                                                                                                                                                                                                                                                                                  3.7%; 5cc
/ 100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                               A; 223
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                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No
                                                                                                                                                                                                                                                                                                                                                               211 G;
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                              NO.
                                                                                                                                                                                                                                                                                                                                                                 242 T;
                                                                                                                                                                                                                                                                                                            DB
37;
                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present
                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                           Length 932;
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                                                                                                                                                                                                                                                                                          Indels
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diagnosis of
                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                          0;
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AAV40259
   Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                              Brevibacterium lactofermentum; lysC; L-lysine; coryneform bacterium; aspartokinase; feedback inhibition; dihydropicolinate reductase; diaminopimelate decarboxylase; aspartate aminotransferase; ds.
                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composite plasmids contg. multiple genes useful for prodn. of aminoacid(s), esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aspC gene; feedback inhibition; amino acid synthesis;
composite plasmid; ss.
 Araki M,
                                                                       05-DEC-1996;
                                                                                                           05-DEC-1997;
                                                                                                                                             22-JUL-1998
                                                                                                                                                                              EP854189-A2
                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV40259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV40259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1293 BP; 322 A; 331 C; 343 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAN71107, AAN71109-11 and AAP70696-97 and AAP70750, AAP70752-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 25; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NUTR-) NUTRASWEET CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUN-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
                                 (AJIN ) AJINOMOTO CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 GCTGTTTGGTAAAGGTAG
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DB; AAP70751.
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 1331
 Nakamatsu T,
                                                                                                                                                                                                                                                                                                                                                                                                                    coli aspC gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   may be inserted into a composite plasmid auction of amino acids. See also AAN71053-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85US-0747732
                                                                       96JP-0325659
                                                                                                           97EP-0121443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86WO-US01353
                                                                                                                                                                                                                                                      Location/Qualifiers
10...1197
                                                                                                                                                                                                                /product= "aspC"
                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.7%;
Sugimoto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hunter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          МG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
 Yoshihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fotheringham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in transcriptional units 
L-phenylalanine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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and

0,:

Gaps

0

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RESULT 12
AAN71109
               Composite plasmids contý. multiple genes in transcriptional units
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                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1987-021998/03.
P-PSDB; AAP70752, AAP71677-8.
                                                                       Edwards MR,
                                                                                    (NUTR-) NUTRASWEET CO.
                                                                                                     24-JUN-1985;
                                                                                                                     24-JUN-1986;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                    15-JAN-1987
                                                                                                                                                    WO8700202-A.
                                                                                                                                                                               CDS
                                                                                                                                                                                                            CDS
                                                                                                                                                                                               CDS
                                                                                                                                                                                                                             Bacillus licheniformis.
                                                                                                                                                                                                                                                       alpha-amylase;
                                                                                                                                                                                                                                           alpha-amylase; feedback inhibition; amino acid synthesis;
composite plasmid; ss.
                                                                                                                                                                                                                                                                      PheA aroF aspC
                                                                                                                                                                                                                                                                                 01-JAN-1980 (first entry)
                                                                                                                                                                                                                                                                                                       AAN71109;
                                                                                                                                                                                                                                                                                                               AAN71109 standard; DNA; 3659 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant DNA autonomously replicable in cells of coryneform bacteria (CB), comprising a DNA sequence coding for an aspartokinase (AK) in which feedback inhibition adhydrodipicolinate reductase (DHPR), a DNA sequence coding for dimydropicolinate synthase (DHPR), a DNA sequence coding for diminopimelate decarboxylase (DHPS), a DNA sequence coding for aspartate aminotransferase (AAT). The present sequence coding for appresent invention, can be used for improving L-lysine products from the by CB. The L-lysine produced can be used as a fodder additive.
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1331 BP; 330 A; 340 C; 350 G; 311 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       252 GCTGTTTGGTAAAGGTAG 269
                                                                                                                                                                                                                                                                                                                                                                 132 GCTGTTTGGTAAAGGTAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA autonomously replicable in coryneform bacteria used to produce L-lysine, codes for e.g. aspartokinase, dihydropicolinate reductase and synthase and di:amino-pimelate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Page 37-38; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1998-379060/33.
DB; AAW69553.
                                                                     Taylor
                                                                                                  85US-0747732.
                                                                                                                 86WO-US01353.
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                      /*tag= a
1259..2329
/*tag= b
2344..3534
                                                                                                                                                                                                                                                               Operon in plasmid pME219.
                                                                                                                                                                                                      Location/Qualifiers 69..1241
                                                                    PP,
                                                                                                                                                                                                                                                                                                                                                                                   3.7%; Su
100.0%; Pr
, Pr
                                                                  Hunter
                                                                                                                                                                                                                                                                                                                                                                                           Score 18;
Pred. No.
                                                                 ΜG,
                                                           Fotheringham IG;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
37;
                                                                                                                                                                                                                                                                                                                                                                                 0;
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         Qγ
                                                                       165 GGCCATTGGTGGTGCTGT 182
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AAQ90655
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                                                                                                                                                                                                                                                                                      CDS
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Query Match
Best Local Similarity
"hohes 18; Conserve
                                                             Sequence 3776 BP;
                                                                Novel EPH-related PTK cDNA clone Cek9 (given in AAQ90655) was isolated from a chick embryo library in lambda. Cek9 protein (AAR75707) is closely related to Cek5 (AAR75712). In adult tis Cek9 expression is predominant in the thymus and detectable in brain, retin, kidney, lung and heart.
                                                                                                                                                        Claim 2; Page 50-53; 129pp; English.
                                                                                                                                                                             Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
                                                                                                                                                                                                                               WPI; 1995-215256/28.
P-PSDB; AAR75707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                       Pasquale EB,
                                                                                                                                                                                                                                                                                         (LJOL-) LA JOLLA CANCER RES
                                                                                                                                                                                                                                                                                                                        03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                  07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                            08-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                    WO9515375-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cek9; Eph;
prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eph-related PTK Cek9 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ90655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ90655 standard; cDNA; 3776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2586 GCTGTTTGGTAAAGGTAG 2603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 GCTGTTTGGTAAAGGTAG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3659 BP; 936 A; 911 C; 947 G; 865 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence may be inserted into a composite plasmid and used for the production of amino acids. See also AAN71053-55, AAN71107, AAN71109, AAN71111 and AAP70696-97 and AAP70750, AAP70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 38; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for prodn. of aminoacid(s), L-tyrosine
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 3.7%; Sc 1 Similarity 100.0%; I 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein tyrosine-kinase; PTK; cancer; diagnosis;
ss.
                                                                                                                                                                                                                                                                   Sajjadi FG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                  93US-0162809
                                             1005 A; 881 C; 941 G; 949 T; 0 other;
                                                                                                                                                                                                                                                                                                                                            94WO-US10140
    100.08; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
290..3311
/*tag= a
 Score 18; DB; Pred. No. 38; 0; Mismatches
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              DB 16;
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38;
                 Length 3776;
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                                                                                          tissues,
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Indels

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RESULT 15
ABL10082
ID ABL10
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AC ABL10
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AAX13059
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                                                                                                                                             Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                  A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosting Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                            2473
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 734-739; 2084pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis; contig; detection; vaccine; attenuation; computer readable me
  ABL10082;
                           ABL10082 standard; cDNA; 10432
                                                                                                                                                                                                Sequence 9813
                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09850555-A2
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                                                                                          1999-045171/04.
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18; Conserv
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                                                                                                                                              Conservative
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                                                                                                                                                                                                BP;
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                3233
                                                                                                                                         3.7%; SC
100.0%; Pr
100.0%; O;
                                                                                                                                                                                                A; 1698 C; 2161 G;
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                                                                                                                                                         Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig SEQ ID NO:122
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                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                              Mismatches
                                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n; Enterococcal infection;
medium; ds.
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Search completed: October Job time: 142.109 secs

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2002,

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Best Local S
Matches 18
                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                           New isolated nucleic a
genes from Drosophila
                                                                                            Sequence
                                                                                                                           (ABB57737-ABB72072).
The sequence data for this patent did not form specification, but was obtained in electronic (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; pharmaceutical; gene; ss.
                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 24728;
                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
P-PSDB; ABB65979.
                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster expressed
                                                                                                                                                                                                                                                                                    interactions
                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
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                        170
TIGGIGGIGCIGITITGG 7035
             TTGGTGGTGCTGTTTTGG
                                            ch 3.7%;
l Similarity 100.0%;
l8; Conservative (
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                                                                                             10432 BP;
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                                                                                                                                                                                                                                                                                                                                                                    Adams M,
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2000US-0614150.
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                                                                                             2894 A;
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                       187
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                                                                                                                                                                                                                                                                                              detection reagent for detecting for elucidating cell signalling
                                                                                             2225 C;
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Mismatches
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AC012273 Homo sapi AP001636 Homo sapi AC090309 Homo sapi AC098770 Rattus no AL513003 Oryza sat AC093459 Homo sapi

AX252413 AF184152

Sequence Piscirick Homo sapi Human DNA

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Title:
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486
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Match Length DB
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        Description
BASE COUNT
ORIGIN
                                                                                     REFERENCE
AUTHORS
                                                                                                                      KEYWORDS
SOURCE
ORGANISM
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AX252413
LOCUS
DEFINITION
ACCESSION
VERSION
                                          FEATURES
                                                                     TITLE
                                                            JOURNAL
                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                  Sequence 5
AX252413
                                                 Burzio,L.

Fish vaccine against piscirickettsia Patent: WO 0168865-A 5 20-SEP-2001; Aqua Health (Europe) Limited (GB)
                                                                                   1 (bases 1 to 489)
Simard.N., Brouwers,H., Jones,S.F., Griffiths,S.,
                                                                                            Piscirickettsia.
1 (bases 1 to 489)
                                                                                                                     Piscirickettsia salmonis.
Piscirickettsia salmonis
                                                                                                                                                  AX252413.1 GI:15985721
                                                                                                              Bacteria; Proteobacteria;
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1151673
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3 4194
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79 c 144 q 127 t
                                         Location/Qualifiers
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161582
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AF184152
AP000516
AL162253
AP0012273
AP001636
AC090309
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AC0903459
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AC016666
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AC007970
AC0166660
                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                               gamma
                                                                                                              subdivision; Piscirickettsia group;
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                                                                   salmonis
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ALG26767 Mus muscu ALG26767 Mus muscu AC09378 Mus muscu U22357 Drosophila AC110102 Rattus no U95370 Bacillus 11 AC018318 Drosophil AC004715 Corynebac AC004715 Drosophil AC004715 Homo sapi AC004715 Homo sapi AC104137 Homo sapi AC104137 Homo sapi AC104137 Homo sapi AC104137 Homo sapi AC104793 Rattus no Sapi AC107966 Homo sapi AC107966 Homo sapi AC107967 Homo sapi AC105755 Homo sapi AC105757 Homo sapi AC105755 Homo sapi AC105755 Homo sapi AC105754 Human DNA AC25833 Homo sapi AC105754 Ho

linear

PAT 05-OCT-2001

Valenzuela, P.

gene <1.501 /gene="alr"	/organism="Piscirickettsia salmonis" /strain="LF-89" /db_xref="txon:1238" /clone="pB12"	JOURNAL Submitted (10-SEP-1999) Biochemistry & Microbiology, University of Victoria, Petch Building, PO Box 3055, Victoria, BC V8W 3P6, Canada source 1. 4983		<pre>Locates 1 CO 4983) Kuzyk,M.A., Burian,J., Thornton,J. Identification of a genus-common F salmonid pathogen Piscirickettsia</pre>	•	_	(OSPA), and transposase (tnpA) g N AF184152 AF184152.1 GT:10441343	4983 bp DNA linear BCT:sia salmonis alanine racemase (alr) gene, pa	T 2	Db 481 GAAAAA 486	QY 481 GAAAAA 486	421 CAAGAGATTTACGGCACTGCATGCCGGAACCGGATGGTCGTTGGCAAGTCATTTCAACA 4		QY 361 GAGCGTCGCCAGCAATATTGTCGAGAATTTTCAGCAAAAGGCGATGATTGCAGGGCAGAAG 420		241	Db 181 GTTTTGGGTGGATTAATTGGTTCTAAAATCGGTCAATCGATGGATCAGCAGGATAAAATA 240 Ov 241 AAGCTAAAACCAACCAACCAACCAACCAACCAACCAACCA		Db 121 GTTGCTGGCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCT 180 Db 121 GTTGCTGGCCAGCTGTTTGGTAAAGGTAGTGGTGGTGGTGCTAGTGCTAGTGGTGGTGGTGGTGGTGGTAAAGGTAGTGGTGGTGGT	61	£ 1 .	Query Match 100.0%; Score 486; DB 6; Length 489; Best Local Similarity 100.0%; Pred. No. 5.2e-248; Matches 486; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OV 1 ATGARGAGAGGAGGATGTTTTGGGGGGGGGGGGGGGGGG
CDS	repeat_region	source .				CDS	gene						CDS	gene					gene CDS			CDS
<pre>/ yelle= LipA" complement(38424561) / yene="tnpA" / codon_start=1</pre>		35604849 /organism="piscirickettsia salmonis" /strain="LF-89" /strain="taxon:1238"	/ "A GILD THE MANGE CLOGSSLITES VELVEC AQNES RQEVGAATGA VVGGVAGQ LECKGSGRVAMA IGGAVLGGLIGSK IGQSMDQODKIKLNOSLEKVKAGQVTRWRNPDT GNSYSVEÞVÆTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGTACRQÞDGRWQVIST EK"	<pre>/product="17 kDa antigen" /protein_id="AAG17000.1" /db_xref="GI:10441346"</pre>	<pre>/note="similar to the rickettsial 17 kDa antigen" /codon_start=1 /transl_table=11</pre>	/evidence=experimental 2834. 3322 /gene="osph"	2834 3322 /gene="ospA"	ORLAMILAVINHGGIASYDODYFINVGGMXITETAADLALLLACVSSLRGKALSOE LIVEGEIGLSGEIRPVQRGLERIKEAVKHGETQAIVPLANCPKQKVDGIEIVGVKHLE DALATL	GIGASTILLIZISVNCTQFGKVLYVTGEESLEQVTLRSKRLGLSQDVDLRLLAETQVER ILKAABIEQPKVLIVDSIQTIFTESLQSAPGGVAQVRESAAILTQFAKRTGTCLFLVG HVTKEGALAGPRVLEHMYDTVLYFEGEQDSRFRLLRAVKNRFGAANELGIFAMTETGL	/translation="MSKOKNOVYCSDCGGIAKKWLGQCPHCQQWNSLSEVKEVLPNRP GRSQRPAGFAGIDAPKVKCLSEITPEQISRQPVGICEEDRVLGGGIVHGAVILLGGDD	/Protein_id="AAG16998.1" /db xref="GT-10/4134"	e=11	/evidence=experimental 1373. 2743 /gene="radA"	1373	ATTUSENTINGITLOKROHILSLIOKKSLSKQEITQLQALAKQYKLNULHEKHODES LLLKRVDIIPNALISAQAINESNWGRSRFAVEGNNFFGMRCHYPGCGIIPKARPANNH WEVANYSSMTASVKAYIHTLNTHNAYQALRDLRAHMRANHQDVSAFKLAEGLTAYSIK GTKYVELIOTITTPSYLSKFGFTSOTT"	/protein_id="AAG17002.1" /db_xref="GI:10441348" /translation="MLSLAVITTAYLAQQPLESAPTSKTOINTAYSODTOSTKOPETT	/transl_table=11 /evidence=not_experimental /product="BAX"	/comp.rement(3201257) /gene="bax" /codon start=1	complement(5261257) /gene="bax" /gene="bax"	/translation="NSAAIFNESYERYDWVRPGIMLYGISPFADKNGVDLELQPVMHVVSRLISVKQLRQGESVGYGATWQCPEDMQVGILSLGYVDGYPRLAASGTPFLVRGQRCALIGRVSMDMIAIDLRRCPDAGVGEAVTVWGQDLPVEEIARHVGTIAYELVCNMPLRAPYTWGE"	/evidence=not_experimental /product="alanine racemase" /protein_id="AAG17001.1" /db xref="GI:104d1747"	<1501 /gene="alr" /codon_start=1 /transl_table=11

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RESULT 3
AP000576
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalla; Eutherla; Primates; Catarrhini; Hominidae; 1 (bases 1 to 121922)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Se Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Saka Homo sapiens 121,922 genomic DNA of 11912
Published Only in DataBase (1999) In press 2 (bases 1 to 121922)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Se
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SEQUENCE, 12
                                                                                                                                                      Homo sapiens
                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:CMB9-6J10.
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HTG; HTGS_PHASE1; HTGS_
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Pred. No. 4.6e-248;
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   Hong-Seog, P.,
                                                                    Hong-Seog, P.,
and Sakaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Direct Submission
Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 118280 bases at least Q30 Consensus quality: 119669 bases at least Q30 Consensus quality: 120421 bases at least Q20 Insert size: 120822; sum-of-contigs Quality coverage: 12.41x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                         Center project Information
Center project name: HumDraftll
Center clone name: CMB9-6J10
                                                                                                                                                                                                                                                                 Sequencing vector: PCR products; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon preserved as it is available and the accession number will be

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
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43637
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111944 1116839: contig of 4896 bp in
116840 116939: gap of 100 bp
116940 119647: contig of 2708 bp in
119648 119747: gap of 100 bp
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103561 103660; gap of 100 k
103661 111843; contig of 8183
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111944 116839; contig of 4896
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25420 43536: contig of 18117 bp in
43537 43636: gap of 100 bp
43637 62163: contig of 18527 bp in
62164 62263: gap of 100 bp
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AL Submitted (20'-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirles: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Puring sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations to the overlapping clone assembly data is compared from overlapping clones. Variation annotation may not be found in the sequence wariations corresponding to the overlapping clone, as we submit sequence with a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
                                                                                                                                                                                                                                                                                                                                                                                                                          70697
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                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                      AL162253

146327 bp DNA linear PRI 21-MAR-2001

Human DNA sequence from clone RP11-574F11 on chromosome 9, complete
                                                                                                                                                                                                                                                                                                 AL162253.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 4.3%; Sc
Similarity 100.0%; F
21; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120912. .121922

/note="assembly_fragment"

23866 c 24325 g 37609 t
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120912. .121922
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119748. .120811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
116940. .119647
                                                                                                                                                                                                                                                                                          GI:13677203
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103661. .111843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
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74571._.84826
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25420. 43536
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/db_xref="taxon:9606"
/chromosome="11"
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Pred. No. 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                           JOURNAL
REFERENCE
                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                         AC012273
                                                                                                                                                                                                       ACCESSION
                                              AUTHORS
                                                                                                                                                                                                                                                                                                          Db 96974
                                                                                                                                                                                                                                                                                                                                      Qy
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Best Local (
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411 AGGGCAGAAGCAAGAGATTTA 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
2 (bases 1 to 160394)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGCCAGAAGCAAGATTTA 96994
                                                                                                                                                                          Puralyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; (bases 1 to 16094)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished

1 (bases 1 to 16094)
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                        AC012273
AC012273.3 GI:14595892
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                 Eukaryota,
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens clone RP11-1K7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is not the entire insert of clone RP11-574F11 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-574F11 is at 146327 in this sequence. The true left end of clone RP11-635N21 is at 62948 in this sequence. The true right end of clone RP11-12D24 is at 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44360 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome, constructed by the Sanger Centre Chromosome 9 mapping http://www.sanger.ac.uk/HGP/Chrg

RPI1-574F11 is from the library RPOI-11.2 constructed by the group http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the abbreviations are used to associate primary accession numbers given the feature table with their source databases: Em:, EMBL; SWI.SSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           data."
84304...84306
//note="Single clone region. Assembly confirmed by restriction digest data."
a 29767 c 29483 g 42717 t
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Anote="Sequence from overlapping clone ba635N21 (AL354744). Assembly confirmed by restriction digest
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/clone_lib="RPCI-11.2"
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/db_xref="taxon:9606"
/chromosome="9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.38;
100.08; Pr
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Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          bp DNA linear I
WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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BASE COUNT
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Query Match
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Consensus quality: 159851 bases at least 030
Consensus quality: 1508051 bases at least 020
Insert size: 162000; agarose-fp
Insert size: 162000; agarose-fp
Ouality coverage: 14.4 in 020 bases; agarose-fp
Ouality coverage: 14.6 in 020 bases; agarose-fp
Ouality coverage: 14.6 in 020 bases; agarose-fp

**NOTE: This is a 'working draff' sequence. It currently
consists of 4 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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                                                                                                                                49405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1474
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97675; contig of 77351 bp in length

97676 97775; gap of 100 bp

97776 160394; contig of 62619 bp in length

Location/Qualifiers

1. .160394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 16762: contig of 16762 bp in length
16763 16863: gap of 100 bp
16863 20224: contig of 3362 bp in length
20225 20324: gap of 100 bp
20325 97675: contig of 77351 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                       /note-"assembly_fragment"
20325. .97675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16863
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/db_xref="taxon:9606"
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                                                                                                                           ector_side:right"
32013 c 31371 g
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    4.38;
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    DB
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'n
Length 160394;
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RESULT 7
AC090309/c
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ORGANISM
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                                                                                                                                       REFERENCE
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                                                                                                                     AUTHORS
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                                                                                                                                                                                               AUTHORS
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Farc,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
                                                                                                                                                                         Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 11, clone RP11-142C4
                                                                                                                                                                                                                                                                                                                                                 IN PROGRESS
AC090309
                                                                                                                                                                                                                                                                                                                                                                 AC090309 161586 bp DNA linear Homo sapiens chromosome 11 clone RP11-142C4 map 11, IN PROGRESS ***, 1 ordered pieces.
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21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa (E-mail:hattori@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
On Dec 7, 2001 this sequence version replaced gi:9927280.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (05-APR-2000) Masahira Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 161582)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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AP001636
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:9606"
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REFERENCE AUTHORS

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RESULT 8
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                                                                                                                           KEYWORDS
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Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                           AC098770

165208 bp DNA linear HTG 20-DEC-2001
***, 62 unordered pieces.

ACO98770

A** SEQUENCING IN PROGRESS
                                                                     Rattus norvegicus
                                                                                                                       AC098770.2 GI:17974352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* provided by the submittor.

* This sequence will be replaced

* the finished sequence as soon as it is available and

161586: contig of 161586 bp in length.
                                                                                                Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lebozky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., McKernan, K., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Hetta, R., K., Rise, C., Rogov, P., Roman, J., Rosetti, M., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Fravers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Zembek, L., Zimmer, A., and Zody, M., Joung, G., Zainoun, J.,
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48496
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All repeats were identified using RepeatMasker:

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
                                                                                                               HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Center project Information
Center project name: L12578
Center clone name: 142_C_4
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/db_xref="taxon:9606"
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100.09; Pr
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TITLE
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Alsbrooks, J. Adams, C., Adio-Oduola, B., All-osman, F. R., Allen, C., Bowie, J. Amaratunge, H. C., Are, J. R., Banks, T., Ban
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 62 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (01-NOV-2001) Human Genome Sequencing Center, Depar of Molecular and Human Genetics, Baylor College of Medicine, Paylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced g1:16572814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished 2 (bases 1 to 165208)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Project Information
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COMMENT

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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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ON CYZA Sativa chromosome 12 clone OSJNBa0009F13, *** SEQUENCING IN PROGRESS ***, in ordered pieces.

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Oryza sativa

Cryza sativa

ISM Oryza sativa

Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryza.

E [ (bases I to 183317)

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Delseny,M., Robert,C., Brottier,P., Wincker,P., Cruaud,C., Artiguenave,F., Saurin,W., Salanoubat,M., Quetier,F. and

Weissenbach,J.
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Sequencing vector: M13; 5%
Sequencing vector: M13; 5%
Chemistry: Dye-primer ET; 0% of reads
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                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
                                                         Center project name: H_NH0499M11
                                                                                           Center: Washington University Genome Sequencing Center code: WUGSC
                                                                                                                      Direct Submission
Submitted (25-AUG-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Feb 7, 2002 this sequence version replaced gi:18308909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 191454)
Materston,R.H.
The sequence of Homo sapiens clone
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Waterston, R.H.
                                                                                                                                                                                                                                                                                         Homo sapiens
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BP 191 91006 EVRY Cedex - FRANCE (E-mail : Seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                               sapiens chromosome 2 clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Organism="Oryza sativa"
/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Clone="OSSNBA0009F13"
/Clone_1ib="CUGI Nipponbare BAC"
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Pred. No. 4.8;
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Db 127210 AAAGCTAAACCAGAGTTTGGA 127190
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         Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Project Information
Center project name: bM421C7
                                                                                       Burton, J.

Direct Submission
Submitted (10-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk which concerns this sequence version replaced gi:16031460.
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                             Mus musculus
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                            Mus musculus chromosome 4 clone RP23-421C7, *** SE AL626767
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21; Conserv
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Insert size: 184000; agarose-fp
Insert size: 19154; sum-of-contigs
Quality coverage: 8.23 in Q20 bases; agarose-fp
Quality coverage: 7.92 in Q20 bases; sum-of-contigs
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75544
75644
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/note="assembly_name:Contig18"
a 36639 c 38791 g 58298 t
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/db_xref="taxon:9606"
/chromosome="2"
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100.08; Pr
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Pred. No. 4.8;
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Length 192810; Indels

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Insert size: 213770; 3.4% error; agarose-fp
Qmailty coverage: 8.22x in Q20 bases; sum-of-contigs Quality
coverage: 7.45x in Q20 bases; agarose-fp
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This record will be updated with the finished sequence
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60178. .(
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57171. .6
                                                 /note="assembly_fragment:04437
fragment_chain:4"
145299. .148627
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fragment_chain:3"
120398. .124934
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fragment_chain:2"
116404...120297
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      /note="assembly_fragment:05331"
148728. .150958
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fragment_chain:2"
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fragment_chain:2"
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/clone_lib="RPCI-23"
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                                                                                                                                                                      Sequencing vector: M13; %
Sequencing vector: M13; %
Sequencing vector: plasmid; %
Chemistry: Dye-primer ET; % of reads
Chemistry: Dye-terminator Big Dye; % of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 249548 bases at least Q40
Consensus quality: 250157 bases at least Q20
Consensus quality: 250759 bases at least Q20
                                                                                     Insert size: 250000; agarose-fp
Insert size: 251971; sum-of-contigs
Quality coverage: 17.62 in Q20 bases; agarose-fp
Quality coverage: 17.54 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-OCT-2001) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Nov 14, 2001 this sequence version replaced gi:16554425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (585571)

McPherson,J.D. and Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC098728 252571 bp DNA linear HTG 14 Mus musculus chromosome UNK clone RP23-3H22, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtmlContact: submissions@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of Mus musculus clone
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AC098728.2 GI:16924170
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                                                                                                                                                                                                                                                                                                                                                                                           Center project name: M_BA0003H22
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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fragment_chain:5"
151059. .161424
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fragment_chain:5"
161525. .186255
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100.0%; Pred. No. 4.8;
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Direct Submission
Submitted (07-MAR-1995) Melissa E. Pepling, Biochemistry and Cell
Biology, SUNY at Stony Brook, 346 Life Sciences Building, Stony
                                                                                                                                     Drosophila pseudoobscura

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ (bases I to 3875)
Pepling, M.E. and Gergen, J.P.

Conservation and function of the transcriptional regulators; Tracky
                                                              Pepling, M.
                                                                                             96016114
                                                                                                                                                                                                                                            Drosophila pseudoobscura.
                                                                                                                                                                                                                                                                                              Drosophila pseudoobscura runt
U22357
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21; Conserv
                                                              (bases 1 to 3875)
ling, M.E.
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                                                                                                       Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 100.0%; ; Conservative 0;
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130985. .252571
/note="assembly_name:Contig40"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="UNK"
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4905: contig of 1160 bp in length
5005: gap of unknown length
23951: contig of 18946 bp in length
24051: gap of unknown length
130884: contig of 106833 bp in length
130884: gap of unknown length
130884: gap of unknown length
252571: contig of 121587 bp in length.
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                                                                                                                    Gergen,J.P.
function of the transcriptional regulatory
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RS Muzny D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buokk, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buokk, J., Burchl, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Davis, C., Davy-Carroll, L., Dederich, D.A., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Bscotto, M., Garrell, J.H., Gaevara, W., Guneratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Haves, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulky, S., Hume, J., Jackson, L. E., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Marhein, P., Martin, P., Maheshwarl, M., Madua, P., Martin, P., Lucier, R., Luna, R., Ma, J., Martin, P., Lucier, R., Luna, R., Ma, J., Martin, P., Martin, P., Lucier, R., Luna, R., Ma, J., Martin, P., Martin, P., Lucier, R., Luna, R., Ma, J., Martin, P., Martin, P., Lucier, R., Luna, R., Ma, J., Martin, P., Martin, P., Lucier, R., Luna, R., Ma, J., Martin, P., Martin, P., Lucier, R., Luna, R., Ma, J., Martin, P., Martin, P., Lucier, R., Luna, R., Ma, J., Martin, P., Martin, P., Lucier, R., Luna, R., Ma, J., Martin, P., Mart
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Mammalia; Eutheria;
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AQSTSLANTSTHSASSSTGSSTPDISATANTTANSSSSSNSNSNTANNTANNGSSNSN
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VIALDDVPDGTLVSIKGRUDENVGGELRNCTTTMKNQVARFNDLÆFVGRSGRGKSFTL
YGYADVERHQAAAQAAVHHPALSKASPSSSSIVSPSASAASSGAGAGAGAAPADYH
YGYADVERHQAAAQAAVHHPALSKASPSSSSIVSPSASAASASGAGAGAGAAPADYH
VSQITPPPSGAPTAAGPAAMMPSPGAAPAAAVAIPQFPENHVAAAAAAAAAQAQOQOH
AKSTPHAEHPYNFAAAACLRARNAAAVLHHGGDATGISHISPASSRSSSPTQOHV
AKSTPHAEHPYNFAAAACLRARNAAAVLHHGDATGISHISPASSRSSSPAQHISPPLR
MRCDLKAPSAIKPLHESAAAATNRQASPETTLPAATKLKNSTVQQKTVWRPY"

MRCDLKAPSAIKPLHESAAAATNRQASPETTLPAATKLKNSTVQQKTVWRPY"

5 a 1207 c 1002 g 766 t 5 others
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8 unordered pieces.
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/db_xref="GI:722345"
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/db_xref="taxon:7237"
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Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 26058)
Worley, K.C.
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be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 18 contigs. The true order of the pieces
is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye: 98% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 15687 bases at least Q40
Consensus quality: 17509 bases at least Q30
Consensus quality: 19045 bases at least Q30
Estimated insert size: 16607; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation
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1 (bases 1 to 28798)

Konz,D., Doekel,S. and Marahiel,M.A.

Molecular and biochemical characterization of the protein template controlling biosynthesis of the lipopeptide lichenysin

J. Bacteriol. 181 (1), 133-140 (1999)
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Bacillus licheniformis
Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                                                                                                                 Germany
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Direct Submission
Submitted (27-MAR-1997) Fachbereich Chemie/Biochemie
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/strain="ATCC 10716"
/db_xref="ATCC:10716"
/db_xref="taxon:1402"
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/product="lichenysin synthetase A"
                                                                 note="LicA"
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Db 27381 CAGGATAAAATAAAGCTAAA 27400 Search completed: October 27, 2002, 21:48:35 Job time: 1558.38 secs

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Q3154 rickettsia
Q9f9f9 rickettsia
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Q930X4	031557	Q98NA9	068681	Q9HU07	098310	046171	Q98P93	8M8A6Ö	Q9SUX1	Q9AL49	Q92NT4	Q9KSR1	Q9XAX8	P76572	Q9CN83	Q92LP2	091762	Q9XCA4	Q9RB08	Q92ST9	Q9RA95	069776	Q9F6B1	Q9A3X8	Q52854	Q9PGX0	Q914S1	09нх13
Q930x4 rhizobium m	O31557 bacillus su	Q98na9 rhizobium l	O68681 bacillus me	Q9hu07 pseudomonas	Q983y0 rhizobium l	046171 nephila cla	Q98p93 rhizobium l	Q9a8m8 caulobacter	Q9sux1 arabidopsis	Q9al49 shigella fl	Q92nt4 rhizobium m	Q9ksrl vibrio chol	Q9xax8 pseudomonas		Q9cn83 pasteurella		Q9i762 pseudomonas	Q9xca4 porphyromon	Q9rb08 pectobacter	Q92st9 rhizobium m	Q9ra95 serratia sp		Q9f6bl edwardsiell	Q9a3x8 caulobacter	H			Q9hxi3 pseudomonas

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Q9F9K8;
Q1-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2001 (TrEMBLrel. 16, L
17 KDA ANTIGEN.
                                                                                                                                                            Kuzyk M.A., Burian J., Thornton J.C., Kay W.W.;
"Identification of a genus-common Rickettsial surface an
salmonid pathogen Piscirickettsia salmonis.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF184152; AAG17000.1;
SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64;
                                                                                                                                                                                                                                                                 Piscirickettsia salmonis.
Bacteria; Proteobacteria;
Piscirickettsia.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                             ERROQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                      ERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK
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Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AAG28452.1; -
SEQUENCE 159 AA; 16497 MW; 34C58020AF470A1F
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MEDLINE=21217364; PubMed=11321078;
                                                                                                                                             Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Pop
Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
                                                                                                                      "Rickettsia felis: molecular characterization of a new member of
                 9 SSLIIISV---FLVGC--AONESROEVGAATGAVVGGVAGOLFGKGSGRVAMAIGGAVLG 63
                                                                                                                                                                                                           Rickettsia felis (Rickettsia azadi),
Bacteria; proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsiaeee; Rickettsia.
                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq)
01-DEC-2001 (TrEMBLrel. 19, Last seq)
17 KDA GENUS-COMMON ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                           Q9F9F2;
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054381
SKIMITALAASMLQACNGPGGMNRQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                                                                           132 KAYGTACRQPDGQWQVV 148
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE-98087556; PubMed-9425244;
Davis M.J., Ying Z., Brunner B.R., Pantoja A., Ferwerda F.H.;
"Rickettsial relative associated with papaya bunchy top disease.";
"Tr. Microbiol. 36:80-84(1998).
                                                                                                                                                                                                                                                                                                                                                                                            77 SQRALEAAPSGSSVQWRNPDNGNYGTVTPSKAY----
                                                                                                                                                                                                                                                                                                                                                                                                 82 LNOSLEKVKAGOVTRWRNPDTGNSYSYEPVRTYORYNKOERROOYCREFOOKAMIAGOKO 141
                                                                                                                                                                                                                                                                                                                                                                                                                                        26 SRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
17 KDA COMMON-ANTIGEN (FRAGMENT).
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                                                                      Similarity
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054381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
                                                           Conservative
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                  34.8%; Score 291; DB 2
38.1%; Pred. No. 1e-18;
tive 28; Mismatches
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41.6%;
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Last annotation updat
                                                                                    34C5B020AF470A1F CRC64;
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Pred. No. 9e-21;
29; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
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                                                                                                                                                                                                                                                                                                      159
                                                              DB_2; Length 159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 148;
                                                                                                                                                    Popov V.L.,
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RESULT 5
Q9K2N6
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SEQUENCE FROM N.A.
Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Bertrand D., Hurst G.D.D., Majerus M.E.N.;
"On the evolution of male-killing: Monophyletic origin and horizontal
transfer of male-killing Rickettsia (a-Proteobacteria) from two con-
generic ladybirds, Adalia bipunctata L. and A. decempunctata L.
COLEOPTER: Coccinellidae).",
EMBL; AJ269518; CAB96383.1;
EMBL; AJ269517; CAB96383.1;
EMBL; AJ269517; CAB96383.1;
NON_TER
144
144
144
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O9K2N6
OPKELMINARY;
OPKENN6;
OPKENN6;
O1-OCT-2000 (Tremblrel 15, Created)
O1-OCT-2000 (Tremblrel 15, Last sequence update)
O1-OCT-2000 (Tremblrel 15, Last sequence update)
ITKDA ANTIGEN (17 KDA ANTIGEN) (FRAOMENT)
Bacteria; Proteobacteria; afrom Adalia bipunctata.
Rickettsiaceae; Rickettsieae; Rickettsia.
Rickettsiaceae; Rickettsieae; Rickettsia.
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Best Local S
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052252
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                                                                                                                                                                                                                                                                                                                      139 QKQEIYGTACRQPD 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Billings A.N., Teltow G.J., Walker D.H.;

Molecular characterization of a novel spotted fever group rickettsial

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                         80 -IKLNOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERROQYCREFQQKAMIAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                7 RGMNKÓGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGÁLLGAVLGGQIGAGMDEÓDRRLA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=69410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsiaceae; Rickettsieae;
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Bacteria, Proteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998
01-DEC-2001
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052252; PRELIMINARY;
01-JUN-1998 (TremBirel.
                                                                                                                                                                                                                                                                                                                      ELTSORALEAAPSGSSTEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTOTVVIGG 121
                                                                                                                                                                                                                                                                                                                                                                                    QNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK--- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 QERROQYCREFOOKAMIAGOKQEIYGTACRQPDGRWQVIS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDA ANTIGEN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
53; Conserv
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23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha subdivision; Rickettsiales;
eae; Rickettsia.
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Pred. No. 1.4
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Last sequence update)
Last annotation updat
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Best Local
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O31065; O9WW02;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-CCT-2001 (TrEMBLrel. 18, Last annotation update)
O1-CTT-2001 (TrEMBLrel. 18, Last annotation update)
I7 KDA ANTIGEN (17 KDA PROTEIN) (FRAGMENT).
Rickettsia honel.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Q9K4W8;
Q9K4W8;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Rickettsia honei sp. nov., the aetiological spotted fever in Australia."; Int. J. Syst. Bacteriol. 48:1399-1404(1998). EMBL; AF027124: AAB81846.1; -. EMBL; AF060706; AAD20231.1; -. EMBL; AF060704; AAD20230.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99045882; PubMed=9828442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                                                                                    KAYGNACROPD 135
                                                                                                                                                                                                                                                                                                                NKQCTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELT
                                                                                                                                                                                                       EIYGTACRQPD 152
                                                                                                                                                                                                                                         SQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQQ
                                                                                                                                                                                                                                                                LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERROQYCREFQQKAMIAGQKQ 141
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                                                                                                                                                                                                                                                                                                                                                                                         Similarity
52; Conserv
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(SEP-1997) to 1
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(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                          PRELIMINARY;
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39.7%;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 259.5; | Pred. No. 5.9e 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         22;
Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raoult
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.9e-16;
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Best Local s
Matches 55
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=93084757; P Baird R.W., Lloyd M "Characterization a
                                                                                                                                                                                                                                                                                                            MEDLINE=93084757; PubMed=1452660;
Baird R.W., Lloyd M., Stenos J., Ross B
"Characterization and comparison of Aus
group rickettsiae.";
J. Clin. Microbiol. 30:2896-2902(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08, CLONE PRB FISF 1), 5' END C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coccinellidae).";
Appl. Environ. Microbiol. 67:270-277(2001).
EMBL; AJ269516; CAB96381.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=20575219; PubMed=11133455; Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K., Bertrand D., Hurst G.D.D., Majerus M.E.N.; "Incidence of male-killing Rickettsia spp. (alpha-Proteobacteria) the Ten-Spot Ladybird Beetle Adalia decempunctata L. (Coleoptera:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 KDA AWTIGEN (FRAGMENT).
male-killing Rickettsia from Adalia decempunctata
Bacteria; Proteobacteria; alpha subdivision; Ricke
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rickettsia sp.
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=120393;
                                                                                                                                                                                                                                                                             SEQUENCE
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QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELT 76
                                                       AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGSYGYVTPNKTYRNSTG
                                                                                                                                                                SSLITISV----FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG 63
                                                                                         GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQRALEAAPSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQQ
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                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                             154 AA;
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                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                             15849 MW;
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                                                                                                                                                                                                     30.1%; score 252; DB 2; J 35.5%; Pred. No. 3.3e-15; tive 29; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
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Last annotation update)
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Pred. No. 6.3e-16;
2; Mismatches 48
                                                                                                                                                                                                                                                                             F5C35855EDB439D2 CRC64;
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Query Match
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Matches 48
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                                                                   STRAIN=CALIFORNIA 2;
ROUX V., RAOULT D.;
Submitted (DEC-1999) to the
EMBL; AF210693; AAG48554.1;
                                                   SEQUENCE
                                                                                                                    Submitted (JAN-2001) to
                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
17 KDA PROTEIN (FRAGMENT).
Rickettsia sp. California 2.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiaee; Rickettsia.)
RUBI-TaxID-147259;
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                       SEQUENCE FROM N.A.
                                                                                                                             Raoult D.;
"A new SFG rickettsia
                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CALIFORNIA 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Nilsson K., Pahlson C.;
"Novel peptide diagnostic reagent and kit for detection rickettsiosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nilsson K.,
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                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
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Q9F9Q9;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                            Local 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia_helvetica.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
                   48;
               Similarity 37.8
48; Conservative
                                                                                                                                                                                                                                                                           RNSTGOYCREYTOTVVIGGKOOKAYGNACROP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                              GLIGSKIGOSMDOODK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                   AVLGGQIVAGMDEQDRRLAELTSQRALEAAPSGSNVEWRNPDNGNYGYVTPNKTY-----
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                                              131
131 AA;
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                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            151 AA;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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          28.4%; 5c.
37.8%; Pre
                                                       131
                                             13374 MW;
                                                                                                              isolated from fleas.";
to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                            29.5%; Score 247; DB 2
36.2%; Pred. No. 9e-15;
         Score 237.5; DB 2
Pred. No. 5.4e-14;
22; Mismatches 48
                                                                     EMBL/GenBank/DDBJ databases
                                      23C8819B29FFF860 CRC64;
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                       Length 131;
        Indels
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RESULT 12
Q9L522
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Q52637
MEDLINE=21091941; PubMed=11157215;
Simser J.A., Palmer A.T., Munderloh U.G.,
                                                                                                                   Q9L522

Q9L522

Q9L522,
Q1-CT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                         STRAIN-DAE100R;
                                                    SEQUENCE FROM N.A.
                                                                                       Bacteria, Proteobacteria, alpi
Rickettsiaceae, Rickettsieae,
                                                                                NCBI_TaxID=47589;
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"Rickettsial relative associated with male killing in the ladybird beetle (Adalia bipunctata).";
J. Bacteriol. 176:388-394(1994).
EMBL; U04162; AAA19235.1; -.
                                                                                                                                                                                                                                                                                   125 KAYGNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=94117373; PubMed=8288533;
Werren J.H., Hurst G.D., Zhang W., Breeuwer J.A.,
                                                                                                                                                                                                                                                                                                                                      82 INOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ
                                                                                                                                                                                                                                                                                                                                                                  10 NKÓGTGTLLGGAGGALLGSQEGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=789;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                               SQRALEAAPSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGOYCREYTOTVVIGGKOO 124
                                                                                                                                                                                                                                                                                                                                                                                          SRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 EIYGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDA ANTIGEN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 NKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131
131 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.48;
                                                                            alpha subdivision; Rickettsiales;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 237.5;
Pred. No. 5.4e
22; Mismatches
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Last annotation updat
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 Kurtti
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EMBL; AF
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MLR7687.
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                                                                            Q985G4
                                                                                                                                                                                                                                                                                                                                                                                            Rickettsiaceae; Rickettsieae; NCBI_TaxID=69475;
Rhizobium loti (Mesorhizobium loti)
                                                                Q985G4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        solation of a spotted fever group rickettsia, Rickettsia peacockii, a Rocky Mountain wood tick, Dermacentor andersoni, cell line."; pl. Environ. Microbiol. 67:546-552(2001).
BL; AF260571; AAF69012.1; -.
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                                                                                                                                             NPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGTACRQPD 152
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                                                                                                                                                                          GQLVGVGV-----
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                     PROTEIN
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48; Conservative
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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37.8%;
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Pred. No. 7.4e
17; Mismatches
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Pred. No. 6.6e-14;
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EMBL; AP003012; BAB54098.1; -
Complete proteome.
SEQUENCE 199 AA; 20517 MW;
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01-JUN-2001 (TrEMBLrel. 17
01-JUN-2001 (TrEMBLrel. 17
17 KDA ANTIGEN (FRAGMENT).
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Kishida Y., Kiyokawa C., Kohara M., Mats
Mochizuki Y., Nakayama S., Nakazaki N.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=MAFF303099; MEDLINE=21082930;
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                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
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Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=785;
                                                                                                                                                                                                                                                                                                                          Rickettsia typhi
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 NPDNGNHGYVTPNKT
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                                                                                                        Similarity 29; Conserv
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Pred. No. 1.6e-05;
3; Mismatches 29;
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Pred. No. 2.9e-05;
5; Mismatches 50;
                                                                                                                                                              B1E447C037263918 CRC64;
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.

SIGNAL 1 19
17 KDA SURFACE ANTIGEN.

LIPID 20 159 AA; 16672 MW; A33D404B65EEB071 CRC64;
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Conservative

35.4%; score 296; DB 1; I 38.1%; Pred. No. 9.9e-19; tive 30; Mismatches 55;

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an email to lic 28482; AAA26378. 1235273; CAA1525 3971; D33971.	S-PROT ent the Swiss ean Bioinfi non-profit and this s	chondria."; re 396:133-140(1998). SUBCELLULAR LOCATION: anchor (Probable).	Vi Vi Vi Vi Wi uen	N.A. E; 71; Tzi eque	00 (Rel. 15, Cr 11 (Rel. 19, La 11 (Rel. 40, La 13 (Rel. 40, p. 13 (Rel. 40, p. 13 (Rel. 40, p. 13 (Rel. 40, p. 13 (Rel. 40, p. 14 (Rel. 40, p. 14 (Rel. 40, p. 14 (Rel. 40, p. 15 (Rel. 40, p. 16 (Rel. 40, p. 16 (Rel. 40, p. 17 (Rel. 40, p. 17 (Rel. 40, p. 18 (Rel. 40, p	STAN	00000000000000000000000000000000000000
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genus-common rickettsial antigen

Barbe V.,

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Furuya Y., Katayama T., Yoshida Y., Kaiho I.;
"Specific amplification of Rickettsia japonica DNA from clinical Specimens by PCR.",
J. Clin. Microbiol. 33:487-489(1995).
-I- SUBGELLULAR LOCATION: Attached to the outer membrane by a lipid
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CONFLICT 146
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PIR: A31836; A31836
PIR: A33971; A33971,
PIR: B33971; B33971,
PROSITE: PS00013; PRO
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EMBL; M28480; AAA26376.1;
EMBL; AE008675; AAL03825.1;
EMBL; J10486; AAA26381.1;
EMBL; J03371; NOT_ANNOTATED
                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration the European Bioinformatics Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no wall or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-30 FROM N.A.

SPECIES-R.rickettsii,
MEDLINE-89008059; PubMed-3139629;
Anderson B.E., Baumstark B.R., Bellini W.J.;
Pappression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii: transcription and posttranslational modification.;
J. Bacteriol. 170:4493-4500(1988).
1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-R.rickettsii,
MEDLINE-87222152; PubMed=3108232;
Anderson B.E., Regnery R.L., Carlone G.M.,
Fu Z.Y., Bellini W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rickettsii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SPECIES-R. Conorii; STRAIN-Malish 7;
MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe
Raoult D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the 17-kilodalton-antigen gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 169:2385-2390(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SPECIES-R. conorii, and R.rickettsii;
MEDLINE-89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
"Comparative Sequence analysis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P05372;

Ol-NOV-1988 (Rel. 09, Created)

Ol-AUG-1990 (Rel. 15, Last sequence update)

17 kDa surface antigen precursor.

OMP OR RC1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=781,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsia conorii, and Rickettsia rickettsii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 171:5199-5201(1989).
                                                                                                     Lipoprotein;
                                                                                                                                                                                                NOT_ANNOTATED_CDS.
                                                                                                              PROKAR_LIPOPROTEIN;
                              159
20
146
153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsieae;
783;
17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
N -> D (IN REF. 3)
G -> E (IN REF 3)
                                                                          DPROTEIN; 1.
Antigen; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha subdivision; Rickettsiales;
eae; Rickettsia.
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Tzianabos T.,

from Rickettsia

McDade J.E.,

В δÃ

В Qy DЬ Ş

(See http://www.isb-sib.ch/announce/

a collaboration

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Best Local S
Matches 55
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                             the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17KD_RICTY STANDARD; PRT; 1
P22882;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
                                                                                                                                                                                                                                                                                                            PROSITE; PS00013; PROKAR_LIPOPROTEIN; Outer membrane; Lipoprotein; Antigen; SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                               EMBL; M28481; AAA26377.1; -. PIR; C33971; C33971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
"Comparative sequence analysis of a gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                              LIPID
                   142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 171:5199-5201(1989). - SUBCELLULAR LOCATION: Attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kDa surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anchor (Probable).
                                                                                                                                         SRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                    NKQGTGTLLGGAGGALLGSQFGHGKGQLVGVGVGALLGAVLGGQIGASLDEQDRKLLELT
                EIYGTACROPDGRWQVIS 159
                                                   SQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQQ
                                                                                    LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN
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                                                                                                                                                                                                                                                          16549 MW;
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38.1%;
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Pred. No. 1.8e
29; Mismatches
                                                                                                                                                                                                                                                        17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PRO)
08973E2648FD8CD8 CRC6
                                                                                                                                                                                    Score 284.5; DB : Pred. No. 9.5e-18; 5; Mismatches 49
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Signal.
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.8e-18;
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CRC64;
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                                                                                                                                  P50927;
01-OCT-1996
01-OCT-1996
01-OCT-1996
17 kDa surfa
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01-OCT-1996
17 kDa surfac
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NON_TER
SEQUENCE FROM N.A. STRAIN-MO 85-1084;
                                                NCBI_TaxID=33989;
                                                                                                    Rickettsia
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NCBI_TaxID=787;
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Rickettsiaceae; Rickettsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane; Lipoprotein; SIGNAL 1 19
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                                                                                                                                                                                                                                                                                       124 ----GYCREYTQTVVIGGKQQKAYGNACRQPDGQ
                                                                                                                                                                                                                                                                                                                               120 QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGR 154
                                                                                                                                                                                                                                                                                                                                                                                                          64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLIIISV---FLVGCAQ--NFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKIMIIALAASMLQACNSPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
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                                                                                surface antigen
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                                          amblyommii.
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(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                  (Rel. 34, Last sequence update) (Rel. 34, Last annotation update)
                                                                                                                                            (Rel. 34, Created)
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                                                                                                                                                                                     STANDARD;
  Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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20
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38.1%;
                                                                              precursor
alpha subdivision;
eae; Rickettsia.
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BY SIMILARITY.
17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 276;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E3AA833346FAC320 CRC64;
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                (Fragment)
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1.9e-17;
nes 55;
                                                                                                                                                                                                                                                                                         154
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                       Rickettsiales
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 154;
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RESULT
17KD_RT
17KD_RT
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CHAIN 20
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Best Local
                                                                                                                               EMBL;
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MACULATUM;

Pretzman C.I., Stothard D.R., Ralph D., Clark J.B., Fuerst P.A.;

Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsiaceae; Rickettsieae; NCBI_TaxID=35792;
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01-OCT-1996 (Rel. 34, I
17 kDa surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                       U17008; AAA82040.1; -
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  mbrane; Lipoprotein; Antigen; Signal.

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20 >154 17 KDA SURFACE ANTIGEN.
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1 19 BY SIMILARITY.
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ace antigen precursor (Fragment).
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Pred. No. 6.
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PROSITE; PSUUULL.
Outer membrane;
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LIPID
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SEQUENCE
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01-OCT-1996 (Re
17 kDa surface (
                            120 QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGR 154
                                                                                                                                                                                                                                                                                                                                                                       EMBL; Ul1020; AAB07706.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.; Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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NCBI_TaxID=33992;
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                                                                                 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK
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                                                      AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYITPNKTY-----
                                                                                                                   SKIMIIALAASMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
                                                                                                                                                 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG 63
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mbrane; Lipoprotein; Antigen; Signal.
1 19 BY SIMILARITY.
20 >154 17 KDA SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PRC
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154 AA;
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15897 MW;
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36.1%;
                                                                                                                                                                                Score 261; DB 1; Lu.
Pred. No. 9.5e-16;
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Pred. No. 9.5e-16;
Pred. No. 97;
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RESULT 9

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17KD_RICCA
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Best Local S
Matches 56
                                                                                                                                                                                               17KD_RICCA
P29697;
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17 kDa surfa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-OHIO 83-441;
Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pres
Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pres
Stothard (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                   Bacteria; Proteobacteria; alp Rickettsiaceae; Rickettsieae; NCBI_TaxID=788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane; stgnaL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
SEQUENCE FROM N.A. MEDLINE-92108069;
                                                                                                                                            Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia montana
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                                                                                                                                               canada.
                                                                                                                                                                                                                (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 34, Last annotation updat
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     PubMed=1729713;
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                                                                                             alpha subdivision;
eae; Rickettsia.
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eae; Rickettsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen; Signal.
BY SIMILARITY.
17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PRO
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Signal.
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RESULT 11 PCP_YEREN
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                    between the Swiss Institute of Bioinformatics and the I
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   PCP_YEREN P31484;
                                                                                                  This
                                                                                                                                                                                          "A lipoprotein of Yersinia uptake in Escherichia coli. J. Bacteriol. 174:1029-1039
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 51872 / WA-C / SEROTYPE
MEDLINE-92121089; PubMed=1732192;
Baeumler A.J., Hantke K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000437; Prok_lipoprot. PROSITE; PS00013; PROKAR_LIPOPROTEIN; Outer membrane; Lipoprotein; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                Outer membrane lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                  -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                NCBI_TaxID=630;
                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                       Yersinia enterocolitica.
                                                                                                                                                                                                                                                                                                                                                     PCP OR PCPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          typhus-like rickettsia found in cat fleas."; Proc. Natl. Acad. Sci. U.S.A. 89:43-46(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Azad A.F., Sacci J.B. Jr., Schmidtmann E.T., Carl M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
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- FUNCTION: FACILITATES FERRIOXAMINE UPTAKE.
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                                                                                                                                        anchor.
SIMILARITY:
                                                                                                                           H.INFLUENZAE
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                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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X60448; CAA42977.1;
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31; Conser
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26, Last sequence 37, Last annotations
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8372 MW;
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                                                                                                                                          AND S.TYPHIMURIUM
                                                                                                                                                                   Attached to the
                                                                                                                                                                                                                                                                                                                          gamma
                                                                                                                                                                                                            enterocolitica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 157; DB 1
Pred. No. 4e-07;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD289A48EAB19E0E CRC64;
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                                                                                                                                                                                                                                                                                                                           subdivision;
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                                noved. Usage by and for (See http://www.isb-sib.
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A Alba H. Baba T. Fujita K., Haysahi K., Inada T., Isono K., A Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kashimoto K., Miki T., Mizobuchi K., Mori H., Mori T., Asai H., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Sanpei G., Seki Y., Sivasundaram S., Ra Tagami H., Takeda J., Takemoto K., Takeuchi Y., Sivasundaram S., Ra Yamamoto Y., Horiuchi T., Takeuchi Y., Makade S., Nashimoto Y., Horiuchi T., Takeuchi Y., Wada C., RT Takeuchi Y., Wada C., RT Takeuchi Y., Wada C., RT Takeuchi Y., Wada C., RT Takeuchi Y., Wada C., RT Takeuchi Y., Wada C., RT Takeuchi T., Wada C., RT Takeuchi Y., Wada C., Yakeuchi Y., Yakeuchi Y., Wada C., Yakeuchi Y., Wada C., Yakeuchi Y., Yakeuchi Y
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STRAIN-K12 / MG1655;

MEDLINE-97426617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., May
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MEDIJINE-96133688; PubMed-8544813;
Ludwig A., Tengel C., Bauer S., Bi
Goebel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSTYN_ECOLI STANDARD; PRT; 155 AA. 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 01-CT-2001 (Rel. 40, Last annotation update) 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete genome sequence of Escherichia coli K-12.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a regulatory protein from Salmonella typhimurium, induces
ytic and pore-forming protein in Escherichia coli.";
en. Genet. 249:474-486(1995).
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37; Conserv
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18 18 N-
155 AA; 15362 MW;
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N-ACYL DIGLYCERIDE (POTENTIAL).
1, 8AD6BE2132E849FA CRC64;
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Pred. No. 0.0041;
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L H., Mori T.,
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RESULT 13
SLYB_SALTY
ID SLYB_SALTY
ID SLYB_SALTY
AC Q53549;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Outer membrane lipoprotein slyB precursor
                                                                                                                                                                                                  DЬ
                                                                                                                                                                                                                                                              DЬ
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Best Local S
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ECOGENE: EG13409; SIJB.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane: Lipoprotein; Signal; Compl.
I 17 POTENTIAL.
I 18 15
F CONFILCT 98 18 N-ACYL DIGLYC
Q SEQUENCE 155 AA; 15602 MW; 543EBBA406;
                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                              119
                                                                                                                                                                                                     98 RNPDTGNSYSVEPVRTYQRYNKQER 122
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EMBL; AB007; BAA15402.1; --
EMBL; AB005587; AAG56630.1; --
EMBL; AP002558; BAB35773.1; --
                                                                                                                                                                                                                                                                                                                  13 IISVELVGCAQN-----FSRQE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch/).
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Hayashi T. Makino K. Ohnishi M. Kurokawa K., Ishii K., Yokoya Hayashi T. Makino K. Ohnishi M., Kurokawa K., Ishii K., Yokoya K., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T. Ida T. Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H., Ogasawara N., Yasunag Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and genomic comparison with a laboratory strain K-12.";

Ol57:H7 and genomic comparison with a laboratory strain K-12.";

-1- SUBCELLULAR LOCATION: Attached to the outer membrane by a li
                                                                                                                                                                       ---DDGNTIMVVQKQGNTRFSPGQR 140
                                                                                                                                                                                                                     LGGFLGNTVGGGTGRSLATAAGAVAGGVAGQGVQSAMNKTQGVEL--EIRK---
                                                                                                                                                                                                                                            VGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRW 97
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MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Posfai G., Hackett J., Klink S., Gregor J., Kirkpatrick H.A.,
Posfac J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=0157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=0157:H7 / E
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SIMILARITY: TO S.TYPHIMURIUM SLYB, H.INFLUENZAE PCP AND
Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                      12.6%;
                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                       Score 105.5; Di
Pred. No. 0.02;
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Tanaka M., Tobe T.,
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

OUTER membrane; Lipoprotein; Signal, Complete proteome.

SIGNAL 17 OUTER MEMBRANE LIPOPROTEIN
CHAIN 18 155 OUTER MEMBRANE LIPOPROTEIN
CHAIN 18 158 N-ACYL DIGLYCERIDE.

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Ludwig A., Tengel C., Bauer S. B. Goebel W.;
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"Complete genome sequence of a multiple enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
-!- SUBCELLULAR LOCATION: Attached to th
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MEDLINE-21534948; PubMed-11677609;
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GCVNNDSLSGDVYTASEAKQVQNVTYGTIVNVRPVQIQGGDDSNVIGAIGGAVLGGFLGN
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LIPID CONFLICT SEQUENCE

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N-ACYL DIGLYCERIDE.
CSLVAEFVF -> VAGRRVRI (IN

CRC64;

REF.

CHAIN

OUTER MEMBRANE

LIPOPROTEIN

Outer membrane; SIGNAL 1

PS00013; PROKAR_LIPOPROTEIN;

Signal;

Complete

proteome

EMBL; M18877; EMBL; U32832; PIR; B28543; B

В28543. AAA24938.1; AAC23228.1; use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (so or send an email to license@isb-sib.ch).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88115138; PubMed=2828309; Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.; Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.; Coloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalto protein from Haemophilus influenzae."; Bacteriol. 170:489-498(1988).
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influenzae Rd.";
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Query Match Best Local Similarity

Conservative

Score 102; DB 1; Length 155; Pred. No. 0.04; 1; Length 155; 9; Mismatches 23; Indels

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                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions. There are no restrictions on its entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                             **Borodovsky M., Rudd K.E., Koonin E.V.;
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**Nucleic Acids Res. 22:4756-4767(1994).**
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-81236546; PubMed=6265208;
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Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamoti T., Saito N.,
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MEDLINE-95075659; PubMed=7984428;
MEDLINE-95075659; Rudd K.E., Koonin J
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STRAIN-KI2 / MG1655;

MEDIJINE-97426617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glaspar J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Kose D.J., "The complete genome sequence of Escherichia coli K-12.";

21 [2]
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  AE000211; AAC74194.1; -. D90746; BAA35925.1; -. V00306; -; NOT_ANNOTATED_
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
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26; Conservative
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                                                                                                                                                                                      EcoGene, EG12444; yciJ.
Hypothetical protein, TRANSMEM 5
                                                     91 AGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQY 126
                                                                    73 GSVLGAVAGGVIGHQFGGGRGKDVATVVGÅLGGGYAGNQIQGSLQESD-----
                                                                                 31 GAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVK 90
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ical protein; Transmembrane; Complete proteome.
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25 25 POTENTIAL.
179 AA; 18920 MW; BA5EB0DB56D45609 CRC64;
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27.1%; Pred. No. 0.082;
"">Mismatches 32;
  2002, 10:56:29
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ALIGNMENTS

															
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Rickettsial common antigen precursor - Ricketsia rickettsii rickettsii C;Species: Rickettsia rickettsii C;Date: 16-Mar-1990 *sequence_revision 16-Ma C;Accession: A33971
R;Anderson, B.E.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Rickettsia conorii
C:Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
C:Accession: B33971
                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-159 <AND>
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J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a A;Reference number: A33971; MUID:89359171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Anderson, B.E.
J. Bacteriol, 17
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                                                                                                                                                                120 RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
                                                                                                                                                                                  120 QERRQOYCREFQQKAMIAGGKQEIYGTACRQPDGRWQVIS 159
                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-Mar-1990 #sequence_revision 16-Mar-1990
                                                                                                                                                                                                                       AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY-----
                                                                                                                                                                                                                                                     GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
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                                                                                                                                                                                                                                                                                     SKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG 64
                                                                                                                                                                                                                                                                                                                   SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY-----
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                    Renesto-Audiffren,
2001
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38.1%;
                                                                                          [imported] -
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                                                                                                                                                                                                                                                                                                                                                                          Score 293;
Pred. No. 1.
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Pred. No. 1.2e-18;
9; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                30-Sep-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rickettsia rickettsii
                          ₽.,
                                                                              Rickettsia conorii (strain Malish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:AAA26376.1; PID:g152458
                                                                                                                                                                                                                                                                                                                                                      DB 2; 1
1.2e-18;
nes 56;
                         Fournier,
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                                                                                                                                                                                                                                                                                                                                                                                  Length 159,
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                       P.E.;
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                    ٧.;
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                  Samson,
                                                                                7)
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R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabo J. Bacteriol. 169, 2385-2390, 1997 A;Title: Seguence analysis of the 17-kilodalton-antigen A;Reference number: A25972; MUID:87222152
                                                                                   C;Species: Rickettsia rickettsii
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change
                                                                                                                                                RESULT
A25972
                                                                                                                      17K antigen precursor - Rickettsia rickettsii
                                                                                                                                                                                                                                     Qy
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                                                                                                                                                                                                                                                                                                Qy
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A:Residues: 1-159 <AND>
A:Cross-references: GB:M28481; NID:g152459; PIDN:AAA26377.1; PID:g152460 C:Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                          Qγ
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A.Title: Comparative sequence analysis of A.Reference number: A33971; MUID:89359171
A.Rocession: C33971
A.Stathue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsial common antigen precursor - Rickettsia C;Species: Rickettsia typhi C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 C;Accession: C33971
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C33971
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J. Bacteriol. 171
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C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia A:Reference number: A97700; MUID:21442074; PMID:11557893 A:Accession: G97860 A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-159 <KUR>
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Best Local
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                                                                                                                                                                                                                              142 EIYGTACROPDGRWQVIS
                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                             27 NKQGTGTLLGGAGGALLGSQFGHGKGQLVGVGVGALLGAVLGGQIGASLDEQDRKLLELT
                                                                                                                                                                                                                                                                                                                                                          26
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                                                                                                                                                                                                  TTYGNACROPDGQWQVVN 159
                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                          SRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary
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                                                                                                                                                                                                                                                                                                                                                                                     55;
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39.9%;
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38.1%;
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Pred. No. 7e-1
%% Mismatches
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Pred. No. 1
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                                                         Tzianabos,
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.2e-18;
                                                                                                                                                                                                                                                     -RNSTGQYCREYTQTVVIGGKQQ
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                           gene from Rickettsia
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                                                      T.; McDade,
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                                                      J.E.;
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                        ricketts
                                                    Fu,
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                                                    Z.Y.
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RESULT 8
A13418
17K surface antigen precursor [imported] - Brucella melitensis (strain 16M)
C.Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: A13418
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Hille: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Accession: A13418
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A;Residues: 1-159 <AND>
A;Residues: 1-159 <AND>
A;Cross-references: GB:M16486; NID:g152467; PIDN:AAA26381.1; PID:g152468
C;Superfamily: rickettsial common antigen
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D83169
A; Molecule type: DNA
A; Residues: 1-131 < KUR>
A; Cross references: GB:AE008917; PIDN:AAL52516.1;
A; Experimental source: strain 16M
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A; Residues: 1-182 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: D83169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE004799; G
A;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNSTGQYCREYTQTVVIGGKQQKAYGDACRQPDEQWQVVN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLIGSKIGOSMDQODK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STVHDSSEKVVGYDVKYMLDGKAGQIRMERDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KLNQSLEKV------KAGQVTRWRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIAGTAIGAVVGGLLGNQIGGGTGKKIATVAGAVGGGYAGNKVQEGMQERDTYTTTETRC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVIS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.4%; Score 128.5; DB 2;
34.8%; Pred. No. 0.0004;
34.8%; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 284; DB 2; I
; Pred. No. 7.7e-18;
29; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AE004091; NID:g9949981; PIDN:AAG07206.1; GSPDB:GN00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
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                              PID:g17983328; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa (strain
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Larbig,
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K.; L
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C;Genetics:
A;Gene: BMEI1335
A;Map position: I
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B83514
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R;Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
                                                                                                                               DЬ
                                                                                                                                                                                                                                                              A;Gene: PA1053
C;Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-154 <STO>
A;Cross-references: GB:AE004537; GB:AE004091; NID:g9946960; PIDN:AAG04442.1;
                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337 A;Accession: B83514 A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein PA1053 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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Best Local
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Best Local
121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 KSVLWSGAGS-NAGDVTAAQPYQ-----VGSQNCRQYSHSFTIGGDQQTVRGTACRNPD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GKGSG--FPSLGGSSQKPETNLLASLGNGLFGNSASQLSAADRRKALEAEYRALEYSPAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 39; Conserv
                                                                                                                                _
                                                                                                                                                                                                                 Local Similarity
                                                                                              VGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL-----
                                                                                                                             MRKSALIVASFTAMALALGGCQSSLTGDTYSREEARTVQTVRMGTIQALRPVKIEGTKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGTACRQPD 152
STRAYVQQVDQGQIFR 136
                              --NQSLEKVKAGQVTR 96
                                                                                                                                                               MNRGCLQGSSLIIISVFLVGC----AQNFSRQE-----
                                                               IGSIAGAGVGGVAGSAVGGGKGSYVAAIIGAVAGGLLGAATEEGLTRTQGVEITVREDDG 120
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                                                                                                                                                                                                               13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.;
                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                               Score 116; DB 2; Pred. No. 0.0042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 125.5; DB 2
Pred. No. 0.00052;
B; Mismatches 43
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                               2;
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Larbig,
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outer membrane lipoprotein precursor - versinia en c; Species: versinia enterocolitica C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 C; Accession: S23787 R; Baeumler, A.J.; Hantke, K. J. Bacteriol. 174, 1029-1035, 1992 J. Bacteriol. 174, 1029-1035, 1992 A; Reference number: S23786; MUID:92121089 A; Accession: S23787

A; Status: preliminary

RESULT 10 S23787

Yersinia enterocolitica

10-Nov-1995

#text_change

29-Sep-1999

facilitates

ferrioxamine uptake

in

A;Residues: 1-155 <BAE> A;Cross-references: EMBL:X60448; NID:g48577; PIDN:CAA42977.1; PID:g48579 C;Superfamily: PAL cross-reacting lipoprotein

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δÃ В

35

10 SLIIISVELVGCAQN-----FSRQE-----

AVAÍAAVTĹTĠĊĀNNNTLSGDVĒŚĀSQĀKQVQTVTYGTLLSVRPVTIQGGDDNNVMĠĀIG 66

Matches

Local Similarity es 37; Conserv

Conservative

13.6%; Score 113.5; DB 24.7%; Pred. No. 0.007;

DB 2;

155;

Mismatches

Indels Length

51; Gaps

4

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A;Molecule Type: DNA
A;Residues: 1-257 <SIM
A;Residues: 1-257 <SIM
A;Cross references: GB:AE003872; GB:AE003849; NID:g9104975; PIDN:AAF82991.1; GSPDB:GN001
A;Experimental source: strain 9a5C
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Alvarenga, R.; A
A;Authors, Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn
Chado, M.A.; Madeira, M.B.N.; Matsukuma, A.P.; Krieger, J.E.; Kuramae, E.C.; Laigu
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Marcoca, E.C.; Myak; E.A.;
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Myak; E.A.;
A;Authors: da Silva, A.C.R.; da Silva, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; Brohn
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, M.C.; Moliveira, M.C.; Brohn
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, M.C.; Moliveira, M.C.; Brohn
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, M.C.; Moliveira, M.C.; Brohn
A;Authors: da Silva, M.C.; de Oliveira, M.C.; Brohn
A;Authors: da Silva, M.C.; de Oliveira, M.C.; Brohn
A;Reference number: adsilva, F.R.; da Silva, M.G.; M.C.; M.C.; Brohn
A;Reference number: adsilva, F.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2
A;Contents: annotation
lipA protein (imported) - Agrobacterium tumefaciens (strain C58, Dupont)
C.Species: Agrobacterium tumefaciens
C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C.Accession. ABZ696
C.Accession. BAZ696
C.Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wood, C.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelj
                                                                                                                                                                                                                                                                                  RESULT 12
AD2696
                                                                                                                                                                                                                                                                                                                                                                                       Ъ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rianonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein xF0178 [imported] - Xylella fastidiosa (strain
                                                                                                                                                                                                                                                                                                                    105 GTAIGALIGGLYGNQFGHGNGRKALTAAGAVAGGFIGNEV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ъ
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;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                       31 GAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 --NOSLEKVKAGOVTRWRNPDTGNSYSVEP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 GAVLGGFLGNTVGGGTGRSLATAAGAVAGGMAGOGVQGAMNRTDGVQLEVRKDDGTTILV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 112; DB 2; Length 257;
Pred. No. 0.016; Length 257;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              0;
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lipA protein – Rhizobium leguminosarum C;Species: Rhizobium leguminosarum

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RESULT 14
S58234
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                                                                                                                                                                                                                                               A; Map position: circular chromosome
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Best Local S
                                                                                                                                                                                                                                                           A;Cross:references: GB:AE007869; PIDN:AAK86781.1; PID:915155981; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <KUR>
                                                                                                                                                                                                                                                                                                                                              A;Reference number: A97359;
A;Accession: D97478
                                                                                                                                                                                                                                                                                                                                                                                                   lipA protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon) C.Species: Agrobacterium tumefaciens (strain C58, Cereon) C.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                       A; Title: Genome Sequence
                                                                                                                                                                                                                                                                                                                                                                                   A.; Liu, F.; Wollam, C.; Al.
Science 294, 2323-2328, 2001
                                                                                                                                                                                                             Matches
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                                         111 GAACRNDDGSW 121
                                                                   145 GTACROPDGRW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-142 <KUR>
A;Cross references: GB:AE008688; PIDN:AAL41986.1; PID:g17739358; GSPDB:GN00186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: circular chromosome
                                                                                         86 LEKVKAGQVTRWRNPDT-GNSYSVEPVRTYORYNKOERROOYCREFQOKAMIAGOKOEIY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Title: The Genome of the Natural Genetic Engineer Agrobacterium
A:Reference number: AB2577; PMID:11743193
                                                                                                                                           30 VGAATGAVVGGVAGQLFGKGSGRVANAIGGAVLGGLIGSKIGQSMDQQDKIKL----NQS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 294, 2317-2323, :
A;Authors: Yoo, H.; Tao,
ster, E.W.
                                                                                                                    2 LSACTTTGTRPAGGSLEGR-SAQPSTPFLANLOGGIVG-KSGVELDRGDOTKALEAEYKA
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                                                                                     LETAPVGTPVIWTGDDVKGQVVANAP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 SILCVSM-LSAC-----TTTGTRPAG--GSLFGR-SAQPSTPFLANLQGGIVG-K 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SLIIISVELVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSK 69
                                                                                                                                                                                                          1 Similarity
36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVELDRGDQTKALEAEYKALETAPVGTPVIWTGDDVKGQVVANAP---YQVGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGOSMDQQDKIKL----NOSLEKVKAGQVTRWRNPDT-GNSYSVEPVRTYQRYNKQERRQ 124
                                                                                                                                                                                                                                                                                                                                                                   Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.;
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 27.2
41; Conservative
                                                                                                                                                                                  13.3%; Score 111; DB 2; I
27.5%; Pred. No. 0.0093;
tive 18; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                of the Plant Pathogen and Biotechnology Agent Agrobacterium
59; PMID:11743194
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27.2%; Pred
21;
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5, Υ.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 111.5; DB 2;
Pred. No. 0.0096;
21; Mismatches 60;
                                                                 -YQVGN-----QNCRQYSHTLTVDGRDTRVR 110
                                                                                                                                                                                                     Length 125;
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RESULT 15
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hypothetical protein CC3073 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Accession: 687629
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koloc
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87629
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Search completed: October 27, 2002, 10:58:39 Job time: 12.6321 secs
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A; Residues: 1-232 <STO>
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A;Molecule type: DNA
A;Residues: 1-139 <YEO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005673; NID:g13424723; PIDN:AAK25035.1; GSPDB:GN00148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 13.2%; Score 110.5; DB 2; Length 232; Best Local Similarity 26.9%; Pred. No. 0.02;
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                                                                                                                                                                                                                   141 AAQEVGGIYKSGGFRYAQTVQAAPLVKIEKKMVTR----STVNL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 QNCRQYTHTLTVDGKDTVARGAACRNDDGSW 136
                                                                                                                                                                                                                                                                                                                        81 VVGCKASGKKQEVGAVVGALLGAAAGSNLAKNDQGTGTAIGAVVGAGAGSLIGCKMQKSD 140
                                                                                                                                                                                                                                                                                                                                                       75 DQQDKIKLNQS------LEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 SLITISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSK 69
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                                                                                                     RAAASTRGERLGAVDSGTTFQĄLG---RTKDGKWILVGQD 217
                                                                                                                                                             RRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTE 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   56; Indels
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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836
1 MNRGCLQGSSLIII
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Match
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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US-09-053-408-8
US-09-067-351-2
US-08-360-490-2
US-08-360-490-2
US-08-360-490-2
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US-08-440-519-12
US-08-440-519-12
US-08-220-151-6
US-08-220-151-6
US-08-220-151-6
US-08-231-188-6
US-09-232-468A-2
US-08-375-709-7
US-09-067-351-1
US-09-360-447-700-2
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Result

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Query Match Best Local Similarity Matches 25; Conservat	US-08-556-978B-19 US-08-556-978B-19 US-08-556-978B-19 Sequence 19, Application US/08556 Patent No. 6268169 GENERAL INFORMATION: NOVEL REC TITLE OF INVENTION: SPIDER SI APPLICANT: FAHNESTOCK, STEPHE TITLE OF INVENTION: SPIDER SI COUNTER OF SEQUENCES: 107 CORRESPONDENCE ADDRESS: ADDRESSE: E. I. DU PONT DE STREET: 1007 MARKET STREET COUNTRY: UNITED STATES OF A ZIP: DELAWARE COMPUTER EADDABLE FORM: MEDIUM TYPE: DISKETTE, 3.50 COMPUTER READABLE FORM: MEDIUM TYPE: MICROSOFT WORD FO COMPUTER APPLICATION UMBER: US/08/5 FILING DATE: MICROSOFT WORD FO CURRENT APPLICATION UMBER: US/08/5 FILING DATE: JUNE 15, 1993 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 08/077, ETLING DATE: JUNE 15, 1993 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 33,692 REFERENCE/DOCKET NUMBER: 33,692 REFERENCE/DOCKET NUMBER: 33,692 REFERENCE/DOCKET NUMBER: 37,016/4 INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 651 amino acids STRANDEDNESS: unknown MOLECULE TYPE: protein US-08-556-978B-19		28 73 8.7 29 73 8.7 30 73 8.7 31 72.5 8.7 32 72.5 8.7 34 72.5 8.7 35 72.5 8.7 36 72.5 8.7 37 72.5 8.7 38 72.5 8.7 39 72.5 8.7 30 72.5 8.7 31 72.5 8.7 32 72.5 8.7 33 72.5 8.7 34 72.5 8.6 40 72 8.6 41 72 8.6 42 72 8.6 43 72 8.6 44 72 8.6 45 72 8.6
9.7%; Score 81.5; DB 4; Length 36.8%; Pred. No. 0.8; ative 3; Mismatches 17; Indel	AHNESTOCK, STEPHEN F. AHNESTOCK, STEPHEN F. NATION: NOVEL RECOMBINANTLY PRODUCED NATION: SPIDER SILK ANALOGS VENCES: 107 E ADDRESS: E. I. DU PONT DE NEMCURS AND COMPANY 107 MARKET STREET INITON AWARE NITED STATES OF AMERICA BLE FORM: DISKETTE, 3.50 INCH ITEM COMPATIBLE FYSTEM: MICROSOFT WINDOWS 95 MICROSOFT WORD FOR WINDOWS 95 MICROSOFT WINDOWS 95 MICR	ALIGNMENTS	254 4 US-09-128-450-26 254 4 US-09-823-494-26 606 4 US-09-247-806-6 479 4 US-09-177-349-3 547 1 US-08-340-203A-3 547 2 US-08-452-567-3 547 2 US-08-452-427-3 547 2 US-08-678-039A-40 101 4 US-08-556-978B-22 101 4 US-08-556-978B-62 101 4 US-08-556-978B-63 101 4 US-08-556-978B-63 101 4 US-08-556-978B-63 101 4 US-09-247-806-5 101 4 US-09-247-806-7 604 4 US-08-556-978B-63
h 651; ls 23; Gaps 2;			Sequence 26, Appli Sequence 26, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 20, Appl Sequence 22, Appli Sequence 62, Appli Sequence 5, Appli Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 63, Appli Sequence 63, Appli Sequence 7, Appli Sequence 63, Appli Sequence 63, Appli Sequence 63, Appli Sequence 63, Appli

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62

US-09-247-806-1

GENERAL

INFORMATION:

Sequence 1, Application US/09247806 Patent No. 6280747

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551 LGGQGAGQ 558

65 LIGSKIGO 72

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APPLICANT: CARSON, Jean-Claude
APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Claude
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
FILE REFERENCE: 6388-0365-0
CURRENT APPLICATION NUMBER: US/09/247,806
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER FILING DATE: 1999-02-11
EARLIER FILING DATE: 1998-02-11
SOFTMARE: Patentin Ver. 2.1
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lewis, Randolph V.
APPLICANT: YU, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COMPANY OF TRANSFORMED CELL
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ZIP: 220.4.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 QGAGAAAAAAVGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
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Pred. No. 0.8;
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                          Query Match
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MOLECULE TYPE: protein
US-08-425-069-2
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
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                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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NAME: MUTPHY Jr., Gerald
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 36.8%;
Matches 25; Conservative
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APPLICANT: Lewis, Randolph V.

APPLICANT: Liewis, Randolph V.

APPLICANT: Yu, Ming

APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK

TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL

TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
FILING DATE: 04-OCT
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.ZIP: 22046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 301 No. 598
CITY: Falls Church
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TELECOMMUNICATION INFORMATION: 1447-106P
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8000
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                                                                                                                                                   amino acid
                                                                                                     TYPE:
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                                                                                                                                                                                                                                                                       (703) 241-2848
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01 No. 5989894th Washington Street
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MBER: 28,977
        9.78;
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Score 81.5;
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Pred. No. 0.91;
3; Mismatches
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RESULT 3 US-08-425-069-2

Sequence 2, Application US/08425069 Patent No. 5728810

GENERAL INFORMATION:

ATTORNEY/AGENT INFORMATION:

DB 2;

Length 718;

APPLICATION NUMBER: US/08 FILING DATE: 19-APR-1995

US/08/425,069

22046

В

551 LGGQGAGQ 558

65 LIGSKIGO 72

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28 QEVGAATGAVVG----GVAGQ------

; ORGANISM: Nephila clavipes US-09-247-806-1

SEQ ID NO 1 LENGTH: 651 TYPE: PRT

Best Local Similarity 36.8 Matches 25; Conservative

9.78;

Query Match

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                                                                                                           Matches
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                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN F
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 1174414
                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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CITY: Palo Alto
551 LGGQGAGQ 558
                                                     491 QGAGAAAAAAVGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
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                            65 LIGSKIGQ 72
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                                                                                                                       Local
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                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                             single
                                                                                                                       9.7%;
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                                                                                                                       Score 81.5;
Pred. No. 0
                                                                                                           Mismatches
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                                                                               ----LFGKGSGRVAMAIGGAVLGG 64
                                                                                                                       .96;
                                                                                                                                   DB 3;
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                                                                                                                                  Length 747;
                                                                                                          Indels
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US-09-553-498-8
; Sequence 8, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 13, Application US/07803633A Patent No. 5369025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
APPLICANT: Schaeffner, Joerg
APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: Process for the production of naturally folded and secreted
FILE REFERENCE: Case 20379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07, FILING DATE: 19911210 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Murphy Jr
                                                                           APPLICANT: Ambrosius, Dorotl
APPLICANT: Rudolph, Rainer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: RECOMBINANT
TITLE OF INVENTION: PROTECTION
NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                                                                                     797
                                                                                                                                                                                                                                                                                  121 ERRQQYCRE-FQQKAMIAGQKQ 141
                                                                                                                                                                                                                                                                                                                                                                                                   688 FMNGLAELFNGMGQVGQAIGKVVVVGAAGAIVSTISGVSAFMSNPFGALAIGLIIIAGLVA 747
                                                                                                                                                                                                                                                                                                                             748 AFL--AYRYVNKLKSNPMKALYPMTTEVLKA-QATRELHGEESDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                        17 FLVGCAQNFSRQ-EVGAATGAVVGGVAGQLFGKGSGRV-----AMAIGGAVLGGLIG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 301 No. 5369025th Washington Street CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                     ERKLEEAREMIKYMALVSAEER 818
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                                                                                                  Dorothee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.3%; Score 78; DB 1; 25.4%; Pred. No. 2.9;
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CURRENT APPLICATION NUMBER: US/09/553,498 CURRENT FILING DATE: 2000-04-20 PRIOR APPLICATION NUMBER: EP99107412.1 NUMBER OF SEQ ID NOS. 10

SEQ ID NOS: 10

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CLONE: 251-2
                                                                                                        TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 255
TYPE: PAT
ORGANISM: E. COll
US-09-553-498-8
                   IMMEDIATE SOURCE:
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                                                                                              SEQUENCE CHARACTERISTICS
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Patent No.
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                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0511 US
                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                   TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                   STREET: J. LTO
CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                        LENGTH:
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                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Baughn, Mariah
                                                                                                                                                                                                                                                                                                                                                                                                                                              TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 SL----TISSMEAEDAATYYCOOWSSNPLTFGAGTKLELKRAAAEO-----KLISEE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 SVEPVRTYQRYNKQERRQQYCREFQQKAMI--AGQKQEIYGTACRQPDGRWQVISTE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 MSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARFSGSGSGTSY 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 LOMTSLRSEDTAMYYCARDYGAY-WGQGTTVTVSSGGGGSGGGGGGGGGGGGGGDIELTQSPAI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LOGSSLIIISVELVGCAONESROEVGAATGAVV----GGVAGOLFGKGSGRVAMAIGGAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 20.9 es 37; Conservative
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5. 5994081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                            551 amino acids
                    CERANOT02
                                             linear
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                                                         single
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US-09-360-490-2
"-quence 2, Ar
                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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                                                                                                                                         TOPOLOGY: line
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LENGTH: 551 amino acids
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54 GASFGSRSLYNLGGAKRVSLNGCGSSCRSGFGGRASNGFGVNSG---FGYGGGVGGGFSG 110
                                                                                                           MMEDIA: KELLIBRARY: KELLIBRARY: 2029060
                                                                                                                                                                                                                                     NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0511 US
TELECOMMUNICATION INFORMATION:
                    8 GSSLIIISVELVGCAQNESRQEVGAATGAVVGGVAGQLEGKGSGRVAMAIGGAVLGGLIG 67
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                Local
                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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                                                                                                                                                                    STRANDEDNESS: Si
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MEDIUM TYPE: Floppy
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 PORTER
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baughn, Mariah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 EQQNK 175
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                                                            Similarity 22.4
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 SK-----IGOSMDQQDKIKLNQSLEKYKAGQVTRWRNPDTGNSYSVEPVRTY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54 GASFGSRSLYNLGGAKRVSLNGCGSSCRSGFGGRASNGFGVNSG---FGYGGGVGGGFSG 110
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                                                                                                                                                                single
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NO: 2:
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                                                                      9.2%;
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                                                             28;
                                                   Score 77; DB 4;
Pred. No. 2;
28; Mismatches 5
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Pred. No. 7
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                                                                       Length 551;
                                                  Indels
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APPLICANT: Hall, Land APPLICANT: Ren, Dejian
APPLICANT: Ren, Dejian
APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
TITLE OF INVENTION: Calcium Channel Subunit
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ANDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
RESULT 11
US-08-95-590-2
; Sequence 2, Application US/08895590
; Patent No. 6207410
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Best Local S
Matches 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel-
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       2508
                                                                                                                                                                        2448 SPPIPDNRLRRVATVTTTNNNNKSQVSQNNSSSLNVRANANSQMNMSPTGQPVQQQSPLR 2507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: McGowan, Malcolm M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19
CLASSIFICATION:
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                                                                                                      GQGNQTYSS 2516
                                                                                                                                      GOKQEIYGT 146
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                                                                                                                                                                                                      -----QSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIA 137
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GY: linear
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ilarity 24.8%; Pred. No. 17;
Conservative 18; Mismatches
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US-07-910-760-12
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                                                                                                                        Sequence 12, Application US/U7910
Patent No. 5683864
GENERAL INFORMATION:
APPLICANT: Houghton, Michael
APPLICANT: Choo, Qui-Lim
APPLICANT: Kuo, George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                      TITLE OF INVENTION: CombinatifITLE OF INVENTION: Antigens NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       2508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an
NUMBER OF SEQUENCES: 101
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2389 IGSSNGSIFGGSAGGLGGAGSGGVG-GLGGSSSIRNAFGGSGSGPSSLSPQHQPYSGTLN 2447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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TOPOLOGY: linear
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                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                       GQGNQTYSS
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SEE: Chiron Corporation: P.O. Box 8097 (Int. Emeryville
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SYSTEM: PC-DOS/MS-DOS
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Antigens for Use
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                 (Int. Prop. R-440)
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Pred. No. 17;
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e in Immunoassays f
                                                                                           Immunoassays for Anti-HCV Antibodies
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        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 1021 minno ac
TYPE: amino acid
; TOPOLOGY: Iinear
MOLECULE TYPE: protein
US-07-910-780-12
                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                 APPLICANT: Choo, Qui-Lim
APPLICANT: Kuo, George
TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
NUMBER OF SEQUENCES: 12
NUMBER OF SEQUENCES: 12
                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: P.O. Box 8097 (Int.)
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: Blackburn Esq., Robert REGISTRATION NUMBER: 30,447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2702
                                                                                                                 COUNTRY:
                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                  970 RRPEGRTWAQPGYPWPLYGNE 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                  852 PAILSPGALYVGVVCAAILRRHYGPGEGAVQWMNRLIAFASRGNHVSPGNSSTNPKPQKK 911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  792 GAATAFVGAGLAGAAIGSVGLGKVLIDILAGYGAGVAGALVAFKIMSGEVPSTEDLVNLL 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 QSL-----EKYKAGQ-VTRWRN-----PDTGNSYSVEPVRTYQRYNKQ 120
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                                                                                                   RY: U.S.A.
94662-8097
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MEDIUM TYPE: Floppy disk
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Choo, Qui-Lim
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US/08/440,519
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20.9%; Pred. No.
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US-08-440-549-12
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                           PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/910,760

FILING DATE: 07-JUL-1992
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                  ATTORNEY/AGENT INFORMATION
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                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: P.O. Box 8097 (Int.)
                                                                                                                                                                                                                                                          TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
                                                                                                                                                                                                                                                                                                               APPLICANT: Houghton, Michael APPLICANT: Choo, Qui-Lim APPLICANT: Kuo, George
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Best Local (
                                                                       FILING DATE: 12
CLASSIFICATION:
                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 94662-8097
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CITY: Emeryville
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APPLICATION NUMBER: US 07/910,760
ETLING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Blackburn Esq., Robert P.
REGISTRATION NUMBER: 30,447
TELEPHONE: COLORET NUMBER: 0101.002
TELEPHONE: (510) 601-2702
TELEPHONE: (510) 601-2702
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                                                                                                                                                                                                                                                                                                                                                                                                                                              970 RRPEGRTWAQPGYPWPLYGNE 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                852 PAILSPGALVVGVVCAAILRRHVGPGEGAVOWMNRLIAFASRGNHVSPGNSSTNPKPOKK 911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
Blackburn Esq., Robert p.
                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                              2, Application US/08440549
6312889
                                                                                                                                                                                                                      CA
                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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GY: linear
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                                                                                   12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1021 amino acids
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NO: 12:
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                                                                                         US/08/440,549
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20.9%; Pred. No. 6;
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RESULT 15
US-08-190-199A-65
US-08-190-199A-65; Sequence 65, Application US/08190199A
; Patent No. 5830663
; GENERAL INFORMATION:
CMMILETON, Michael J.
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-440-549-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (510) 655-35 INFORMATION FOR SEQ ID NO:
                    INFORMATION FOR SEQ ID NO: 65:
                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9212419.7
FILING DATE: 11-JUN-1992
                                                                                                                                                            FILING DALL:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/GB92/01483
                                                      FILING DATE: 11-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 13-JUL-1994
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1021 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2702
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                  APPLICATION NUMBER: PCT/
FILING DATE: 10-AUG-1992
                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
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                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WINTER, Gregory P.
VENTION: TREATMENT OF CELL POPULATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOROCHOV, Guy
                                                                                                                                                                                                                                                                                      Microsoft Word
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                                      10-AUG-1991
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                                                                                                                                                                                                                                                                                          Query Match 9.0%; Score 75; DB 2; Best Local Similarity 19.6%; Pred. No. 1.1; Matches 31; Conservative 27; Mismatches 7
201 L----TISSMEAEDAATYYCQQWSSNPLTFGAGTKLEL 234
                                                                                                141 SASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARFSGSGSGTSYS 200
                                                108 VEPVRTYQRYNKQERRQQYCREFQQKAMI -- AGQKQEI 143
                                                                                                                                                 63 GGLIGSKIGQSMDQQDKIK-LN-------QSLEKVKAGQVTRWRNPDTGNSYS 107
                                                                                                                                                                                                 81 LQMTSLRSEDTAMYYCARDYGAYWGQGTLVTVSAGGGGSGGGGGGGGGGGQIVLTQSPAIM 140
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                               6 LQGSSLIIISVFLVGCAQNFSR---QEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL 62
                                                                                                                                                                                                                                                                                               76;
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Search completed: October 27, 2002, 11:00:27 Job time: 10.3938 secs

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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB DB
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Match
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Gapop 10.0 , Gapext 0.5
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                    100.0
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SIDSI/gcgdata/geneseq/geneseqp-embl/AA198.DAT:

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Listing first 45 summaries
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                Piscirickettsia sa OspA antigen amino Optimised OspA pro C17E2 OspA constru OspA B-cell epitop Moraxella catarrha Porphorymonas ging PBOMP-2 gene prod.
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Corynebacterium gl	AAB76750	22	346	9.1	76	45
C glutamicum prote	AAG92057	22	346	9.1	76	44
Corynebacterium gl	AAB76751	22	324		76	43
Merozite surface a	AAR05878	11	300		76	42
Drosophila melanog	ABB61076	22	2516		76.5	41
Invertebrate calci	AAW01884	17	2516	9.2	76.5	40
Neuronal invertebr	AAW01875	17	2516	9.2	76.5	39
Pseudomonas aerugi	AAU36520	22	514		76.5	38
Drosophila melanog	ABB61254	22	1251	9.2	. 77	37
Human keratin KERT	AAY52398	21	551		77	36
Antigenic protein	AAP90064	10	429	9.2	77	35
Drosophila melanog	ABB69847	22	147		77	34
Novel human diagno	ABG28648	22	900		77.5	33
E. carotovora PelB	AAY72020	22	255			32
Expression plasmid	AAB70769	22	255	9.3	77.5	31
	AAB74199	22	255			30
E. coli expression	AAB11398	21	255	9.3	77.5	29
Marek's Disease Vi	AAR30169	14	865		78	28
Nephila clavipes s	AAW27178	18	646	9.3	78	27
Human prostate can	AAB56803	21	618		79	26
Neisseria meningit	AAY75098	21	2599		80	25
Novel human diagno	ABG06301	22	2017		80	24
H. pylori ORF 01cp	AAY11028	19	116	9.6	80	23
Drosophila melanog	ABB70501	22	542	•		22
Drosophila melanog	ABB65791	22	542			21
Drosophila melanog	ABB65790	22	542		80.5	20
Human polypeptide	AAM40157	22	302			19
Human polypeptide	AAM41943	22	102	•	•	18
N. clavipes spider	AAY59070	21	718	9.7	•	17
	AAW53346	19	718	9.7	•	16
S	AAR14308	12	718	9.7		15
ij	AAY40097	20	651	9.7	81.5	14
	ABB58019	22	666	9.8	82	13
Drosophila melanog	ABB66232	22	2309	10.3	86.5	12

ALIGNMENTS

RESULT 1 AAG78025

Piscirickettsia salmonis polypeptide P10.6

15-JAN-2002 (first entry)

AAG78025;

AAG78025 standard; Protein;

162

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Simard Burzio Piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial; septicaemia; SRS; surface antigen; vaccine; antibacterial; fish; ATCC VR-1361. WPI; 2001-639050/73. N-PSDB; AAH79040. 11-MAR-2000; 2000GB-0005838. 01-JUL-2000; 2000GB-0016080. 01-JUL-2000; 2000GB-0016082. 29-JUL-2000; 2000GB-0018599. 12-MAR-2001; 2001WO-GB01055 20-SEP-2001. WO200168865-A2. Piscirickettsia (AQUA-) AQUA HEALTH EURO LTD ŗz Brouwers H, salmonis. Jones s Griffiths Ś Valenzuela P;

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RESULT
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ID AAA
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                     Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                               (KAYW/) KAY W W.
(BURI/) BURIAN J.
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                                                                                                                                                                                                                                                                                                                          17-SEP-1999;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB81126 standard; Protein; 162 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to protect fish against P. salmonis which causes piscirickettsiosis, also known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Fig 5; 25pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids encoding an amino acid sequence homologous to the surface antigen present on Piscirickettsia salmonis are useful to protect fish against piscirickettsiosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                    2001-316844/34.
DB; AAF86246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERROQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERROOYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ 120
                                                                                                                                                                                                               KUZYK M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162;
                                                                                                                                                                        Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                 99CA-2281913
                                                                                                                                                                                                                                                                                                                    99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fish; Piscirickettsia salmonis; rickettsial pathogen; salmonid rickettsial septicaemia; rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         /label= B_cell_epitope
                                                                                                                                                                        Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 836; DB 22;
Pred. No. 3.2e-80;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162;
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DЬ
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RESULT 3
AAB81127
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Method for protecting poikilothermic fish against salmonid rickettsepticaemia and other rickettsial diseases comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                WPI;
                                                                                                                                                    (KAYW/)
(BURI/)
                                                                                                           Kay WW,
                                                                                                                                                                                           17-SEP-1999;
                                                                                                                                      (KUZY/)
                                                                                                                                                                                                                           17-SEP-1999;
                                                                                                                                                                                                                                                      17-MAR-2001
                                                                                                                                                                                                                                                                                   CA2281913-A1
                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                            Piscirickettsia salmonis Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                 Poikilothermic fish; Piscirickettsia salmonis; rickettsial pavaccine; OspA; salmonid rickettsial septicaemia; rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Optimised OspA protein 17E2 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB81127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB81127 standard; Protein; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a OspA in the form of a vaccine. The method is used for protecting animals, P. salmonis. The method is used for protecting animals, P. salmonis. The method is also useful for protecting against salmonid sequence represents P. salmonid (SRS) and other rickettsial diseases. The present N-terminal fusion partner is used in a vaccine to create an anti-OspA antihody response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 2B;
                                                              2001-316844/34
DB; AAF86247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERROQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERRQQYCREFQOKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                 KAY W W.
BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNRGCLOGSSLITISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGA
                                                                                                                                   KUZYK M A.
                                                                                                    Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                         99CA-2281913
                                                                                                                                                                                                                      99CA-2281913
                                                                                                                                                                                                                                                                                                      /label= B_cell_epitope
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
109..128
                                                                                                   Kuzyk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                    MA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 836; DB 22;
Pred. No. 3.2e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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              rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162;
                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
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RESULT 4
AAB81128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Pisciriokettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The presence represents optimised P. salmonis OspA protein 17E2. The DNA encoding OspA 17E2 (AAF86247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                             C17E2
                                                                                                                                                                                                                                                                  SRS;
                                                                                                                                                                                                                                                                            Poikilothermic fish; Pis vaccine; OspA; salmonid
                                                                                                                     CA2281913-A1
                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                            Piscirickettsia
                                                                                                                                                                                                                                                                                                                                    11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                        AAB81128;
                                                                                                                                                                                                                                                                                                                                                                             AAB81128 standard;
                                                                          17-SEP-1999;
                                                                                                                                                                           Region
                                                                                                                                                                                                Region
         (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                   122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                 RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OspA construct with N-terminal fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     containing
                                                                                                                                                                                                                                                                 OspA; sal
2; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,
                                                                          99CA-2281913
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٠٠
                                                                                                                                                                          /label= Undefined_N-terminal_fusion_partner
96..256
                                                                                                                                                                                                                                            salmonis
                                                                                                                                                                 /label- C17E2_OspA
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                  construct.
                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.5%;
                                                                                                                                                                                                                                                                           Piscirickettsia salmonis; rickettsial pathogen; nid rickettsial septicaemia; rickettsial disease
                                                                                                                                           "Product of OspA gene optimised Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OspA protein
                                                                                                                                                                                                                                                                                                                                                                             256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 815; DB 22;
Pred. No. 5.1e-78;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                             partner
                                                                                                                                                                                                                                                                                                                                                                                                                                   161
                                                                                                                                                                                                                                                                                                                                                                                                                                                         162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 161;
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                                                                                                                                                       for expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                             disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                animals,
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Matches 158; Query Match

Local

Similarity

97.5%; 98.8%;

Score 815; DB 22; Pred. No. 9.3e-78;

Length Indels

Conservative

۳.

Mismatches

0;

Gaps

0;

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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a P. salmonis OspA construct optimised for expression in Escherichia coli, fused to an undefined N-terminal fusion partner. The fusion protein is used in a vaccine to create an anti-OspA antibody response.
Sequence
                                                                                                                                                                                                                                                                                                                                   Example 4; Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                               vaccine
                                                                                                                                                                                                                                                                                                                                                                                                      septicaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-316844/34.
                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                               containing the OspA protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF86248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burian
                                                                                                                                                                                                                                                                                                                                                                             protecting poikilothermic fish against salmonid rickettsial a and other rickettsial diseases comprises administering a ntaining the OspA protein of Piscirickettsia salmonis
256 AA;
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QΥ
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                   (KAYW/)
(BURI/)
(KUZY/)
                                                                                   CA2281913-A1
                                                                                                Piscirickettsia
                                                                                                             SRS; antibody
                                                                                                                  Poikilothermic vaccine; OspA;
                                                                                                                                      OspA B-cell
                                                                                                                                                                            AAB81130
                                            17-SEP-1999;
                                                         17-SEP-1999;
                                                                      17-MAR-2001.
                                                                                                                                                                                                             217
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       , WW
                                                                                                                                                                                                           RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                              RGCLQGSSLITISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                   KAY W W.
BURIAN J.
KUZYK M A.
                                                                                                                                                                            standard;
       Burian
                                                                                                                                      epitope
                                                                                                                                                   (first entry)
                                                                                                                   fish; Piscirickettsia salmonis; rickettsial pathogen; salmonid rickettsial septicaemia; rickettsial disease
                                             99CA-2281913
                                                         99CA-2281913
                                                                                                                                                                            Peptide;
                                                                                                                                     peptide
                                                                                                                                      #2
                                                                                                                                                                            20
                                                                                                                                                                            Å
                                                                                                                                                                                                                                                               156
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2001-316844/34.

This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, piscirickettsia salmonis. The method comprises administering an immunogenic amount of a OspA in the form of a vaccine. The method is used for protecting animals particularly polkilothermic fish, against the bacterial pathogen animals. The method is also useful for protecting animals, rickettsial septicaemia (SRS) and other rickettsial diseases. The present san immunogenic epitope of the p. salmonis OspA protectin. The peptide is used to raise rabbit anti-OspA antibodies.

Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -

Page 17; 35pp; English.

δ

Matches

Y Match Tocal Similarity

13.48;

Score 112; DB 22; Pred. No. 4.9e-05;

Length 20; Indels

0; Gaps

0;

Conservative

0,

Mismatches

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The present sequence is that of BASB113 protein from Moraxella catarrhalis strain Mc2931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adults. The invention provides BASB113 polypeptides, and polynucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB113 composition comprising a BASB113 polypeptide, an immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                   Claim 1; Page 67; 86pp; English.
                                                                                                          New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterium, infections such as otitis media and pneumonia
                                                                                                                                                                                                           Thonnard J;
                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                   23-JUN-2000; 2000WO-EP05851.
                                                                                                                                                                                                                                                                                             04-JAN-2001.
                                                                                                                                                                                                                                                    25-JUN-1999;
                                                                                                                                                                                                                                                                                                                   W0200100836-A1
                                                                                                                                                                                                                                                                                                                                    Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                           BASB311; infection; otitis media; pneumonia; therapy; diagnosis; antibacterial; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                   Moraxella catarrhalis BASB113 protein
                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB20105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB20105 standard; Protein; 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 PVRTYQRYNKQERRQQYCRE 129
                                                                                                                                                                        2001-112458/12.
)B; AAF30043.
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AAY34318 to the

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RESULT 7
AAY34487
AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AA: AAX34583. AAX91802 to AAX91989 represent PCR primers used in th
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                                              Claim 1; Page 469; 588pp; English
                                                                          gingivitis
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                                                                                                                                                                                  22-MAY-1998;
29-JUL-1998;
                                                                                                                                                                                                               30-JAN-1998;
10-MAR-1998;
09-APR-1998;
23-APR-1998;
                                                                                                                                                                                                                                                      04-AUG-1998;
10-DEC-1997;
31-DEC-1997;
                                                                                                                                      Ross
                                                                                                                                               Agius
                                                                                                                                                             (CSLC-) CSL LTD.
                                                                                                                                                                                                        05-MAY-1998;
                                                                                                                                                                                                                                                                                            10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                    Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                                            Porphorymonas gingivalis protein PG3.
                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                       25-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY34487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY34487 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment of a BASB113 polypeptide, or a polypeptide having at least 85% amino acid sequence identity to BASB113, or comprising a polypuciacide encoding such a polypeptide. A claimed method of polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection comprises at least polypeptides also have utility in raising specific BASB113 polypeptides. BASB113 polypeptides also have utility in raising specific antibodies,
                                                                                                    1999-385613/32.
DB; AAX91705.
                                                                                                                               BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKTGRDAILGAAVGAAAGAYMERQAK----QIEQQMQGTGŸTVTHDTDTGN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVVLLASSMALAGCANTGT---TGNGTGFGGANVNKAVIGAVAGAL---GGTAISKATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 104
                                                                        Porphorymonas gingivalis peptides
                                                                                                                                Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                     monas gingivalis; PG; periodontal disease;
antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
36; Conserv
                                                                                                                                                                                                98AU-0002264
98AU-0002911
98AU-0003128
98AU-0003338
                                                                                                                                                                                                                                      98AU-0005028.
97AU-0000839.
97AU-0001182.
98AU-0001546.
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                                                                                                                              Hocking D
Webb EA;
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                                                                                                                                      DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches
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Pred. No. 0.
                                                                                                                                Margetts MB,
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0.0028;
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                                                                      preventing
                                                                                                                               Patterson
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Best Local
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31-DEC-1997;
30-JAN-1998;
10-MAR-1998;
09-APR-1998;
23-APR-1998;
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22-MAY-1998;
29-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAX91802 to AAX91899 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can
                                                                                                                                                                    Ross
                                                                                                                                                                                                                                                                                                                            04-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphorymonas
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                                                                              Claim 1; Page 325-326;
                                                                                                                                   N-PSDB;
                                                                                                                                                                               Agius
                                                                                                                                                                                                                                                                                                                                                 10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine;
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                                                                                                              Antigenic Porphorymonas
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                                                                                                                                                                                                    (CSLC-) CSL
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                                                                                                                                                                  BC,
                                                                                                                                     1999-385613/32
DB; AAX91580.
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antigenic.
                                                                                                                                                                    Rothel
                                                                                                                                                                  Barr IG,
Rothel LJ,
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                                                                                                                                                                                                     LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                 gingivalis
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98AU-0002264.
98AU-0002911.
98AU-0003128.
98AU-0003338.
98AU-0003654.
98AU-0004917.
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97AU-0001182.
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                                                                                                                                                                  Hocking DN
Webb EA;
                                                                           588pp;
                                                                                                            gingivalis peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                PG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105.5; DB, 
Pred. No. 0.0051; 
2; Mismatches 3
                                                                                                                                                                             DM,
                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                periodontal disease;
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                                                                                                                                                                               MB,
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                                                                                                              preventing
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30 VGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIĞSKIGQSMDQQDKIKL

Query Match Best Local S Matches 21

. Similarity 21; Conser

Conservative

9

Score 102; DB 11; Pred. No. 0.0074; 9; Mismatches 23;

Length 154;

Indels

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Gaps

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12.2%;

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RESULT 9
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                                             The PBOMP proteins were isolated from a PBOMP-enriched insoluble cell wall fraction from physically disrupted cells of H. influenzae and then solubilising the PBOMP from the cell wall fraction by heating in the presence of a detergent or digesting the cell wall fraction with lysozyme, opt. in the presence of a detergent. The genes encoding the PBOMP proteins were isolated by screening a DNA library with an oligonucleotide probe based on the amino acid sequence of the PBOMP protein, or using antibodies to PBOMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Outer membrane proteins; PBOMP-2
Praxis Biologics Outer Membrane
     Sequence
                                                                                                                                                                                                                                                                                                                  diagnosis.
                                                                                                                                                                                                                                                                                                                                      Outer membrane protein ep.
the prodn. of antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-115815/15
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21-AUG-1989;
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                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to detect Porphorymonas gingivalis in standard hybridisation Porphorymonas gingivalis is involved in periodontal disease
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     154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 AA,
                                                                                                                                                                                                                                                                Fig 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              influenzae.
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89US-0396572.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RC,
                                                                                                                                                                                                                                                                   164pp; English.
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es, in vaccines and for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PBOMP-2;
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prodn. of reagents for
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The invention relates to isolated polynucleotide (I) and CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or impartitating a polypeptide in tissue, as molecular weight markers and as cCC quantitating a polypeptide in tissue, as molecular weight in medical companies of sites expressing (II). (I) and (II) are useful in medical composities, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations can be produce other types of data and products dependent on DNA and CC amino acid sequences of their protest and products dependent on DNA and CC specification, but was obtained in electronic format directly from WIPO CC at fits wiso.int/pub/published oct sequences.
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ABG15906
                                                                                13 IISVFLVGCAQNFSR-----QEVGAATGAVVGGVAGQLFGKG--SGRVAMAIGGAVLGGL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID No 46265; 103pp; English.
                                                         IISILPAKVAVDNSQNKRNAQAFGALIGAVAGGVIGHNVGSGSNSGTTAGAVGGGAVGAA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #15897.
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                                                                                                                                                                                                                        309 AA;
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2000US-0649167.
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                                                                                                                                                                11.7%;
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                                                                                                                                      Score 98; DB 22;
Pred. No. 0.047;
1; Mismatches 35
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                                                                                                                                                                    Length 309;
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                                                                                                                           Gaps
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                             Cells or other biological samples (such as non-recombinantly derived cells), and enrich the purity and yields of structural proteins by hydrolysing many of the macromolecules while leaving the structural proteins intact. In the case of silk proteins, the chromatography and processed into an aqueous-based mixture for fibre spinning. In the present case, the pETNoDS gene was cloned containing denaturant (3 M quanidine-Hcl) and by affinity of containing denaturant (3 M quanidine-Hcl) and by affinity of methods of the invention can be used in the construction of many surface. Products obtained using the materials including films films films woven articles surface.
materials including films, fibres, woven articles, sutures, ballistic protection, parachutes and parachute cords. The method has the following advantages over prior art: it invofewer steps, requires less time and smaller volumes of reag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
AAB82611
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Query Match Best Local

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Sequence

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The present sequence is that of the orb-weaver spider (Nephila clavipes) recombinant silk protein pETNCDS. The invention structural proteins. Organic acids are used to lyse recombinant
                                                                                                                                                                                                                                                                                                                                                                                           Recovering structural polypeptides in a biological sample, useful for purifying and spinning spider silks and other structural proteins, comprises treating the sample containing the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with an activation of the polypeptides with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide with a polypeptide
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N-PSDB; AAH26304.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) MELLO C M.
) ARCIDIACONO S.
) BUTLER M M.
) US SEC OF ARMY.
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RESULT 12
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Matches 34
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Best Local
 2124
                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), approach the sequences (ABL16176-ABL30511).
                                                                                                 Sequence
                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 25488;
                                                                                                                                                                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
interactions -
                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
N-PSDB; ABL10335.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 results in better recovery of protein at higher purity (70-99%), is easy to scale up, and the fibres are spun in an environmentally benign solution reducing hazardous waste accumulation and cost.
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                        23
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QQQQQRQVGGGNGPSMNALGGRGSGAVGSGSGN-----GGGGGGGGAGGSQVGGNGGGNGV 2178
                      QNFSRQEVGAATGA----VVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEVGAATGAVVGGVAGQ--LFGKGSGRVAMAIGGAVLGGLIGSKIGQ
                                                                                                                                                                                                                                                                                                                                                                                       JC,
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                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
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                                                 Conservative
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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                                                                                                                                                                                                                                                                                                                                                                                       PWD,
                                                                                                                                                                                                                                                                                                             detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Pred. No.
                                                           Score 86.5;
Pred. No. 9
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                                                 Mismatches
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Best Local
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
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11-JUL-2000; 2000US-0614150
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                                                                                                      AAR14308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the natural spider silk protein spidroine major 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions have use as hair or skin care products; and make up or sunscreens. As the protein is a good, persistent film-formers on the skin agents that are generally difficult to administer, e.g. vitamins, and hair moisturizers or agents for treating disorders of the
                                                                                                                                                                                                                       551 LGGQGAGQ 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                  491 OGAGAAAAAYGAGQEGIROOGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
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36.88;
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                                                                                                                                   Sequence
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                             491 OGAĞAAAAAYGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG
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                                                                                                                                                                                                                                                                DNA encoding spider silk protein-1 and 2 and variants - isolated from Nephila clavipes, for prodn. of spider silk protein and fibres having desired characteristics
                                                                                                                                                                                                                                                 Claim 15; Page 23; 48pp; English.
                  65 LIGSKIGQ 72
                                                28 QEVGAATGAVVG----GVAGQ------LFGKGSGRVAMAIGGAVLGG 64
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Search completed: October 27, 2002, 10:57:54 Job time: 23.8238 secs

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01-MAR-2001 (TrEMBLrel. 16, 1
01-MAR-2001 (TrEMBLrel. 16, 1
17 KDA ANTIGEN.
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"Identification of a genus-common Rickettsial surface ar
almonid pathogen Piscirickettsia salmonis.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF184152; AAG17000.1;
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SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piscirickettsia salmonis.
Bacteria; Proteobacteria;
Piscirickettsia.
NCBI_TaxID=1238;
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                                                                                                                                                                                                                                                                   ERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                               ERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
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Pred. No. 9.6e-68;
; Mismatches 0;
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Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AAG28452.1; -
SEQUENCE 159 AA; 16497 MW; 34C5B020AF470A1F
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=21217364; PubMed=11321078;
Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,
Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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"Rickettsia felis: molecular characterization of a new member
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Rickettsiaceae; Rickettsieae; Rickettsia
NCBL_TaxID=42862;
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Bacteria; proteobacteria; alpha subdivision;
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SKIMITALAASMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG 64
                                                       SSLIIISV---FLVGC--AQNESRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
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MEDLINE~98087556; PubMed=9425244;
Davis M.J., Ying Z., Brunner B.R., Pan
"Rickettsial relative associated with
Curr Microbiol 36:80-84(1998).
EMBL; U76907; AAC02809.1; -.
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=789;
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                                                                                                                                                       Similarity 38.1
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-JUN-1998 (TremBLrel. 06, Last sequence update)
-NOV-1998 (TremBLrel. 08, Last annotation update)
KDA COMMON-ANTIGEN (FRAGMENT)
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(TrembLrel 16, Last seq
(TrembLrel 19, Last ann
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Pred. No. le-18;
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top disease.";
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Schulenburg H.J.G.V.D., Habiq M., Sloggett J.J., Webberley M.K.,
Bertrand D., Hurst G.D.D., Majerus M.E.N.;

"On the evolution of male-killing: Monophyletic origin and horizontal generic ladybirds, Adalia bipunctata L. and A. decempunctata L. (Coleoptera: Coccinellidae).",

Submitted (APR-2000) to the EMBL, AJ269518; CAB96383.1;

EMBL: AJ269517; CAB96383.1;

EMBL: AJ269517; CAB96382.1;

NON_TER 144 144
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Billings A.N., Teltow G.J., Walker D.H.;
"Molecular characterization of a novel spotted fever gro
Species from Ixodes scapularis in Texas.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF031534; AAB95267.1;
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(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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Pred. No. 1.4
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Q9K4WB;
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O31065; Q9WW02;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-OCT-2001 (TrEMBLrel. 18, Last annotation update)
17 KDA ANTIGEN (17 KDA PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                          Stenos J., Roux V., Walker D., Raoult D.;
"Rickettsia honei sp. nov., the aetiological agent
spotted fever in Australia.";
Int. J. Syst. Bacteriol. 48:1399-1404(1998).
EMBL: AF027124; AAB81846.1;
EMBL: AF060706; AAD20331.1;
                                                                                                                                                                                                                                                                                                                                                                                               Rickettsia honei.
Bacteria; Proteobacteria; alpha subdivision;
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STRAIN-TT-118;
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NCBI_TaxID=37816;
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                                                                                                                                                         NKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEQDRRLAELT
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                                                                                                                     SQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQQ
                                                                                                                                     LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ
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(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 19,
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NCBI_TaxID=789;
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                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=120393;
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52; Conserv
                                                                                                            Similarity
                                                                                                                                       154 AA;
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MEDLINE-93084757; PubMed=1452660; Baird R.W., Lloyd M., Stenos J., Ross B "Characterization and comparison of Ausigroup rickettslae.";
J. Clin. Microbiol. 30:2896-2902(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20575219; PubMed=11133455; Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K., Bertrand D., Hurst G.D.D., Majerus M.E.N.; "Incidence of male-killing Rickettsia spp. (alpha-Proteobacteria) the Ten-Spot Ladybird Beetle Adalia decempunctata L. (Coleoptera:
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Bacteria; Proteobacteria; alpha subdivision;
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01-NOV-1998 (TrEMBLrel.
(CLONE PRB FISF 1), 5' E
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male-killing Rickettsia from Adalia decempunctata
Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsiaee; Rickettsia.
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Appl. Environ. Microbiol. 67:270-277(2001).
EMBL; AJZ69516; CAB96381.1; -.
120 QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ
::|| :| | || || || || || :||
SQRALEAAPSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQQ
                                                                 AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGSYGYVTPNKTYRNSTG
                                                                                                        GLIGSKIGQSMDQQDK----IKLNQSLEKYKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                              SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
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                                                                                                                                                       SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
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. 01, Last sequence update)
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END CDS (FRAGMENT).
                                                                                                                                                                                                                                           29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS (FRAGMENT).
                                                                                                                                                                                                                                         Score 252; DB 2;
Pred. No. 3.3e-15;
9; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 259.5; DB 2
Pred. No. 6.3e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Ross B.C., Stewart R.S., Dwy of Australian human spotted
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QD-----CRVYTQTVVIGGKQQKAYGNACRQPDGQ 154

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RESULT 10
Q9F0Q1
AC Q9F0Q
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O9F001, O1-MAR-2001 (Tremblrel 16, C1)
O1-MAR-2001 (Tremblrel 16, L4)
O1-MAR-2001 (Tremblrel 16, L4)
O1-MAR-2001 (Tremblrel 16, L4)
O1-MAR-2001 (Tremblrel 16, L4)
O1-MAR-2001 (TREMBLE)
                                                                                                                  EMBL; AI
NON_TER
NON_TER
                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CALIFORNIA 2;
ROUX V., RAOULT D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
EMBL; AF210693; AAG48554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                    SEQUENCE
                                                                                                                                                                                                               Raoult D.;
"A new SFG rickettsia isolated from fleas.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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STRAIN-CALIFORNIA 2;
                                                                                                                                                                                                                                                                                                                                 Rickettsia sp. California 2.
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=147259;
                                                Local
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01-MAR-2001 (TremBLrel. 16, Last annotation update)
0UTER MEMBRANE PROTEIN (FRAGMENT).
Rickettsia helvetica.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettslaceae; Rickettsieae; Rickettsia.
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Q9F9Q9;
Q1-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nilsson K., Pahlson C.,
"Novel peptide diagnostic reagent and kit for detection rickettsiosis.";
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                                 l Similarity
48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNSTGOYCREYTOTVVIGGKOOKAYGNACROP 151
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131 AA;
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                            Conservative
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(TrEMBLrel. 16, Last sequence up)
(TrEMBLrel. 16, Last annotation
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                                                                                   131
; 13374 MW;
                                         28.4%;
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                          22;
                   Score 237.5;
Pred. No. 5.4e
22; Mismatches
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                                                                            23C8819B29FFF860 CRC64;
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Pred. No. 9e-15;
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                                .4e-14
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                                                DB 2;
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                   48;
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                                              Length 131;
              Indels
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          Gaps
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RESULT 12
Q9L522
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O9L522 PRELIMINANI,
O9L522; O9L522;
O1-OCT-2000 (TremBLrel. 15, Created)
O1-OCT-2000 (TremBLrel. 15, Last sequence update)
O1-DEC-2001 (TremBLrel. 19, Last annotation updat
17 KDA SURFACE ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
 SEQUENCE FROM N.A.
STRAIN-DAE100R;
MEDLINE-21991941; PubMed-11157215;
Simser J.A., Palmer A.T., Munderlo
                                                                  Rickettsia peacockii.
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=47589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                    125 KAYGNAC
                                                                                                                                                                                                                                                                             142 EIYGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beetle (Adalia bipunctata) ", ", Bacteriol 176:388-394(1994).
EMBL: U04162; AAA19235.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-94117373; PubMed-8288533; Merren J.H., Hurst G.D., Zhang W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
17 KDA ANTIGEN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                   "Rickettsial relative associated with male killing in
                                                                                                                                                                                                                                                                                                                                    10 NKOGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLGAVLGGQIGAGMDEODRRLAELT
                                                                                                                                                                                                                                                                                                                                                          26 SRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK
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48; Conservative
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131 AA;
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Kurtti
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Т.J.;
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01-OCT-2001
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EMBL; AF
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NON_TER
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031208;
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MEDLINE-98367252; PubMed-9701930;

Billings A.N., Yu X.J., Teel P.D., Walker D.H.;

"Detection of a spotted fever group rickettsia
(Acari: Ixodidae) in south Texas.";

J. Med. Entomol. 35:474-478(1998).
                                                                                                                                                                                                                                                                                                                                                                                                         Ol-JAN-1998 (TREMBLRel. 05, Last sequence upd Ol-DEC-2001 (TREMBLRel. 19, Last annotation u 17 KDA ANTIGEN (FRAGMENT).

Rickettsia sp. 'La Copita'.

Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.

NCBI_TaxID=69475;
           MLR7687
MLR7687.
                                                                              Q985G4
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Rhizobium loti (Mesorhizobium
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a Rocky Mountain wood tick, Dermacentor andersoni, cell line.";
pl. Environ. Microbiol. 67:546-552(2001).
BL; AF260571; AAF69012.1; -.
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                                                                                                                                   GQLVGVGV-----GALLGAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWR
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47; Conservative
                       PROTEIN.
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18; Conservative
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1 (TrEMBLrel. 18,
1 (TrEMBLrel. 18,
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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11236 MW;
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41.2%; Pred. No. 7.4e-13;
tive 17; Mismatches 33;
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Pred. No. 6.6e-14;
22; Mismatches 48
 loti).
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01-JUN-2001
01-JUN-2001
17 KDA ANTICE
                                                                                                                                                                SEQUENCE FROM N.A.
Paspaliaris V., Liedtke B., Vitetta L., Whiting J.L.;
Paspaliaris v., Liedtke B., Vitetta L., Whiting J.L.;
"Rickettsia typhus and Rickettsia felis rickettsioses in
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF336794; AAK21272.1; -
NON_TER 1
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NON_TER 77
77
                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia. NCBI_TaxID=785;
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                                                                                                                                                                                                                                                                                                          Rickettsia typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome structure of the nitrogen-fixing Mesorhizobium loti.";
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                                                                                                                                                      SEQUENCE
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NPDNGNHGYVTPNKT
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AP003012; BAB54098.1; -.
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Maximum Match 100%
Listing first 45 summaries
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K1CJ_BOVIN
K1CJ_BOVIN
KNDO_BACSU
YOBO_BACSU
OSMB_SALTY
CYSH_SALTY
STXG_RAT
VF5_BTV11
Y615_BV11
Y615_BV1N
NU57_FAST
SPD1_NEPCLL
CANS_RABIT
YKR3_CABEL
CANS_RABIT
ATPA_BOVIN
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Q52764 rickettsia
P05372 rickettsia
P22882 rickettsia
                                         P33476
066867
P13135
P48837
P19837
P46724
P34309
                                                                                                                                        P50930
P50931
P50929
P50929
P314897
P551441
Q53549
P10326
P06394
P45931
P45931
P37723
Q97158
Q00310
P06813
P19482
P15999
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6 escherichia
4 bos taurus
4 bacillus su
1 bacillus su
1 salmonella
3 escherichia
                                                                               bluetongue
aquifex aeo
bos taurus
saccharomyc
                                       nephila cla
mycobacteri
caenorhabdi
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l escherichia
l salmonella
                                                                                                                                                      salmonella
rattus norv
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rickettsia
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              oryctolagus
bos taurus
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	P25705 homo sapien P13645 homo sapien P19483 bos taurus Q03265 mus musculu P18538 marek's dis P37665 escherichia O88456 mus musculu P14593 plasmodium P12405 anabaena sp P41167 thiobacillu P17854 escherichia	

ALIGNMENTS

RESULT 1 17KD_RICPR

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Query Match
Best Local S
Matches 61
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01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17 kDa surface antigen precursor.
0MP OR RP833.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-MADRID E;

MEDLINE-99039499; PubMed-9823893;

Andersson S.G.E., Zomorodipour A., Andersson J.O.,

Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.I

Eriksson A.-S., Winkler H.H., Kurland C.G.;

"The genome sequence of Rickettsia prowazekii and the origin of

mitochondria.";
                                                                           CHAIN
LIPID
                                                                                                                                             EMBL; AJ235273; can
PIR; D33971; D33971
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia. NCBI_TaxID=782;
                                                                                                         Outer membrane; Lipoprotein; SIGNAL 1 19
                                                                                                                                                                 EMBL; M28482; AAA26378.1; ALT_SEQ. EMBL; AJ235273; CAA15258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-MADRID E;
MEDLINE-89359171; PubMed-2768201;
Anderson B.E., Tzianabos T.;
                                                                                                                     PROSITE; PS00013; PROKAR_LIPOPROTEIN;
Outer membrane; Lipoprotein; Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Comparative sequence analysis of a genus-common rickettsial antigen
gene_":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsia prowazekii.
                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 171:5199-5201(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L7KD_RICPR
                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Attached to the
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20
159
                                                             A,
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                                                           159
20
16672
              35.4%; Score 296; DB 1; 38.1%; Pred. No. 9.9e-19;
                                                             MW;
                                                        17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PRO
; A33D404B65EEB071 CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Signal; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                 outer membrane by a lipid
                                                                            (PROBABLE).
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Similarity 61; Conserv

Conservative

30;

Mismatches

Length 159;

Indels

14;

Gaps

4

RESULT 2 17KD_RICJA

17KD_RICJA Q52764;

STANDARD;

PRT;

01-NOV-1997 (Rel. 01-NOV-1997 (Rel. 01-NOV-1997 (Rel. 17 kDa surface anti-

Created)

kDa surface

antigen

precursor.

Rickettsia japonica. Bacteria; Proteobacteria;

ckettsiaceae;

Rickettsieae;

В Ş Дb

120 120 Qy В õ

9

65 64 G

63

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Seno ....

ABL; D16515; BAA03965.1; ...

ROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.

JULET membrane; Lipoprotein; Antigen; Signal.

SIGNAL 1 1 9 8 SIMILARITY

CHAIN 20 159 17 KDA SURFACE ANTIGEN.

20 20 N-ACYL DIGLYCERIDE (PROBABLE).

16554 MW; CDDCE7CEBDCD6B41 CRC64;

Length 159;
                                                                                                                                                                                                                        65 AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no we see that the swiss is a superior of the swiss in the swiss content is in no we have the swiss content in the swiss content in the swiss content is in no we have the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss content in the swiss conte
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                                                                                                                                                                                                                                             GLIGSKIGOSMDQODK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                   SKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGTGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                                            SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QERROQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVLGGQIGASHDEQDRRLLELTSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY-----
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                                                                                                                                                                                                                                                                                                                                                                                          35.2%; Score 294; DE 38.1%; Pred. No. 1.56 tive 30; Mismatches
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Last annotation
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eae; Rickettsia.
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hes 55;
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MBL outstation -
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                                       Outer membrane; I
SIGNAL 1
CHAIN 20
LIPID 20
CONFLICT 146
CONFLICT 153
                                                                                                                                             EMBL; M28479; AAA26379.1;
EMBL; M28480; AAA26376.1;
EMBL; AE008675; AAL03825.1;
EMBL; M16486; AAA26381.1;
EMBL; J03371; NOT_ANNOTATED_CDS.
PIR; A25972; A25972.
PIR; A31836; A31836.
PIR; B33971; B33971.
PIR; B33971; B33971.
PIR; B33971; B33971.
                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through, between the Swiss Institute of Bioinformatics and the EMT the European Bioinformatics Institute. There are no restrementing by non-profit institutions as long as its content modified and this statement is not removed. Usage by and or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89008059, PubMed-3139629;
Anderson B.E., Baumstark B.R., Bellini W.J.,
"Expression of the gene encoding the 17-kilodalton antigen
Rickettsia rickettsii: transcription and posttranslational
modification.",
J. Bacteriol. 170:4493-4500(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-30 FROM N.A. SPECIES=R.rickettsii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=R.rickettsii;
MEDLINE=87222152; PubMed=3108232;
Anderson B.E. Regnery R.L., Carl
Fu Z.Y., Bellini W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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01-NOV-1988 (Rel. 09, Created)
01-AUG-1990 (Rel. 15, Last sequence
01-MAR-2002 (Rel. 41, Last annotati
17 kba surface antigen precursor.
OMP OR RG1287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=R.conorii; STRAIN=Malish 7
MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Samson D., Roux
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ogata H., Audic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-R. conorii, and R.rickettsii; MEDLINE-89359171; PubMed=2768201; Anderson B.E., Tzianabos T., "Comparative sequence analysis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mechanisms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 169:2385-2390(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anchor (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3acteriol 170:4493-4500(1988).
SUBCELLULAR LOCATION: Attached
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 171:5199-5201(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isms of evolution in Rickettsia conorii and R. prowazekii.";
293:2093-2098(2001).
                        Lipoprotein;
1 19
0 159
0 20
146
146
                                                                                                       PROKAR_LIPOPROTEIN; ipoprotein; Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S., Renesto-Audiffren P., Fournier P.-E.,
V., Cossart P., Weissenbach J., Claverie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09, Created)
15, Last sequence update)
41, Last annotation update)
17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
N -> D (IN REF. 3).
G -> E (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carlone G.M., Tzianabos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the outer membrane by a lipid
                                                                      1.
Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                  noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genus-common rickettsial antigen
                                                                                                                                                                                                                                                                                                                                                                                          restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL
                                                                                                                                                                                                                                                                                                                                                                                                         h a collaboration
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anchor (Probable).

MEDLINE=95229950; PubMed=7714214; Furuya Y., Katayama T., Yoshida Y.,

SEQUENCE FROM N.A.

RESULT 3
17KD_RICCN
ID 17KD_RICCN

STANDARD;

PRT;

159

γ 밁 δÃ DЬ QΥ

64

G 9

120

Matches Query Match Best Local

Conservative

Foca1

CHAIN LIPID

PROSITE;

SEQUENCE

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17KD_RICTY
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Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-89359171; PubMed-2768201;
Anderson B.E., Tzianabos T.;
"Comparative sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17KD_RICTY P22882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsia typhi.
Bacteria; Proteobacteria;
Rickettsiaceae; Rickettsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAB
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01-AUG-1991 (Rel. 19,
01-OCT-1996 (Rel. 34,
17 kDa surface antigen
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                     Outer membrane;
                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                  PIR; C33971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=785;
                                                                                                                                                                                                                                                         LIPID
                 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 171:5199-5201(1989).
- SUBCELLULAR LOCATION: Attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anchor (Probable).
                                                                                                                                SRQEVGAATGAVVGGVAGQLEGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVIS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVIGGQIGAGMDEQDRRIAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
EIYGTACRQPDGRWQVIS
                                                                  LNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSLITISY---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
                                                SQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQQ
                                                                                                             NKQGTGTLLGGAGGALLGSQFGHGKGQLVGVGVGALLGAVLGGQIGASLDEQDRKLLELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN
                                                                                                                                                                                                                                                                                                                                                 M28481; AAA26377.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
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                                                                                                                                                                                                                                                                                                971; C33971.
PS00013; PROKAR_LIPOPROTEIN;
mbrane; Lipoprotein; Antigen;
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159
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159
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16549 MW;
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eae; Rickettsia.
                                                                                                                                                                         25;
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Pred. No. 1.8e
29; Mismatches
                                                                                                                                                                       Score 284.5; DB 1
Pred. No. 9.5e-18;
5; Mismatches 49
                                                                                                                                                                                                                                    17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outer membrane
                                                                                                                                                                                                        DB 1;
                                                                                                                                                                           49;
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                                                                                                                                                                                                                                       (PROBABLE)
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rickettsial
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17KD_RICAU
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01-OCT-1996
01-OCT-1996
17 kDa surfa
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01-0CT-1996
01-0CT-1996
01-0CT-1996
17 kDa surfac
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LIPID
NON_TER
 SEQUENCE FROM N.A.
STRAIN-MO 85-1084;
                                                             Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Outer membrane; SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baird R.W., Ross B., Submitted (OCT-1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsiaceae;
NCBI_TaxID=787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P50928;
                                                                                            Rickettsia amblyommii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsia australis
                                             NCBI_TaxID=33989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M74042; AAA26394.1; -
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                                                                                                                                                                                                     7KD_RICAM
                                                                                                                                                                                                                                                                                     124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Attached
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                                                                                                                                                                                                                                                                                                                  QERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGR 154
                                                                                                                             surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 59; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154
154 AA;
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(Rel.
(Rel.
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                                                                                                                           antigen
                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     >154

    Last sequence update)
    Last annotation update)

                                                                                                                                                                       34, Created)
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154
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                                                                                                                          precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                             alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
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                                                                                                                           (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
                         AVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTYRNSN-
                                                                                           SKIMIIALAASMLQACNSPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
                                                                                                                                           SSLIIISV---FLVGCAQ--NFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 surface antigen precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 34, Last sequence update) (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dwyer B.; to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                       POPROTEIN; 1.
; Antigen; Signal.
BY SIMILARITY.
17 KDA SUNFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROF
                                                                                                                                                                                                                  Score 276; DB 1;
Pred. No. 4.9e-17;
                                                                                                                                                                                                                                                                                           E3AA833346FAC320 CRC64;
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                                                                                                                                                                                                                                           Length 154;
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Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

-: SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid

Stothard D.R.,

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RESULT 7
17KD_RICPA
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMBL outstation is a constant of the EMBL outstation. There are no restrictions on its by non-profit institutions as long as its content is in no way or send an email to license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Outer membrane; Lipoprotein; Antigen; Signal.
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BY SIMILARTTY.
CHAIN 20 >154 17 KDA SURFACE ANTIGEN.
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PROSITE; PS00013; PROKAR LIPOPROTEIN; 1
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seque
01-OCT-1996 (Rel. 34, Last annot
17 kDa surface antigen precursor
                                                                                                                                     STRAIN-MACULATUM;
Pretzman C.I., Stothard D.R., Ralph D., Clark J.B., Fuerst P.A.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-! SUBCELL/LIAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Rickettsia parkeri.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Best Local :
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les 57; Conserv
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                                                                                                                                                                                                                                                           Last sequence update;
Last annotation update;
n precursor (Fragment).
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36.8%; Pred. No. 6.4e-16;
tive 27; Mismatches 57;
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120 RNSTGOYCREYTQTVVIGGKQQKAYGNACLQPDGQ
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                                         65 AVLGGQIGAGNDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYITPNKTY-----
                                                                  64 GLIGSKIGOSMDQODK----IKLNOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYORVNK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C., Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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Best Local
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01-CCT-1996 (Rel. 34 Last sequence update)
01-CCT-1996 (Rel. 34 Last annotation update)
17 kDa surface antigen precursor (Fragment).
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                         QERROQYCREFOQKAMIAGQKQEIYGTACRQPDGR 154
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P50931;
                                                                                                 SKIMITALAASMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
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154
154 AA;
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                                                                                                                                                         31.2%; Score 261; DB 1; Length 154,
36.1%; Pred. No. 9.5e-16;
tive 28; Mismatches 57; Indels
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154
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17KD_RICMO
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
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Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pressubmitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
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   SEQUENCE FROM N.A. MEDLINE-92108069;
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Rickettsiaceae; Rickettsieae;
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       PubMed=1729713;
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RESULT 11 PCP_YEREN
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                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                     Baeumler A.J., Hantke K.;

**A lipoprotein of Yersinia enterocolitica faci
uptake in Escherichia coli.";

J. Bacteriol. 174:1029-1035(1992).

-!- FUNCTION: FACILITATES FERRIOXAMINE UPTAKE.
                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew
                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-ATCC 51872 / WA-C / SEROTYPE 0:8; MEDLINE-92121089; PubMed-1732192;
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SEQUENCE
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                                                                      the European Bioinformatics Institute.
                                                                                                                                     -!- SIMILARITY: TO
                                                                                                                                                             -!- SUBCELLULAR LOCATION:
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InterPro; IPR000437; Prok_lipoprot.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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A Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
RA Oshima T., Saito N., Sampei G., Seki Sivasundaram S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RY Tamamoto Y., Horiuchi T.,
RY Torkesponding to the 28.0-40.1 min region on the linkage map.",
RL DNA Res. 3:363-377(1996).
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                                                                                                                                                                                                                                                                                                                                           STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R. Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J.L., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Glasner J.D., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "SlyA, a regulatory protein from Salmonella typhimurium, induces Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=96133688; PubMed=8544813;
Ludwig A., Tengel C., Bauer S., Bi
Goebel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 --NOSLEKVKAGQVTRWRNPDTGNSYSVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 GAVLGGFLGNTVGGGTGRSLATAAGAVAGGNAGQGVQGANNRTDGVQLEVRKDDGTTILV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVAIAAVTLTGCANNNTLSGDVFSASQAKQVQTVTYGTLLSVRPVTIQGGDDNNVNGAIG
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37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83334;
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155 OUTER MEMBRANE LIPOPROTEIN PCP.
18 N-ACYL DIGLYCERIDE (POTENTIAL).
15362 MW; 8AD6BE2132E849FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.6%;
24.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 113.5;
Pred. No. 0.(
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RESULT 13
SLYB_SALTY
ID SLYB_S,
AC Q53549
DT 01-NOV
DT 01-MAR
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Q53549;
01-WOV-1997 (Rel. 3
01-WOV-1997 (Rel. 3
01-MAR-2002 (Rel. 4
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Best Local
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PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

OUTET membrane; Lipoprotein; Signal; Complete proteome.
CHAIN

CHAIN

18
155
APPROKAR LIPOPROTEIN; 1.

POTENTIAL

INTERPORTOTEIN

CONFLICT

98
98
N-ACYL DIGLYCERIDE.

SEQUENCE
155
AA; 15602 MW; 543EBBA4069A5FA3 CRC64;
                                                                                                                                                               98 RNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                              10 MVGĹSĽVČCVNNDTLSGDVYTASEAKQVQNVSYGTIVNVRPVQIQGGDDSNVIGÁIGGAÝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial correst a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                            70
                                                                                                                                                                                                                                                      13 IISVFLYGCAQN------FSRQE------VGAATGAV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-0157-H7 / RIMD 0509952,
MEDLINE-21156231, PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyar Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Tobe T. "Complete genome sequence of enterohemorrhagic Escherichia coli -1- 3UBACELIULAR LOCATION: Attached to the outer membrane by a li
                                                                                                                                                                                                                                                                                                                             Local
V-1997 (Rel. 35, Created)
V-1997 (Rel. 35, Last sequence update)
R-2002 (Rel. 41, Last annotation update)
membrane lipoprotein slyB precursor.
                                                                                                                                       ---DDGNTIMVVQKQGNTRFSPGQR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perna N.T., Plunkett G. III., Perna N.T., Plunkett G. III., Postand V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Postand G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Apodaca J., Anantharaman T.S., Lin A., Dimalanta E.T., Potamousis K., Welch R.A., Blattner F.R.; S., Lin J., Yen G., Schwartz D.C., Nature 409:529-533(2001).
                                                                                                                                                                                LGGFL6NTVGGGTGRSLATAAGAVAGGVAGQGVQSAMNKTQGVEL--EIRK---
                                                                                                                                                                                                   VGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGOSMDQODKIKLNQSLEKVKAGQVTRW 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=0157:H7 / F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anchor (Potential).
SIMILARITY: TO S.TYPHIMURIUM SLYB, H.INFLUENZAE PCP AND
Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                        Conservative
                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                    12.6%;
                                                                                                                                                                                                                                                                                                  21;
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                   Pred
                                                                                                                                                                                                                                                                                                                       Score 105.5;
                                                                                                                                                                                                                                                                                                                                            543EB8A4069A5FA3 CRC64;
                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                No.
                                                                      155
                                                                                                                                                                                                                                                                                                           0.02;
                                                                    AA
                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                 Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishii K., Yokoyama K.,
Tanaka M., Tobe T.,
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Best Local S
Matches 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ludwig A., Tengel C., Bauer S., B
Goebel W.;
                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a multiple enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-S.typhi; STRAIN-CT18; MEDLINE-21534947; PubMed-11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC MEDILINE-21534948; PubMed-11677609;
                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Ngyan E., Sun H., Florea L., Miller W., Stoneking T., Nha
                                                                                                        SEQUENCE
                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                EMBL; S80790; AAB35871.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "SlyA, a regulatory protein from Sahaemolytic and pore-forming protein Mol. Gen. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-S. typhimurium;
MEDLINE-96133688; PubM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium, Salmonella typhi.
                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston
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                                                                                                                          J.; S80790; AAB35871...,
BL; AE008762; AAL20367.1; -.
BL; AL627271; CAD01922.1; -.
CYGene; SG10573; S1yB.
CYGENE; PS00013; PROKAR_LIPOPROTEIN; 1.
POTENTIAL.
POTENTIAL.
POTENTIAL.
TOTAL
17
                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Attached
                        GCLQGSSL----
GCVNNDSLSGDVYTASEAKQVQNVTYGTIVNVRPVQIQGGDDSNVIGAIGGAVLGGFLGN
                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             (Potential)
                                                                                                        155
                                                    Conservative
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18
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                                                                                                        15548 MW;
                                                                                                                       18
                                                                 12.6%;
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                                                    19;
                         ----IIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQ
                                                                 Score
Pred.
                                                                                                        N-ACYL DIGLYCERIDE.
82FDDCDCBABD55A7 CRC64;
                                                                                                                                   OUTER MEMBRANE LIPOPROTEIN
                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subdivision; Enterobacteriaceae;
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                                                                 105.5;
No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                drug resistant
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                                                                            Length
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Sebaihia M.,
                                                                                                                                   SLYB
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01-NOV-1995
       CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAINARD / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Fine C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDILINE=88115138; PubMed=2828309;

Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;

Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;

"Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalto protein from Hammophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane lipoprotein PCP precursor (15 cross-reacting lipoprotein). PCP OR LPP OR HI1579.
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LIPID
                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                     EMBL; M18877; EMBL; U32832;
                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Query Match Best Local Similarity

Matches

Conservative

Score 102; DB 1; Length 155; Pred. No. 0.04; 9; Mismatches 23; Indels

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      EMBL; AE000211; AAC74194.1; -. EMBL; D90746; BAA35925.1; -. EMBL; V00306; -; NOT_ANNOTATED
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its pon-profit institutions as long as its content is in no was entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  IDENTIFICATION.

MEDLINE-95075659; PubMed-7984428;
BOROGOVSKY M., Rudd K.E., Koonin E.V.;
"Intrinsic and extrinsic approaches for detecting genes in bacterial genome.";
Dacterial genome. ", Nucleic Acids Res. 22:4756-4767(1994),
-!- SIMILARITY: TO RICKETTSIA 17 kDa SURFACE ANTICEN.
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YCFJ_ECOLI
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MEDLINE-81236546; PubMed-6265208;
Young J. G., Rogers B.L., Campbell H.D., Jaworowski A., Shaw D.C.,
"Nucleotide sequence coding for the respiratory NADH dehydrogenase of Escherichia coli. UUG initiation codon.";
Eur. J. Biochem. 116:165-170(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Anno M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97061202; PubMed=8905232;
Oshima T. Aiba H. Baba T. Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-63 FROM N.A.
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STRAIN-KL2 / MG1655;

MEDILINE-97426617; PubMed=9278503;

MEDILINE-97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P37796; P75951;
01-OCT-1994 (Rel. 30, Created)
01-MOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical protein ycfJ.
YCFJ OR BIllo.
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Maximum Match 100%
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1: pir1:*
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D33971
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A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971; MUID:89359171
A;Accession: D33971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Rickettsia prowazekii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 03-Nov-2000
C;Accession: D33971; B71645
                                                                                                    Вþ
                                                                                                                                        δõ
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A; Residues: 1-159 < AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names: 17kD surface antigen; outer membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Anderson, B.E.; Tzianabos, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rickettsial common antigen precursor - Rickettsia prowazekii
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ALIGNMENTS

(omp); RP833

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RESULT 2
B33971
Rickettsial common antigen precursor -
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C; Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499
A;Accession: B71645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M28482; NID:9152461
A;Note: the sequence in GenBank entry RIRANT17KC,
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson,
Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15258.1; PID:g386
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-159 <AN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                     64
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                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                           SKIMIIALAASMLQACNGQSGMNKQGTGTLLGGAGGALLGSQFGQGKGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                                              SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG
                                                                                                                   RNSAGQYCREYTQTVIIGGKQQKTYGNACRQPDGQWQVVN 159
                                                                                                                                                                                                                                                     GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           35.4%;
                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                         Score 296; DB 2; I
Pred. No. 6.8e-19;
O; Mismatches 55;
    Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             release 109.0, (PID:g152462) omits J.O.; Sicheritz-Ponten, T.; Alsmar
                                                                                                                                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 159;
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/Species: Rickettsia conorii
/Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999

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17k surface antigen precursor [imported] - Rickettsia conorii (strain Malish C; Species: Rickettsia conorii.
C; Species: Rickettsia conorii.
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C; Accession: G97860
R; G9ata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samesto-293, 2093-2098, 2001
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C;Superfamily: rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial A;Accession: A33971; MUID:89359171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: A33971
R; Anderson, B.E.; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
A33971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsial common antigen precursor - C; Species: Rickettsia rickettsii
                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Molecule type: DNA;Residues: 1-159 <AND>
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A; Residues: 1-159 <AND>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen A;Accession: B33971; MUID:89339171
A;Accession: B33971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Anderson, B.E.; 7
J. Bacteriol. 171,
                                                                                                                                                                  120 RNSTGOYCREYTOTVVIGGKOOKAYGNACROPDGOWOVVN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Cross-references; GB:M28479; NID:g152463; PIDN:AAA26379.1; PID:g152464;
;Superfamily: rickettsial common antigen
                                                                                                                                                                                          120 QERRQQYCREFQQKAMIAGQKQETYGTACRQPDGRWQVIS 159
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                                                                                                                                                                                                                         65 AVLGGOIGAGMDEODRRLAELTSORALETAPSGSNVEWRNPDNGNYGYVTPNKTY---
                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                5 SKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQLVGVGVGALLG
                                                                                                                                                                                                                                                                                                             9 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLG 63
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                                                                                                                                                                                                                                               GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-Mar-1990 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRVNK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       GB:M28480; NID:9152457; PIDN:AAA26376.1; PID:9152458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                    35.0%; Score 293; DB 2; L
38.1%; Pred. No. 1.2e-18;
70. Mismatches 56;
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38.1%;
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Pred. No. 1.2e-18;
9; Mismatches 56
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                                                                                                                                                                                                                                                                                                                                                                                Length 159;
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           V.; Samson,
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             D.;
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          Rq
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R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabc
J. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen
A;Reference number: A25972; MUID:87222152
                                                                17K antigen precursor - Rickettsia rickettsii C:Species: Rickettsia rickettsii rickettsii C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change C:Accession: A25972
                                                                                                                                                          RESULT 6
A25972
                                                                                                                                                                                                                     Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-159 <AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Accession: C33971 A33971; MUID:89359171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsial common antigen precursor - C:Species: Rickettsia typhi
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C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE006914; PIDN:AAL03825.1; PID:g15620425; GSPDB:GN00173
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A; Residues: 1-159 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                     142 TTYGNACRQPDGQWQVVN 159
                                                                                                                                                                                                                               142 EIYGTACRQPDGRWQVIS
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                                                                                                                                                                                                                                                                                                                            26 SRQEVGAATGAVVGGVAGOLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK----IK 81
                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                NKQGTGTLLGGAGGALLGSQFGHGKGQLVGVGVGALLGAVLGGQIGASLDEQDRKLLELT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 GLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 119
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55; Conserv
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61; Conservative
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                 34.0%; Score 284.5; DB
39.9%; Pred. No. 7e-18;
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38.1%;
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Pred. No. 1.2e-18;
29; Mismatches 56
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                                                         Tzianabos,
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                                                T.; McDade, J.E.;
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                 from Rickettsia ricketts
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RESULT 8
AI3418
17K surface antigen precursor [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AI3418
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Bruce A;Accession: AI3418
A;Status: preliminary
**Latence of the facultative intracellular pathogen Bruce A;Accession: AI3418
A;Status: preliminary
**Latence of the facultative intracellular pathogen Bruce A;Accession: AI3418
A;Status: preliminary
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A;Gene:
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B83169

conserved hypothetical protein PA3819 [imported] -
c;Species: Pseudomonas aeruginosa
c;Species: Pseudomonas aeruginosa
c;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opp
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A;Residues: 1-159 <AND>
A;Cross-references: GB:M16486; NID:g152467; PIDN:AAA26381.1; PID:g152468
C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                       В
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A; Residues: 1-182 <STO>
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A;Cross-references: GB:AE008917; PIDN:AAL52516.1; A;Experimental source: Strain 16M
                                         A; Molecule type: DNA
A; Residues: 1-131 <KUR>
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Pred. No. 0.0004;
.3; Mismatches 28;
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Pred. No. 7.7e-18;
9; Mismatches 57;
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                   PID:g17983328;
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                                                                                                                                                                           G.; Mujer, C.; Los, 1.,
Hagius, S.; O'Callaghan,
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                     GSPDB:GN00190
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RESULT
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R:Stover, C:K.; Pham, x.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; (
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein PA1053 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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B83514
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A; Gene: BMEI1335
A; Map position:
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C;Superfamily: PAL cross-reacting lipoprotein
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A;Residues: 1-154 <STO>
A;Cross-references: GB:AE004537; GB:AE004091; NID:g9946960;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Complete genome
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les 39; Conserv
                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                           1 MNRGCLQGSSLIIISVFLVGC----AQNFSRQE-----
                                                                                                                                                             VGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGTACRQPD 152
                                                               STRAYVQQVDQGQIFR
                                                                                             -- NOSLEKVKAGOVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSVLWSGAGS-NAGDVTAAQPYQ-----VGSQNCRQYSHSFTIGGDQQTVRGTACRNPD 124
                                                                                                                               IGSIAGAGVGGVAGSAVGGGKGSYVAAIIGAVAGGLLGAATEEGLTRTQGVEITVREDDG 120
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of Pseudomonas
50; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.0%;
                                                                                                                                                                                                                                                                          13.9%;
                                                                                               96
                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                          Score 116; DB 2,
Pred. No. 0.0042,
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 125.5; DB 2
Pred. No. 0.00052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                         Length 154;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                        PIDN:AAG04442.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAO1,
                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic
                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                             82
                                                                                                                                                                                                                            29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    þa
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outer membrane lipoprotein precursor - Yersinia en C; Species: Yersinia enterocolitica C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 C; Accession: S23787 R; Baeumler, A.J.; Hantke, K. J. Bacteriol. 174, 1029-1035, 1992 J. Bacteriol. 174, 1029-1035, 1992 A; Reference number: S23786; MUID:92121089 A; Accession: S23787

Yersinia enterocolitica

10-Nov-1995

#text_change

29-Sep-1999

facilitates

ferrioxamine uptake

A;Status: preliminary A;Molecule type: DNA

```
C;Accession: AD2696
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks,
erage, G.; Gillet, W.; Grant, C.; Guenthner, I
, Karp, P.; Romero, P.; Zhang, S.
                                                                                                                                                            lipA protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens (strain C58, Dupont) C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2003
                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental Source: Strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Asheno, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lieju, Chado, M.A.; Madeira, A.M.B.N.; Matsukuma, A.Y.; Marchos: Earrins, E.M.E.; Matsukuma, A.Y.; Marchos: Martins, E.M.E.; Matsukuma, A.Y.; Marchos: Marchos, M.C.; Frohm A; Authors: Martins, E.M.E.; Matsukuma, A.Y.; Marchos, C.L.; Marques, M.V.; Martins, E.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Mathors: da Silva, A.J.; de N.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.B., Vanda, A.C.R.; da Silva, A.M.; Salvasak A.B., Vanda, A.C.R.; da Silva, A.M.; Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Silva, A.M.; Savasak A.B., Vanda, A.C.R.; da Silva, A.M.; Vanda, S.; Vettore, A.L.; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE003872; GB:AE003849; NID:g9104975; PIDN:AAF82991.1; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The genome sequence of the plant Pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below A;Accession: B82837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein xF0178 [imported] - xylella fastidiosa (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ДЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-155 <BAE>
A;Cross-references: EMBL:X60448; NID:948577; PIDN:CAA42977.1; PID:948579
C;Superfamily: PAL cross-reacting lipoprotein
                                                                                                                                                                                                                                                                                                                                      105 GTÁIGALIGGLYGNOFGHGNGRKÁLTAAGÁVAGGFIGNEV 144
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XF0178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 VOKOGPTRFSVGQ--RVMLASSGSTVTVSP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 GAVYGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AVAIAAVTLTGCANNNTLSGDVESASQAKQVQTVTYGTLLSVRPVTIQGGDDNNVMGAIG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 50.(
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --NOSLEKVKAGQVTRWRNPDTGNSYSVEP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAVLGGFLGNTVGGGTGRSLATAAGAVAGGMAGQGVQGAMNRTDGVQLEVRKDDGTTILV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLIIISVELVGCAQN-----FSRQE------------VGAAT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.48; 50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.6%; Score 113.5; DB 24.7%; Pred. No. 0.007;
                                                                                        Guenthner, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 112; DB 2; Length 257;
Pred. No. 0.016;
8; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Mismatches
                                                                                                                      D.;
                                                                           Kutyavin, T.; Levy,
                                                                                                      Chen, L.; Wood,
                                                                                                                                              #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 155;
                                                        G.E.; Chen, Y.; Woo,
vy, R.; Li, M.; McClel
                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9a5c)
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                                                                              RESULT 14
S58234
lipA protein – Rhizobium leguminosarum
C;Species: Rhizobium leguminosarum
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QУ Ъ Qy Ъ Qy

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A; Map position: circular chromosome
                                                                                                                                                                                                                                                                              C; Genetics:
A; Gene: AGR_C_1782
                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE007869; PIDN:AAK86781.1; PID:g15155981; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                  R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrot
                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-125 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                        lipA protein [imported] - Agrobacterium tumefaciens (strain C58, Gereon) C;Species: Agrobacterium tumefaciens (C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
D97478
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE008688; PIDN:AAL41986.1; PID:g17739358; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-142 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: AE
A; Accession: AD2696
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 294, 231
A; Authors: Yoo,
111 GAACRNDDGSW
                             145 GTACROPDGRW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                    60 LETAPVGTPVIWTGDDVKGQVVANAP---YQVGN-----QNCRQYSHTLTVDGRDTRVR 110
                                                                   86 LEKVKAGQVTRWRNPDT-GNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 144
                                                                                                                                 30 VGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL----NQS 85
                                                                                                    2 LSACTTTGTRPAGGSLFGR-SAQPSTPFLANLQGGIVG-KSGVELDRGDQTKALEAEYKA 59
                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 QNCRQYSHTLTVDGRDTRVRGAACRNDDGSW 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 QYCREFQQKAMIAGQKQEIYGTACRQPDGRW 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 SLIIISVELVGCAQNESRQEVGAATGAVVGGVAGQLEGKGSGRVAMAIGGAVLGGLIGSK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
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Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVELDRGDQTKALEAEYKALETAPVGTPVIWTGDDVKGQVVANAP---
                                                                                                                                                                                         Similarity 27.5
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGQSMDQQDKIKL----NQSLEKVKAGQVTRWRNPDT-GNSYSVEPVRTYQRYNKQERRQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SILCVSM-LSAC------TTTGTRPAG--GSLFGR-SAQPSTPFLANLQGGIVG-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2317-2323,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.; Tao,
                                                                                                                                                                              13.3%; Score 111; DB 2;
27.5%; Pred. No. 0.0093;
tive 18; Mismatches 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001
), Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Ka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.3%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 111.5; DB 2;
Pred. No. 0.0096;
21; Mismatches 60;
                                                                                                                                                                                  61;
                                                                                                                                                                                                           Length 125;
                                                                                                                                                                         Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56
                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                Markelz,
                                                                                                                                                                                                                                                                                                                                                                                                                                  B.; Goldm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
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Дb Qy В Qy DЪ Qy

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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
G87629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein CC3073 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: G87629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Date: 13-Jan-1996 *sequence_revision 01-Mar-1996 *text_change 08-Oct-1999 C:Accession: S58.234 R:Yeoman, K.H.; Delgado, M.J.; Downie, J.A.; Johnston, A.W.B. submitted to the EMBL Data Library, July 1995 A;Reference number: S58232 A;Accession: S58234
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Search completed: October 27, 2002, 11:11:35 Job time: 10.3523 secs
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A;Gene: CC3073
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A; Residues: 1-232 <STO>
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                                                                                                                  181
                                                                                                                                                122 RRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTE 161
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                                                                                                                                                                                                                                                                                                                                         81 VVGCKASGKKQEVGAVVGALLGAAAGSNLAKNDQGTGTAIGAVVGAGAGSLIGCKMQKSD 140
                                                                                                                                                                                                                                                                                                                                                                                              18 LVGCAQNFSRQEVGAATGAVVGGVAGQLFGK---GSGRVAMAIGGAVLGGLIGSKIGQSM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 13.2%; Score 110.5; DB 2; Length 232; Local Similarity 26.9%; Pred. No. 0.02; les 43; Conservative 22; Mismatches 56; Indels 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 IGQSMDQQDKIKL----NQSLEKVKAGQVTRWRNPD-TGNSYSVEPVRTYQRYNKQERRQ 124
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                                                                                                               RAMASTRGERLGAVDSGTTFQALG---RTKDGKWILVGQD 217
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/AB_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
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Gapop 10.0 , Gapext 0.5
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US-09-057-351-2
US-09-360-490-2
US-08-895-590-2
US-08-895-590-2
US-08-440-519-12
US-08-440-519-12
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US-08-220-151-6
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US-08-232-468A-2
US-08-375-709-7
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; MOLECULE TYPE:
US-08-556-978B-19
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                                                  Query Match
Best Local Similarity
Matches 25; Conserv
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Length 651; Indels 23;

Score 81.5; DB Pred. No. 0.8; 3; Mismatches

9.7%;

unknown protein

55 08/07/ 15, 199 15, 199 15, 199 15, 199 16, AXAMET AXAMET 13,6 MBER: 00MATIO 00MATIO 164 164 165 165 165 165 165 165 165 165	Sequence 19, Application US/U855978B Patent No. 6288169 GENERAL INFORMATION: APPLICANT: FAHNESTOCK, STEPHEN F. TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED TITLE OF INVENTION: SPIDER SILK ANALOGS UMMBER OF SEQUENCES: 107 CORRESPONDENCE ADDRESS: ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINTON STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA ZIP: 19898 COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER: IBM PC COMPATIBLE CORPUTER: MICROSOFT WORD FOR WINDOWS 95 SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 CURRENT APPLICATION NUMBER: 1087556 078B	28 73 8.7 254 4 US-09-128-450-26 29 73 8.7 254 4 US-09-823-494-26 30 73 8.7 666 4 US-09-923-696-6 31 72.5 8.7 479 4 US-09-177-349-3 32 72.5 8.7 547 1 US-08-340-203A-3 33 72.5 8.7 547 2 US-08-452-427-3 35 72.5 8.7 547 2 US-08-452-427-3 36 72.5 8.7 547 3 US-08-911-364-1 37 72.5 8.7 731 2 US-08-911-364-1 37 72.5 8.7 792 2 US-08-911-364-1 38 72.5 8.6 101 4 US-08-556-978B-20 40 72 8.6 101 4 US-08-556-978B-22 41 72 8.6 101 4 US-08-56-978B-62 41 72 8.6 101 4 US-09-247-806-5 43 72 8.6 101 4 US-09-247-806-7 44 72 8.6 101 4 US-09-247-806-7 44 72 8.6 604 4 US-09-247-806-7 45 72 8.6 604 4 US-09-556-978B-63 45 72 8.6 604 4 US-08-556-978B-63 45 72 8.6 604 4 US-08-556-978B-21 US-08-556-978B-19
		Sequence 26, Appl Sequence 26, Appl Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appl Sequence 21, Appli Sequence 5, Appli Sequence 7, Appli Sequence 5, Appli Sequence 7, Appli Sequence 21, Appli

В

23;

Gaps

2

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: Patentin Release #1.0, Ver
APPLICATION DATA:
FILING DATE: 19-APR-1995
CLASSIFICATION: 435
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US-08-425-069-2
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: TYPE: PRT
: ORGANISM: Nephila clavipes
US-09-247-806-1
                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/084250
Patent No. 572810
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: YU, Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-09-247-806-1
Sequence 1, Application US/09247806
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CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER FILING DATE: 1998-02-11
SOFTWARE: PSEQ ID NOS: 14
SEQ ID NO 1 patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
NUMBER OF SEQUENCES: 69
CORPRECIAMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJUKESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5728810th Washington Street STATE: Vizginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
FILE REFERENCE: 6388-0365-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 QEVGAATGAVVG----GVAGQ------LFGKGSGRVAMAIGGAVLGG 64
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Pred. No. 0.
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                                                                                       US-08-317-844B-2
                                 Query Match
                                                                                                                                                                                      TELEFAX: (70) 241-12848
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 mino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/317,844B
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
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US-08-317-844B-2
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                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-425-069-2 Protein
                                                                                                                                TYPE: amino acids TOPOLOGY: ];...
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STATE: Viry..
COUNTRY: U.S.A.
TIP: 22046
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APPLICANT: Xu, Ming
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APPLICANT: Xu, Ming
APPLICANT: Author of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first of the first o
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Best Local
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CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch CITY: Falls Church
STATE: Virginia
COMMEDV. Friginia
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SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: amino acid
TYPE: amino acid
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REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 144
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 LIGSKIGQ 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2, Application US/08317844B
5. 5989894
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                                                                                                                                                                                                                                                                                                                  . (703) 241-2848
                                                                                                               protein
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                9.78;
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Score 81.5;
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Pred. No. 0.91;
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                                                                                                                        Query Match
Best Local Similarity
                                                                                                             Matches
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                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0486 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: GI 1174414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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CTTY: Palo Alto
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                                                                          28 QEVGAATGAVVG----GVAGQ-------LFGKGSGRVAMAIGGAVLGG 64
                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
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LGGQGAGQ 558
                          LIGSKIGQ 72
                                                    QGAGAAAAAAVGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
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                                                                                                          Score 81.5; DB Pred. No. 0.96; 3; Mismatches
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Matches
                                                                                                      Sequence 8, Application Patent No. 6309861 GENERAL INFORMATION:
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Query Match
                                                                        APPLICANT: Ambrosius, APPLICANT: Rudolph, F
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 865 amino acids
TYPE: AMINO ACID
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TELECOMMUNICATION INFORMATION: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                  797
                                                                                                                                                                                                                                                                             748
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                                                                                                                                                                                                                                           121 ERRQOYCRE-FOOKAMIAGOKO 141
                                                                                                                                                                                                                                                                                                                                       688 FMNGLAELFNGMGQVGQAIGKVVVGAAGAIVSTISGVSAFMSNPFGALAIGLIIIAGLVA 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 36; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                  ERKLEEAREMIKYMALVSAEER 818
                                                                                                                                                                                                                                                                                                          SKIGQSMDQQDKIKLN------QSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: BIRCH, STEWART, KOLASCH & BIRCH 301 No. 5369025th Washington Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YANAGIDA, No. 5369025oru
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OGAWA, Ryohei
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                                                                        Rainer
                                                                                           Dorothee
                                                                                                                                      US/09553498
                                                                                                                                                                                                                                                                                                                                                                                                                 9.3%; Score 78; DB 1; 25.4%; Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/07/803,633A
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                            the production
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                              of naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 865;
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                              folded and
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                              secreted
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202 SL----TISSMEAEDAATYYCOOWSSNPLTFGAGTKLELKRAAAEQ-----KLISEE 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 MSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARFSGSGSGTSY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 LGGLIGSKIGQSNDQQDKIK-LN-------QSLEKVKAGQVTRWRNPDTGNSY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 LOMTSLRSEDTAMYYCARDYGAY-WGQGTTVTVSSGGGGSGGGGGGGGGGGSDIELTQSPAI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LOGSSLIIISVFLVGCAQNFSRQEVGAATGAVV----GGVAGQLFGKGSGRVAMAIGGAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                  TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KERANOTO2
CLONE: 2029060
US-09-360-490-2
                                 B
                                                      δÃ
                                                                            Matches
                                                                                                 Query Match
                                                                                                                                                                                                INFORMATION FOR SEO ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 551 amino acids
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Patent No.
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54 GASFGSRSLYNLGGAKRVSLNGCGSSCRSGFGGRASNGFGVNSG---FGYGGGVGGGFSG 110
                                                                                                                                                                                                                                              REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PE-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                      8 GSSLIIISVELVGCAQNESRQEVGAATGAVVGGVAGQLEGKGSGRVAMAIGGAVLGGLIG 67
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/067,351
                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                      Local
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Best Local Similarity 22.49
Conservative
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                    NAME: CERRONE, MICHAREGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 POF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 PSEPVCPPGGIOEVTVNQSLLTPLHLQIDPTIORVRAEEREQIKTLNNKETSFIDKVRFL 170
                                                                 Similarity 22.4
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 SK-----IGOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTY 114
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                                                                                                                                                                                          amino acid
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                                                                                                                                            KERANOT02
                                                                                                                                                                                                                                            (650)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang, Y. Tom
                                                                                                                                                                             single
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, 845-4166
NO: 2:
                                                                                                                                                                                                                                                                                                MICHAEL
                                                                              9.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN KERATINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.2%;
                                                                  28;
                                                                 Score 77; DB 4; Length 551; Pred. No. 2;
                                                                                                                                                                                                                                                                  PF-0511 US
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
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                                                          53;
                                                      Indels
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RESULT 8 US-09-067-351-2

Sequence 2, Application US/09067351 Patent No. 5994081 GENERAL INFORMATION:

APPLICANT: Hiliman, APPLICANT: Corley, I

Jennifer L.

UMBER OF SEQUENCES:

ADDRESSEE:

TLE OF INVENTION:

Baughn, Mariah Corley, Neil C

HUMAN KERATINS

APPLICANT:

В Qγ

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Matches Query Match

Local Similarity es 37; Conserv

9.3%;

Conservative

28;

Score 77.5; DB Pred. No. 0.65; 28; Mismatches

DB 4;

Length 255;

81; Indels

LENGTH: 255; TYPE: PRT; ORGANISM: E. coli

CURRENT APPLICATION NUMBER: US/09/553,498
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: EP99107412.1
NUMBER OF SEQ ID NOS: 10
LENGTH: 255
TWONE: NEW TOWNS: NEW TOWN

US-09-067-351-2

IMMEDIATE SOURCE

TOPOLOGY: STRANDEDNESS: LENGTH:

linear

Single

MMEDIA. LIBRARY: KEAL CNE: 2029060

KERANOT02

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TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

: 551 amino acids amino acid

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555

PF-0511 US

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0

COMPUTER: Floppy disk
OPERATING SYSTEM PC COMPAtLble
SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS 6.2
APPLICATION NUMBER: US/09/067.351
FILING DATE: Herewith

STREET: 3174 PORTER CITY: PALO ALTO STATE: CALIFORNIA CORRESPONDENCE ADDRESS:

E: INCYTE PHARMACEUTICALS, INC.

COUNTRY:

USA

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RESULT 11
US-08-895-590-2
; Sequence 2, Application US/08895590
; Patent No. 6207410
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                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 2516 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
                                                                                                          2508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zheng, Wei
APPLICANT: Dubald, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Invertebrate Alphal
TITLE OF INVENTION: Calcium Channel Subunit
                                                                                                                                                                                                                                            2389 IGSSNGSIFGGSAGGLGGAGSGGVG-GLGGSSSIRNAFGGSGSGPSSLSPQHQPYSGTLN 2447
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          2448 SPPIPDNRLRRVATVTTTNNNNKSQVSQNNSSSLNVRANANSQMNMSPTGQPVQQQSPLR 2507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                        138 GQKQEIYGT 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 699 Princ
CITY: Alexandria
                                                                                                                                                                                                                                                                            30 VGAATGAVVGGVAGOLFGKGSGRVAMAIGG--AVLGGLIGSKIGQS----MDQQDKIKLN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 19-JACLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                               Local Similarity
les 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 39, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                          GQGNQTYSS 2516
                                                                                                                                                                                                          -----QSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SK-----IGOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McGowan, Malcolm M.
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                                                                                                                                                                                                                                                                                                               Conservative
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Ren, Dejian
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                                                                                                                                                                                                                                                                                                            9.2%; Score 76.5; 1
24.8%; Pred. No. 17;
tive 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                              Length 2516;
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US-07-910-760-12
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                 STREET:
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; MOLECULE TYPE: protein US-08-895-590-2
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Best Local Similarity 24.8
Matches 32; Conservative
                                                                                                                                                                                         Patent No. 5683864
GENERAL INFORMATION:
                                                                                                                                                                                                               sequence 12, Application US/07910760 Patent No. 5683864
                                                      APPLICANT: Houghton, Michael
APPLICANT: Choo, Qui-Lim
APPLICANT: Kuo, George
TITLE OF INVENTION: Combinatio
TITLE OF INVENTION: Antigens;
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCGGWAN, MALCOLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hall, Linda M.
APPLICANT: Ren, Dejian
APPLICANT: Zhen, Wei
APPLICANT: Dubald, Manuel
TITLE OF INVENTION: Genes
                                                                                                                                                                                                                                                                                                                                   2508 GQGNQTYSS 2516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2389 IGSSNGSIFGGSAGGLGGAGSGGVG-GLGGSSSIRNAFGGSGSGPSSLSPQHQPYSGTLN 2447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              2448 SPPIPDNRLRRVATVTTTNNNNKSQVSQNNSSSLNVRANANSQMNMSPTGQPVQQQSPLR 2507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                        138 GOKQEIYGT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 -----QSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIA 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                      ADDRESSEE:
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SEE: Chiron Corporation: p.O. Box 8097 (Int. Emeryville
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                                                                                               Antigens
                                                                                             Combinations
Antigens for
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                  (Int. Prop. R-440)
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Pred. No. 17;
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                                                                                               Of Hepatitis C virus (HCV)
Use in Immunoassays for An
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                                                                                             for Anti-HCV Antibodies
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RESULT 13
US-08-440-519-12
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' MOLECULE TYPE:
US-07-910-760-12
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: P.O. Box 8097 (Int. |
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                      APPLICATION
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APPLICATION NUMBER: US/07//
FILING DATE: 07-JUL-1992
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COUNTRY:
ZIP: 94662-809,
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
MEDLIUM TYPE: Floppy disk
MEDLIUM TYPE: FLOPPY DISK
MEDLIUM TYPE: FC-DOS/MS-DOS
TYPE SYSTEM: PC-DOS/MS-DOS
TYPE SYSTEM: PC-DOS
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                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 912 NKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPI--PKA 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 QSL-----EKYKAGO-VTRWRN-----PDTGNSYSVEPVRTYORYNKO 120
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                                                                                                                                                                                                 94662-8097
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                                                                                                                                                                                                                                                 CA
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Choo, Qui-Lim
                                                             Patentin
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                                       DATA
                                                                                                                                                                                                                                                                                                                                                      Combinations of Hepatitis C virus (HCV)
Antigens for Use in Immunoassays for Anti-HCV Antibodies
12
                                    Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            655-3542
US/08/440,519
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Pred. No.
                                                                                                                                                                                                                                                                          Prop. R-440)
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RESULT 14
US-08-440-549-12
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            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,760
FILING DATE: 07-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-440-519-12
ATTORNEY/AGENT INFORMATION:
                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,549

FILING DATE: 12-MAY-1995
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    STREET: P.C. STREET: P.C. CITY: Emeryville
                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                 APPLICANT: Choo, Qui-Lim
APPLICANT: Kuo, George
TITLE OF INVENTION: Combinations of Hepatitis C virus
TITLE OF INVENTION: Antigens for Use in Immunoassays f
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Best Local
                                                              CLASSIFICATION:
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                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (510) 655-3542 INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                      ADDRESSEE:
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LENGTH: 1021 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 QSL-----EKVKAGQ-VTRWRN-----PDTGNSYSVEPVRTYQRYNKQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,760
FILING DATE: 07-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Blackburn Esq., Robert P. REGISTRATION NUMBER: 30,447
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CLASSIFICATION:
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94662-8097
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42; Conservative
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GY: linear
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O. Box 8097 (Int.
                                                                                                                                                                                                                                                                                                                                                               Houghton, Michael
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                                                                       UMBER: US/08/440,549
12-MAY-1995
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20.9%; Pred. No. 6;
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Esq., Robert P.

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RESULT 15
US-08-190-199A-65
; Sequence 65, Application US/08190199A
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Best Local
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                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,199A
FILING DATE: 13-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01483
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (510) 601-27/
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: EMBLET
APPLICANT: GOROCH
                                      FILING DATE: 10-AUG-19 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1021 amino act
SEQUENCE CHARACTERISTICS: LENGTH: 236 amino acid
                                                                                           APPLICATION NUMBER: GB 9: FILING DATE: 11-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JONES, F
APPLICANT: WINTER,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                970 RRPEGRTWAQPGYPWPLYGNE 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 RQPDGR------WQVISTE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         912 NKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPI--PKA 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  852 PAILSPGALVVGVVCAAILRRHVGPGEGAVQWMNRLIAFASRGNHVSPGNSSTNPKPQKK 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                792 GAATAFVGAGLAGAAIGSVGLGKVLIDILAGYGAGVAGALVAFKIMSGEVPSTEDLVNLL 851
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 9.1%; Score 76; DB Local Similarity 20.9%; Pred. No. 6; nes 42; Conservative 24; Mismatches
                                                      APPLICATION NUMBER: GB 9 FILING DATE: 10-AUG-1991
                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 QSL-----EKVKAGQ-VTRWRN-----PDTGNSYSVEPVRTYQRYNKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 GAATGAVVGGVAGQLFGK-GSGRVAMAI----GGAVLGGLIGSKI--GQSMDQQDKIKLN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 0101.002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: PILLSBURY MADISON & SUTRO, L.L.P. 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBLETON, Michael J. GOROCHOV, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JONES, Peter T.
WINTER, Gregory P.
VENTION: TREATMENT OF CELL POPULATIONS
                                                                                                                                                                                                                                                                                                               Microsoft Word
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                                                                                                                                      GB 9212419.7
                                                                             GB 9117352.6
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                                                                                                                                                                                                                                                                  Query Match 9.0%; Score 75; DB 2; Best Local Similarity 19.6%; Pred. No. 1.1; Matches 31; Conservative 27; Mismatches 7
201 L----TISSMEAEDAATYYCQQWSSNPLTFGAGTKLEL 234
                                                                                     141 SASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARFSGSGSGTSYS
                                        108 VEPVRTYORYNKQERROQYCREFQQKAMI--AGQKQEI 143
                                                                                                                                63 GGLIGSKIGQSMDQQDKIK-LN------QSLEKVKAGQVTRWRNPDTGNSYS 107
                                                                                                                                                                             81 LQMTSLRSEDTAMYYCARDYGAYWGQGTLVTVSAGGGGSGGGGGGGGGGGGGQIVLTQSPAIM 140
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                          6 LQGSSLIIISVFLVGCAQNFSR----QEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL 62
                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                                                                                                                    Length 236;
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Search completed: October 27, 2002, 11:12:12 Job time: 9.39378 secs

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Title:
Perfect score:
Sequence:
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Gapop 10.0 , Gapext 0.5
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    AAG78025
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              Piscirickettsia sa
OSPA antigen amino
Optimised OSPA pro
C17E2 OSPA constru
OSPA B-cell epitop
Moraxella catarrha
Porphorymonas ging
Porphorymonas ging
PBOMP-2 gene prod.
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  recombinant
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			2222222222 200000000000000000000000000	
300 324 346 346	429 551 1251 514 2516 2516 2516	255 255 255 255 255 255 267	102 302 542 542 116 2017 2599	2309 666 651 718 718 718
11 22 22 22	10 21 22 22 17 17	114 22 22 22 22	22 22 22 21 21	22 22 20 19 19
AAR05878 AAB76751 AAG92057 AAB76750	AAP90064 AAY52398 ABB61254 AAU36520 AAW01875 AAW01884 ABB61076	AAW27178 AAR37169 AAR31398 AAB11398 AAB74199 AAB70769 AAB70769 AAY72020 ABG28648	AAM41943 AAM40157 ABB65790 ABB65791 ABB70501 ABB70501 AAY11028 ABG06301 AAY75098	ABB66232 ABB58019 AAN740097 AAR14308 AAN53346 AAN53370
Merozite surface a Corynebacterium gl C glutamicum prote Corynebacterium gl	Antigenic protein Human keratin KERT Drosophila melanog Pseudomonas aerugi Neuronal invertebr Invertebrate calci Drosophila melanog	a clavipe a clavipe s Disease i express cFvOxazol sion plas otovora F human dia	Human polypeptide Human polypeptide Human polypeptide Drosophila melanog Drosophila melanog Drosophila melanog H. pylori ORF Olcp Novel human diagno Neisseria meningit	Drosophila melanog Drosophila melanog Spider silk protei N.clavipes draglin Nephila clavipes s N. clavipes spider

ALIGNMENTS

RESULT 1 AAG78025

Piscirickettsia salmonis polypeptide P10.6.

15-JAN-2002 (first entry)

AAG78025;

AAG78025 standard; Protein; 162

A

Simard Burzio 11-MAR-2000; 2000GB-0005838. 01-JUL-2000; 2000GB-0016080. 01-JUL-2000; 2000GB-0016082. 29-JUL-2000; 2000GB-0018599. Piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial; septicaemia; SRS; surface antigen; vaccine; antibacterial; fish; ATCC VR-1361. WPI; 2001-639050/73. N-PSDB; AAH79040. 12-MAR-2001; 2001WO-GB01055 20-SEP-2001. WO200168865-A2 Piscirickettsia (AQUA-) AQUA HEALTH EURO LTD ŗz Brouwers H, salmonis. Jones ß Griffiths s Valenzuela P;

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Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis.
                                                                                                       (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
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                                                                                                                                                  17-SEP-1999;
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                                                                                                                                                                                                            CA2281913-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 162;
                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                  Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                  Poikilothermic vaccine; OspA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                        OspA antigen amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                   11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                AAB81126 standard; Protein; 162 AA.
                                                         2001-316844/34
DB; AAF86246.
                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ERROQYCREFQOKAMIAGQKOEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to protect fish against p. salmonis which causes piscirickettsiosis, also known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Fig 5; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids encoding an amino acid sequence homologous to the surface antigen present on Piscirickettsia salmonis are useful to protect fish against piscirickettsiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                   Burian J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                             99CA-2281913.
                                                                                                                                                                 99CA-2281913.
                                                                                                                                                                                                                                                                              fish; Piscirickettsia salmonis; rickettsial pathogen; salmonid rickettsial septicaemia; rickettsial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                    Location/Qualifiers
110..129
                                                                                                                                                                                                                      /label= B_cell_epitope
                                                                                  Kuzyk MA;
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Pred. No. 3.2e-80;
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AAB81127
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           N-PSDB;
                                       Kay ww,
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DЬ Qy

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(KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                  Method for protecting septicaemia and other
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Best Local S
                                                                                                                                                    17-SEP-1999;
                                                                                                                                                                         17-SEP-1999;
                                                                                                                                                                                               17-MAR-2001.
                                                                                                                                                                                                                    CA2281913-A1.
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                                                                                                                                                                                                                                                                                        Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                         Poikilothermic fish, Piscirickettsia salmonis, rickettsial pa
vaccine; OspA; salmonid rickettsial septicaemia; rickettsial
                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                              Optimised OspA protein 17E2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                          AAB81127;
                                                                                                                                                                                                                                                                                                                                                                                                                      AAB81127 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a OSPA in the form of a vaccine. The method cospic can immunogenic fragment of particularly poikilothermic fish, against the bacterial pathogen animals, rickettsial septicaemia (SRS) and other fiskettsial gainst salmonid recember 1. Sequence represents P. salmonis OSPA protecting against salmonid N-terminal fusion partner is used in a vaccine to create an anti-OSPA anti-hodu resonness.
                                                  2001-316844/34.
)B; AAF86247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ERRÓQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ERRQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VLGGLIGSKIGOSMDQODKIKLNOSLEKVKAGOVTRWRNPDTGNSYSVEPVRTYORYNKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 2B; 35pp; English.
                                                                                 Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQ
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                               99CA-2281913
                                                                                                                                                                     99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                               Location/Qualifiers 109..128
                                                                                                                                                                                                                                      /label=
                                                                               Kuzyk MA;
poikilothermic fish against salmonid rickett.
rickettsial diseases comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 836; DB 22; 100.0%; Pred. No. 3.2e-80; tive 0; Mismatches 0;
                                                                                                                                                                                                                              B_cell_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                                                                                                                     AΑ
                                                                                                                                                                                                                                                                                                                 salmonis; rickettsial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
            rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162;
                                                                                                                                                                                                                                                                                                         disease;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents optimised P. salmonis OspA protein 17E2. The DNA encoding OspA 17E2 (AAR86247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                 Poikilothermic fish; Piscirickettsia vaccine; OspA; salmonid rickettsial sSRS; 17E2; fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a
        (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                        C17E2 OspA construct with N-terminal fusion
                                                                                                                                                                                                                                                                                                                                  AAB81128 standard;
                                                                  17-SEP-1999;
                                                                                                        CA2281913-A1
                                                                                                                                                       Region
                                                                                                                                                                         Region
                                                                                                                                                                                                                Piscirickettsia
                                                                                                                                                                                                                                                                                             11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                17-SEP-1999;
                                                                                     17-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine
                                                                                                                                                                                                                                                                                                                                                                                  122
                                                                                                                                                                                                                                                                                                                                                                                                    123
                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to a method for the protection against infect polkilothermic fish by the bacterial pathogen, Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK
                                                                                                                                                                                                                                                                                                                                                                                                   ROOYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK
                                                                                                                                                                                                                                                                                                                                                                                                                      GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                           (first entry)
                                                                  99CA-2281913
                                                                                                                                                                                                                salmonis
                                                                                                                                           /label= Undefined_N·terminal_fusion_partner
96..256
/label= C17E2_OsbA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ن</u>
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the OspA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.5%;
                                                                                                                         "Product of OspA gene
Escherichia coli"
                                                                                                                                                                                                                                          scirickettsia salmonis; rickettsial pathogen; rickettsial septicaemia; rickettsial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 815; DB 22;
Pred. No. 5.1e-78;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                  256
                                                                                                                                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                        partner
                                                                                                                                    optimised
                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                                                                                                                                                                                                                                                                    162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                    for expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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(KAYW/) (BURI/) (KUZY/)

KAY W W. BURIAN J.

KUZYK M A.

17-SEP-1999;

99CA-2281913 99CA-2281913

17-SEP-1999;

17-MAR-2001.

Kay WW,

Burian J,

Kuzyk

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RESULT 5
AAB81130
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Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a P. salmonis OspA construct optimised for expression in Escherichia coli, fused to an undefined N-terminal fusion partner. The fusion protein is used in a
                                                                                                                                                                          OspA B-cell
CA2281913-A1
                                                                                   Poikilothermic fish; vaccine; OspA; salmor SRS; antibody.
                                                                                                                                                                                                                      11-JUL-2001
                                                                                                                                                                                                                                                                  AAB81130
                                                                                                                                                                                                                                                                                                              AAB81130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for protecting septicaemia and other
                                         Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                           217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 158; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                        RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for protecting poikilothermic fish against salmonid rickettsial emia and other rickettsial diseases comprises administering a containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Fig 5; 35pp;
                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 AA;
                                                                                                                                                                        epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                    (first entry)
                                                                                                            salmonid
                                                                                                                                                                                                                                                                                                            Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuzyk MA;
                                                                                                                                                                          peptide
                                                                                                                              Piscirickettsia salmonis; rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.5%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                          rickettsial septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 815; DB Pred. No. 9.3e
                                                                                                                                                                             #2
                                                                                                                                                                                                                                                                                                              20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
).3e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                           256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156
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2001-316844/34.

Example 2; Page 17; 35pp; English.

Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis

This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an Immunogenic amount of a particularly poikilothermic fish, against the salmonis specific antigen termed OspA, or an immunogenic fragment of particularly polkilothermic fish, against the bacterial pathogen animals, rickettsial septicaemia (SRS) and other ricketting against salmonid sequence represents an immunogenic epitope of the p. salmonis OspA protein. The peptide is used to raise rabbit anti-OspA antibodies.

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RESULT 6
AAB20105
ID AAB2
XX
AC AAB2
XX
The present sequence is that of BASB113 protein from Moraxella Catarrhalis strain Mc2931 (ATCC 43617), a Causative agent of otitis media in children and pneumonia in adults. The invention provides BASB113 polypeptides, and polynucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB113 Composition comprising a BASB113 polypeptide, an immunogenic
                                                                                                     Claim 1; Page 67; 86pp;
                                                                                                       New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia.
                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                         Thonnard J;
                                                                                                                                                                                                                                                 25-JUN-1999;
                                                                                                                                                                                                                          (SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                              23-JUN-2000; 2000WO-EP05851.
                                                                                                                                                                                                                                                                                           04-JAN-2001.
                                                                                                                                                                                                                                                                                                               W0200100836-A1
                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                             BASB311; infection; otitis media; pneumonia; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                             Moraxella catarrhalis BASB113 protein.
                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB20105;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB20105 standard; Protein; 224
                                                                                                                                                                     2001-112458/12.
DB; AAF30043.
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                           99GB-0015044.
                                                                                                                                                                                                                  BEECHAM BIOLOGICALS
                                                                                                    English.
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AAY34318

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RESULT 7
AAY34487
AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAI AAX34583. AAX31802 to AAX91989 represent PCR primers used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Д
                                               Claim 1; Page 469; 588pp; English.
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                                                                        Antigenic Porphorymonas gingivalis peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888888888<del>%</del>&
                                                                                                    WPI; 1999-385613/32.
N-PSDB; AAX91705.
                                                                                                                                       Ross
                                                                                                                                                                                  23-APR-1998;
05-MAY-1998;
22-MAY-1998;
29-JUL-1998;
                                                                                                                                                                                                                        04-AUG-1998;
10-DEC-1997;
31-DEC-1997;
30-JAN-1998;
10-MAR-1998;
09-APR-1998;
                                                                                                                                                            (CSLC-) CSL LTD.
                                                                                                                                                 Agius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                           10-DEC-1998;
                                                                                                                                                                                                                                                                                                             17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                  Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                   Porphorymonas gingi
vaccine; antigenic.
                                                                                                                                                                                                                                                                                                                                                                                          Porphorymonas gingivalis protein PG3
                                                                                                                                                                                                                                                                                                                                                                                                                      25-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY34487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY34487 standard; Protein;
                                                                                                                               , CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment of a BASB113 polypeptide, or a polypeptide having at least 85% amino acid sequence identity to BASB113, or comprising a polypeptide encoding such a polypeptide. A claimed method of a polypeptide or antibody. A claimed therapeutic composition useful in treating humans with M. catarrhalis infection comprises at least 1 antibody directed against a BASB13 polypeptides also have utility in raising specific antibodies, and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVVLLASSMALAGCANTGT---TGNGTGFGGANVNKAVIGAVAGAL---GGTAISKATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSSLIIISVFLYGCAQNESRQEVGAATG-----AVVGGVAGQLFGKGSGRVAMAIGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AVLGGLIGSKIGOSMDOODKIKLNOSLEKVKAGGVTRWRNPDTGN 104
                                                                                                                                 Barr IG,
Rothel LJ,
                                                                                                                                    Rothe1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
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                                                                                                                                                                                                98AU-0002264
98AU-0002911
98AU-0003128
98AU-0003338
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                               98AU-0004917
                                                                                                                                                                                                                                                                                                                                                              gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                               gingivalis
                                                                                                                                                                                                                                       98AU-0001546
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97AU-0001182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                      98WO-AU01023.
                                                                                                                              Hocking DI
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%;
                                                                                                                                        DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 108; DB 22
Pred. No. 0.0028;
                                                                                                                                    Margetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                  MΒ,
                                                                    for preventing
                                                                                                                               Patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35,
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                                                                                                                               MA,
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В QΥ

110 PVRTYQRYNKQERRQQYCRE 129

1 PVRTYQRYNKQERRQQYCRE 20

Matches

Local

Similarity

13.48; 5-100.08; Pr

Score 112; DB 22; Pred. No. 4.9e-05;

Length 20; Indels

Mismatches

0;

0; Gaps

0,

Conservative

Query Match

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AAY34362
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Best Local (
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                                                                                                                                                                                                                                                             04-AUG-1998;
10-DEC-1997;
31-DEC-1997;
30-JAN-1998;
10-MAR-1998;
09-APR-1998;
23-APR-1998;
AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can
                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                  W09929870-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphorymonas gingivalis; vaccine; antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY34362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY34362 standard;
                                                                                                       gingivitis
                                                                                                                Antigenic Porphorymonas gingivalis
                                                                                                                                                    WPI;
                                                                                                                                                                          Ross
                                                                                                                                                                                   Agius
                                                                                                                                                                                                                                                                                                                                                       10-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphorymonas gingivalis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                        (CSLC-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : ||: ||:| |
66 ALIGKKMDKQKK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                        1999-385613/32
DB; AAX91580.
                                                                                                                                                                         ВС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKIGQSMDQQDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASVLAVALVFAGCGLN--NMAKGGLIGAGVGGAIGAGVGNVAGNTAVGAIVGTAVGGAAG
                                                                                                                                                                                 CT,
                                                                               1; Page 325-326;
                                                                                                                                                                                                          CSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                        Rothel
                                                                                                                                                                        Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        gingivalis.
                                                                                                                                                                                                                             98AU-0005028
97AU-0001182
97AU-0011546
98AU-000254
98AU-0002128
98AU-0003128
98AU-0003128
98AU-0003338
98AU-0003338
                                                                                                                                                                                                                                                                                                                                                       98WO-AU01023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.6%;
36.1%;
                                                                                                                                                                        Hocking DM, Webb EA;
                                                                              588pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 105.5; DB Pred. No. 0.0051;
                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
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                                                                                                                                                                                  Margetts MB,
                                                                                                                 peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                  for
                                                                                                                 preventing
                                                                                                                                                                                   Patterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                   MA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
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δÃ

21;

Conservative

9;

Indels

Gaps

0,

82 0;

Similarity

30 VGAATGAVVGGVAGQLEGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKL

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AARO5799
ID AARC
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Best Local S
Matches 21
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Best Local
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                                                                                    The PBOMP proteins were isolated from a PBOMP-enriched insoluble cell wall fraction from physically disrupted cells of H. Influenzae and then solubilising the PBOMP from the cell wall fraction by heatiful in the presence of a detergent or digesting the cell wall fraction with lysozyme, opt. In the presence of a detergent. The genes encoding the PBOMP proteins were isolated by screening a DAN library with an oligonucleotide probe based on the amino acid sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
                                                                         with lysozyme, opt. in the presence of a detergent. The encoding the PBOMP proteins were isolated by screening with an oligonucleotide probe based on the amino acid s PBOMP protein, or using antibodies to PBOMP.
                                                                                                                                                                                                                  Outer membrane protein epitopes of Haemophilus the prodn. of antibodies, in vaccines and for p
                                                                                                                                                                                                                                                                                                                                      01-SEP-1988;
21-AUG-1989;
                                                   Sequence
                                                                                                                                                                                Disclosure; Fig 15;
                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                        Anilionis A,
                                                                                                                                                                                                                                                                                                               (PRAX-) PRAXIS BIOLOGICS IN
                                                                                                                                                                                                                                                                                                                                                                        31-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                       WO9002557-A
                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Outer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PBOMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR05799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR05799 standard; Protein; 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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DB; AAQ03870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKIGQSMDQQDK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane proteins;
s Biologics Outer Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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                                                    154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              influenzae.
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                                                                                                                                                                                                                                                                                                                                     88US-0239572.
89US-0396572.
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                                                                                                                                                                                164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                  12.
39.
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               . 68
                                                                                                                                                                                                                                                                                         Deich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PBOMP-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
    Score 102; DB Pred. No. 0.00 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105.5; DB Pred. No. 0.0053; 2; Mismatches 3
                                                                                                                                                                                                                                                                                        RΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunisation;
                                                                                                                                                                                                                                                                                        Zlotnick GW,
DB 11.
0.0074;
23;
                                                                                                                                                                                                                   prodn.
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                                                                                                                                                                                                                    influenzae- used
prodn. of reagents
                                                                                                                                                                                                                                                                                          Green
                          Length 154;
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                                                                                                                                                                                                                   reagents
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62

VGTLGGGALGGIAGSTIGGGRGQAIAAVVGAIGGAIAGSKIEEKMSQVNGAEL 114

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(MELL/) MELLO C M.
(ARCI/) ARCIDIACONO S.
(BUTL/) BUTLER M M.
(USSA) US SEC OF ARMY.
                                                                                                    20-JAN-2000; 2000US-0490291
                                                                                                                              01-NOV-2000; 2000WO-US30086.
                                                                                                                                                                                                                                        Misc-difference 522 rencoded by CGA
                                                                                                                                                                                                                                                                Misc-difference 427 encoded by TAT'
                                                                                                                                                                                                                                                                                                  Misc-difference 417
                                                                                                                                                                                                                                                                                                                                                  Spider; orb-weaver; silk protein; pETNcDS; structural protein; purification; fibre; spinning.
                                                                                                                                                                                                                                                                                                                                           Nephila clavipes
                                                                                                                                                                                                                                                                                                                                                                                                       Spider recombinant silk protein pETNCDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB82611 standard; Protein; 528
                                                                                                                                                                                                              /note= "encoded by GAG"
Butler MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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Drmanac RT, Liu C, (HYSE-) HYSEQ INC.

Tang

2001-639362/73

31-MAR-2000; 23-AUG-2000;

2000US-0540217. 2000US-0649167.

30-MAR-2001; 2001WO-US08631.

11-OCT-2001. W0200175067-A2 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Novel human diagnostic protein #15897.

(first entry)

18-FEB-2002 ABG15906;

ABG15906 standard; Protein; 309

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RESULT 11 AAB82611

AAB82611;

Дb

δÃ

The invention

Claim 20; SEQ ID No 46265; 103pp; English.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations biodiversity.

WO200153333-A1

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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC to restore normal activity of (II) or to treat disease states involving or imaging or sites expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or imaging of sites expressing (II). (II) and its binding partners are useful for restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful in tissue, as molecular weight markers and as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical consisting of sites expressing (II). (I) and (II) are useful for treating or disorders involving aberrant protein expression or biological activity. CC and to produce other types of data and products dependent on ECC and to produce other types of data and products dependent on DNA and CC specification, but was obtained in electronic format directly from WIPO CC at ftp. wipo.int/pub/published pot sequences of the invention.
                                                                                                      185 IISTLPAKVAVDNSQNKRNAQAFGALIGAVAGGVIGHNVGSGSNSGTTAGAVGGGAVGAA 244
                                                                                                                                 13 IISVFLVGCAQNFSR------QEVGAATGAVVGGVAGQLFGKG--SGRVAMAIGGAVLGGL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relates to isolated polynucleotide (I) and II) sequences (I) is useful as hybridisation
                                                                                                                                                                                                                         Score 98; DB;
Pred. No. 0.04;
11; Mismatches
                                                                                                                                                                                                                       DB 22;
0.047;
hes 39;
                                                                                                                                                                                                                                                            Length 309;
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                                                                                                                                                                                                       w
••
                                                                CC Clavips) recombinant silk protein pETNCDS. The invention of the orb-weaver spider (Nephila CC clavips) recombinant silk protein pETNCDS. The invention of structural proteins. Organic acids are used to lyse recombinant CC cells or other biological samples (such as non-recombinant) of the structural proteins. Organic acids are used to lyse recombinant CC proteins by hydrolysing many of the macromolecules while leaving CC the structural proteins intact. In the case of silk proteins, the criminal proteins intact. In the case of silk proteins, the criminatography and processed into an aqueous-based mixture for into vector pET24 for recombinant expression in Escherichia coli, and recombinant silk protein was obtained using formic acid containing denaturant (3 M guanidine-HCl) and by affinity cometors of the invention can be used in the construction of many the invention can be used in the construction of many cometorials including films, fibres, woven articles, sutures, method has the following advantages over prior art: it involves can be steps, requires less time and smaller volumes of reagents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 41-42; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recovering structural polypeptides in a biological sample, useful for purifying and spinning spider sliks and other structural proteins, comprises treating the sample containing the polypeptides with an acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mello CM,
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DB; AAH26304.
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Query Match Best Local : Matches

Local

Similarity

11.78; 34.08;

Conservative

Sequence

309 AA;

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RESULT 12
ABB66232
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Matches 34
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Best Local
                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 25488; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                   New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB66232 standard;
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is easy
2124 QQQQQRQVGGGNGPSMNALGGRGSGAVGSGSGN-----
                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                           Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      benign
                                                                                                                                                        (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 QGAGAAAAAAAAGGAGQGGLGGQGAGAAAAAAAGGAGQGGLGGQGAGQ 366
                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 QEVGAATGAVVGGVAGQ--LFGKGSGRVAMAIGGAVLGGLIGSKIGQ
                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                     QNFSRQEVGAATGA---VVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDK
                                                                                                                                                                                                                                                                                                                                                    2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s in better recovery of protein at higher purity (70-99%), y to scale up, and the fibres are spun in an environmentally solution reducing hazardous waste accumulation and cost.
                                             Similarity 27.
                                                                                                                                                                                                                                                                                                                                         ABL10335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster polypeptide SEQ ID NO 25488
                                                                                              2309
                                                                                                                                                                                                                                                                                                                                                                           Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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                                                        10.3%;
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                                                                                                                                                                                                                                                                                                                                                                           PWD,
                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 for elucidating cell signalling and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biology;
                                              18;
                                            Score 86.5; D
Pred. No. 9.9;
18; Mismatches
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Pred. No. 0.51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell signalling; insecticide;
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                                                    DB
3.9;
-GGGGGGGAGGSQVGGNGGGNGV 2178
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RESULT 13
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                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signaling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmacceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes from Drosophila and interactions
                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2179
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 849; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL02122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
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11-JUL-2000; 2000US-0614150
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                                                  91 AGOVTRWRNPDTGNSYSV----
                                                                                                                             31 GAATGAVVGGVAGQLFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVK
                                                                                                                                                                                                                                   Local
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SGSGSHPGTPTSLHAHSANGTSSSLLGGGLHLATPHQMVAAGGSPVMLHQQQQQQQQHQQQ
                                                                                                     GPQTGGAGGGGGSSSGNGAGTLAVS-GSVTTGAGAGSGTGSSNSNSNSGGSSGSVSGSV
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                                                                                                                                                                                                        1 Similarity 30; Conserv
                                                                                                                                                                                                                                                                                                                 999
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                                                                                                                                                                                                                              Score 82;
Pred. No.
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                                                  ---- EPVRTYQRYNKQERRQQ 125
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RESULT 14 AAY40097

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126 YCREFQQKAMIAGQKQ 141 :: ||: ||:| 582 QQQQQQQHQQQQQQQ 597

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RESULT 15
AAR14308
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       15-JAN-1992
                            AAR14308;
                                           AAR14308 standard;
                                                                                                                                                                                                                                The present sequence represents the natural spider silk protein spidroine major 1. The protein improves the moisturizing/softening action of the compositions. The protein, and its fragments are used in cosmetic or dermatological compositions. These compositions are used as hair or skin care products; and make-up or sunscreens. As the protein is a good, persistent film-formers on the skin agents that are generally difficult to administer, e.g. vitamins, which and hair
                                                                                             551 LGGQGAGQ 558
                                                                                                                    491 QGAGAAAAAAVGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
                                                                                                                                                                                                                         Sequence
                                                                                                                  65 LIGSKIGQ 72
                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 1; 32pp; French.
                                                                                                                                       28 QEVGAATGAVVG----GVAGQ------LFGKGSGRVAMAIGGAVLGG 64
                                                                                                                                                                                                                                                                                                                                                        Cosmetic or dermatological composition containing spider silk protein, for hair or skin care, in make-up or sunscreens
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-510729/43.
                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                               Philippe M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2774588-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nephila clavipes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spider silk protein; spidroine major 1; cosmetic; make-up; dermatological compositions; hair care; skin care; sunscreen; hormone; moisturizer; skin disorder; skin disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spider silk protein spidroine major 1.
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                                                                                                                                                                                        Similarity
(first entry)
                                                                                                                                                                                                                      651 AA;
                                                                                                                                                                            Conservative
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                                         Protein;
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                                                                                                                                                               Score 81.5; DB 20;
Pred. No. 6.7;
3; Mismatches 17;
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Search completed: October 27, 2002, 11:09:11 Job time : 22.544 secs
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                                                                                                                                                                       The spider silk protein contains a basic 34 amino acid repeat. The repeat itself contains 3 regions. The first comprises 0-9 amino acids with a sequence AGR(GGX)2. This region is not highly conserved. The second region has a sequence GAG(A)x which is highly and is 8-10-amino acids long. The third segment is (GGX)5 and is 15 amino acids long and is very highly conserved. In most in a silk having lower elasticity.
                                                  551
                                                                     491 QGAGAAAAAAVGAGQBGTRGQGAGQGGTGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
                                                                65 LIGSKIGQ 72
                                                                                                                                                                                                                                                                                          DNA encoding spider silk protein-1 and 2 and variants - isolated from Nephila clavipes, for prodn. of spider silk protein and fibres having desired characteristics
                                                                                    28 QEVGAATGAVVG----GVAGQ--------LFGKGSGRVAMAIGGAVLGG
                                                                                                                                                                                                                                                                               Claim 15; Page 23; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-312199/43.
                                                                                                                                                                                                                                                                                                                                                                                                  (UYWY-) UNIV OF WYOMING.
                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nephilia clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein superfibre; major ampullate silk; orb web spider.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.clavipes dragline silk protein-1.
                                               LGGQGAGQ 558
                                                                                                                                 25;
                                                                                                                           Similarity 36.8
25; Conservative
                                                                                                                                                                                                                                                                                                                                                   AAQ14183.
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                                                                                                                                                                                                                                                                                                                                                                             Hinman M;
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                                                                                                                     Score 81.5; D
Pred. No. 7.6;
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Result
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Maximum Match 100%
Listing first 45 summaries
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      12243210987654321
76543210987654321
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Copyright (c) 1993 - 2002 Compugen Ltd.
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                            6748477542 residues
 BG240789
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BG713858
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BG240789 OV1_38_CO
BG356895 OV2_11_ED
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BF587805 FM1_40_CO
BF587805 FM1_40_CO
BF587805 FM1_20_CO
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BF58880 DG1_67_A0
BF58888 DG1_67_A0
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                                                                                                                                  source
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Sorghum bicolor

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Sorghum.

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1 (bases 1 to 238)
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EST.
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BG240789
                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
                                                                                                                                                                                       Seq primer: PolyTMix
High quality sequence start: 3
High quality sequence stop: 230
                                                                                                                                                                                                                                                       Email: nmpratteuga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
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Plant Sciences Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG240789 238 bp mRNA linear EST 15-OV1_38_C06.gl_A002 Ovary 1 (OV1) Sorghum bicolor cDNA, mRNA
                                                                                                                                                                                                                                                                                                                                           Tel: 706 542 1860 Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An EST database from Sorghum: ovaries of varying immature stages
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Ovary 1 (OV1)"
/note="Ovary 1 (OV1)"
/note="Organ: Mix of ovaries of varying immature stages from 8-week-old plants; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
                                                                                                                                               Location/Qualifiers
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BASE COUNT ORIGIN

63

from

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Query Match
Best Local Similarity
"-+ hes 72; Conserv
                                                         CGGCGAGAAGCTGACCGACGAGGAGGTCGACGAGATGATCCGTGAGGCTGACGTCGATGG 199
                                                                         CGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGGCGGCCACCGGTGCGGTTGTGGGGGGTGT 119
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Tel: 706 542 1860
Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An EST database from Sorghum: ovaries of varying Unpublished (2000)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Sorghum.
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Sorghum bicolor
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OV2_11_D01.91_A002 Ovary 2 (OV2) Sorghum bicolor cDNA,
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                                                                                                                                   Conservative
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.primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Georgia
                                                                                                                                                                            /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="ovary 2 (ov2)"
/note="ovary 2 (ov2)"
/note="ovary 3 (ov2)"
/note="ovary 5 (ovaries of varying immature stages from 8-week-old plants; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision."
a 82 c 117 g 96 t
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were prepared by mass excision."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: PolyTMix
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Plant Sciences Building, F
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Sequences have been tr
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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Contact: Cordonnier-Pratt MM
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DG1_11_E11.g1_A002 Dark Grown
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                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                               /Organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="bark Grown 1 (DG1)"
/note="Organ: 5-164y-Old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
Clones to be sequenced were prepared by mass excision."
a 82 c 116 g 119 t
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Pred. No. 0.25;
0; Mismatches 50;
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CDNA, mRNA

140

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BASE COUNT ORIGIN

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FEATURES

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COMMENT

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AUTHORS

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RESULT 2 BG356895

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BG052290
         Sorghum propinquum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 446)
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The University of Georgia
Plant Sciences Building, F
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1 (bases 1 to 428)
Reid,S.P., Cordonnier-Pratt.M.-M. Ginela
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RHIZ2_12_G04.g1_A003 Rhizome2
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Sequences have been trimmed
below Phred quality 16. The
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High quality sequence stop: 427
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                                                                                                         Sorghum propinguum.
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80 c 119 g 126 t
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/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: xhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
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/db_xref="taxon:4558"
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Gingle, A.,
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(RHIZ2) Sorghum propinquum
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 Paterson, A.,
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 Sudman, M.
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RESULT 6
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Best Local
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                                                                                                                                                                   Department of Botany
The University of Georgia
Plant_Sciences_Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72; Conservative
Seq primer: PolyTMix
High quality sequence start: 8
High quality sequence stop: 495
                                                                        Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                              Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                    Cordonnier-Pratt, M.-M., Gingle, A.,
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BF586874
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FM1_31_E06.91_A003 Floral-Induced Meristem 1 (FM1) Sorghum
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Seq primer: PolyTMix
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706 542 1805
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/db_xref-"taxon:132711"
/db_xref-"taxon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizome2; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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Pred. No. 0.25;
0; Mismatches
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                                                                                                                                                                                                                                                                                                      Sudman, M., Marsala, C.
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                                                                                                                                                         High quality sequence start: 95
High quality sequence stop: 507
POLYA=Yes
                                                                                                                                                                                                                   Email: mmpratt@uga.edu
Seq primer: T7
                                                                                                                                                                                                                              The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
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Sorghum propinguum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                  Department of Botany
                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                              An EST database from Sorghum: Sorghum propinguum rhizomes
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RHIZ2_11_C03.91_A003 Rhizome2
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/organism="Sorghum propinguum"
/db_xref="taxon:132711"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda 2ap II; Site_1: XhOI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda 2AP II.
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/db_xref="taxon.132711"
/db_xref="taxon.132711"
/clone=lib="Floral-Induced Meristems (FM1)"
/clone="Organ: Floral-Induced Meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; mature plants were placed in a growth chamber for induced by short-day conditions); Id days after being is returned to the greenhouse under natural long days during library was made from poly-A RNA in the cloning vector mass excision."

Clones to be sequenced were prepared by 134 t
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22 (RHIZ2) Sorghum propinguum cDNA, mRNA
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Ouery Match Best Local; Matches 7; Oy 60 CGC; Oy 120 TGCC Oy 120 TGCC Oy 181 CGAC	Source BASE COUNT ORIGIN	FEATURES	ORGANISM ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 8 BGO53014 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	BASE COUI ORIGIN Query Mest LC Matches Qy 60 Db 54 Qy 120 Db 114 Qy 180 Db 174
h Similarity 59.0%; Pred. No. 0.27; 72; Conservative 0; Mismatches 50; I CCAGAACTTCAGCCGCCAGGAACTTGGCGGCGCACCGGTGCGG (1111 1 1 1 1 1 1 1 1	// Clone_lib="Rizone2" (RHIZ2)" // Clone_lib="Rhizone2" (RHIZ2)" // Clone_lib="Rhizone2" (RHIZ2)" // Clone_lib="Rhizone2" (RHIZ2)" // Clone="Organ: Rhizone3" (Vector: pBluescript II from Forgan: Rhizone3" (Vector: pBluescript II from from poly-A RNA in the cloning vector lambda ZAP II. 122 a 101 c 152 g 154 t 2 others	The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 542 1805 Email: mmpratt@uga.edu Seq primer: PolyTMix High quality sequence start: 42 POLYA=NO.	Sorghum p Sorghum p Eukaryota Eukaryota Spermatopi clade; Pau 1 (bases Cordonnies ,L.H. An EST dat Unpublishe Contact: C	N ON	Clones to be sequenced were prepared by mass exclements and the propagation of the propag
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                                                                                                                                                                180 TC
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                                                                                                                                                                                                 CGACGGCCAGATCAACTATGAAGAGTTTGTTAAGGTTATGATGGCCAAGTGAGGAGCGGT
                                                                                                                                                                                                                   TGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTCGGTGTGTCGGCCATCGGCGGTGCGGT 179
                                                                                                                                   င္ပ
BF587805 561 bp FM1_40_G05.gl_A003 Floral-Induced proplinguum cDNA, mRNA sequence. BF587805
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EM1_20_C08.g2_A002 Embryo
                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence start: 62
High quality sequence stop: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 706 542 1860
Fax: 706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Botany
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                                                                                                                                                                                                                                                                                                                                     Conservative
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/db_xref="taxon:4558"
/dlone_lib="Embryo 1 (EM1)"
/clone_lib="Embryo 1 (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
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98 c 152 g 169 t
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59.0%;
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Pred. NO. 0.27;
0; Mismatches 50
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                                                                                                       sequence.
BG673858
BG673858.1
sorghum.
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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Sequences have been trimmed
below Phred quality 16. The
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Plant Sciences Building, F
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                BG673858
EM1_20_C08.g1_A002 Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Similarity 59.072; Conservative
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                                                                                           EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An EST database from Sorghum:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Ploral-Induced Meristem 1 (FM1)"
/clone_lib="Ploral-Induced Meristems; Vector:
/note="Organ: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda ZAP II. Clones to be sequenced were prepared by
mass excision."
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/db_xref="taxon:132711"
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                                                                                                           GI:13919511
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Pred. No. 0.28;
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bicolor cDNA, mRNA
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Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 542 1860
Fax: 706 542 1805
                                                          An EST database from Sorghum: dark-grown seedlings Contact: Cordonnier-Pratt MM
                                                                                                             Sorghum.

Sorghum bicolor

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 582)
                                                                                                   Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
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                                                                                                                                                                                                                                           BE356763
582 bp mrNA linear EST 20-JUL-2000
DG1_12_B12.g1_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mrNA
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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1 (bases 1 to 577)
Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A
An EST database from Sorghum: developing em
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/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Embryo | (EM1)"
/note="Organ: Embryos germinated for 24 hr; Vector: Beluescript II from Lambda Zap II; Site_1: XhoI; Site_2: Vector lambda Zap II. Clones to be sequenced were a 106 c 166 g 176 t
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59.08;
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BE356800
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                                                                                                                                                           High quality sequence start: 10 High quality sequence stop: 557 POLYA=NO.
                                                                                                                                                                                                                                                                     Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                               Sequences have been trimmed below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                          Email: nmpratt@uga.edu
Sequences have been tri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
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Sorghum bicolor
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72; Conserv
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High quality sequence stop: 553
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
/organism≈"Sorghum bicolor"
/db_xref≈"taxon:4558"
                                                                                                                Location/Qualifiers
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//db_xref="taxon:4558"
//clone_lib="Dark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
Clones to be sequenced were prepared by mass excision."
a 116 c 166 g 155 t
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Pred. No. 0.28;
0; Mismatches 50; Indels
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BASE COUNT
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Best Local S
Matches 72
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Best Local :
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 267
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CGGCGAGAAGCTGACCGACGAGGAGGTCGACGAGATGATCCGTTGAGGCTTGACGTCGATGG 326
                              CGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGCGCCACCGGTGCGGTGTTGTGGGCGGTGT 119
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RHIZ2_34_H05.g1_A003 Rhizome2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                                 The University of Georgia Plant Sciences Building, Rm. Tel: 706 542 1805 Pax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG102589.1 GI:12617422
                                                                                                                                                                                                                                                                                                                                                                               Email: mmpratt@uga.edu
Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clade; Panicoideae; Andropogoneae;
1 (bases 1 to 597)
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                                                                                                                                               /organism="Sorghum propinquum"
/db_xref="taxon:132711"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizome2; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 130 c 170 g 148 t
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Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 114 c 168 g 163 t
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                                                                  Score 42; DB 1
Pred. No. 0.29;
0; Mismatches
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Pred. No. 0.29;
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AW672446
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LG1_359_D09.g1_A002 Light Grown
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Sequences have been tr
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The University of Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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Sorghum bicolor
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706 542 1805
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/dlone_lib="light Grown 1 (LG1)"
/clone_lib="light Grown 1 (LG1)"
/note="Gragan: 10 - to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: Eco
; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
a 128 c 173 g 146 t
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                                                                                                                                                                                                                                                                 8.7%;
                27,
                                                                                                                                                                                                                                                   Score 42; DB 9 Pred. No. 0.29; 0; Mismatches
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1 (LG1) Sorghum bicolor cDNA, mRNA
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Page 8

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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483
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383533 seqs, 122816752 residues
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    atgcgtggttgcctgcaggg.....aggtgattagcaccgaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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                             4 US-08-556-978B-80

4 US-08-556-978B-81

5 4 US-09-103-840A-1

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4 US-08-765-907A-16

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3 US-08-231-818-10

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6 5187077-4

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US-09-530-212A-1

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Sequence 80, Appl
Sequence 2, Appli
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Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 27, Appli
Sequence 1, Appli
Sequence 6, Appli
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                                           Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
ZIP: 198
85 GTTGGCGCGCCACCGGTGCGGTGTGTGGGCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGC
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sequence 90, Appi	~	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 2, Appli				-	Sequence 100, App	-	Sequence 100, App	Sequence 1, Appli	Sequence 14, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 7, Appli

ALIGNMENTS

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; LENGTH: 303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomi
                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,600

FILING DATE: JUNE 15, 1993

ATTORNEY/AGENT INFORMATION:

NAME: FLOYD, LINDA AXAMETHY

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: CR-9389-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-892-8112

TELEPAX: 302-73-0164

INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:

IFNORM: 303 baso 5116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80, Application US/08556978B Patent No. 6268169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY
TITLE OF INVENTION: SPIDER SILK ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS
SOFTWARE: MICROSOFT WORD FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
COMPUTER: IBM PC COMPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1007 MAR
CITY: WILMINTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNITED STATES
                                                                                          DNA (genomic)
7.68;
57.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107
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Score 36.6; DB 4; Pred. No. 0.043; 0; Mismatches 49;

Length 303; Indels

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US-09-103-840A-2/c
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                                                                                                              GENERAL INFORMATION:
                                                                                                                      Sequence 2, Application US/09103840A
Patent No. 6294328
                                                APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-92-8112
INFORMATION FOR SEQ ID NO: 81:
LENGTH: 303 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-08-556-978B-81

Sequence 81, Application US/08556978B
Patent No. 6268169
Patent No. 6268169
                                                                                                                                                                                   147 GCTGGTGCAGCAGCAGCTGCCGCTGGCGGTGCAGGCCAAGGTGGATATGGTGGCT 201
                                                                                                                                                                                                             145 TCTGGTCGTGTGTGGATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGCT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ъ
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                               85 GTTGGCGCGCCCACCGGTGCGGGTTGTGGCCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 0
FILING DATE: JUNE 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                        GCTGCGGCAGCTGGTGGTGGTCAGGGCGGTCTTGGCTCACAAGGGGCCGGTCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: WILMINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 GÉTEGTECAGCAGCAGCTGÉCGCTGCCGGTGCAGGCCAAGGTGGATATGGTGGCT 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 TCTGGTCGTGTGTCGATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGCT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 GCTGCGGCAGCTGGTGGTGCTGGTCAGGGCGGTCTTGGCTCACAAGGGGCCGGTCAAGGC
                                                                                                                                                                                                                                                                                                                        66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                               Similarity 57.4
66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: E. I. DU PONT DE NEMOURS AND COMPANY
1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAHNESTOCK, STEPHEN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISKETTE, 3.50 INCH
                                                                                                                                                                                                                                                                                                                           7.6%;
57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOVEL RECOMBINANTLY PRODUCED SPIDER SILK ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08/077,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/556,978B
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                                                                                                                                                                                                                                                                                                                    Score 36.6; DB /
Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR-9389-A
                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                           DB 4; Length 303;
                                                                                                                                                                                                                                                                                                  49; Indels
                                                                                                                                                                                                                                           146
                                                                                                                                                                                                                                                                                             0,
Db 2061410 GGGCGCCGGTGGGCTCGGCGGCAAAGCCGGGCTGATCGGCGACGGCGGTGACGGCGGCGC 2061351
                                                                                                          Db 2061470 CACTGCGGGCCTGCTTTGGTGCCGGCGGCGCGCGGCGGATTCGGCTTCGGCGGTGCCGG 2061411
                                                                                                                                                                        Qy
                                                                                                                                                                                                                                            ; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                        Query Match
Best Local Similarity 48.9%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                       SOFTWARE: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                           159 GATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCAT 218
                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                      LENGTH: 4411529
                                                                        99 CGGTGCGGTTGTGGGCGGTGTTGCGGCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGTC 158
                                                                                                                                     39 CTCTGTTTTCCTGGTGGGTTGGGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGGCCAC 98
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2.1

0;

Mismatches

Score 33.6; Pred. No. 18;

DB 4; 94;

Length 4411529;

0;

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US-09-103-840A-1/c
                                                                                                                                                                                                                                                                             Db 2884584 AAAAGCGGTGGGCGCGATGTTGACCTCGATGA 2884553
                                                                                                                                                                                                                                                                                                                            Db 2884644 GAGTCGGGCCAGGCGCGCTTGTTGATACAGGGTTTGCAGCTGTTGCCGTTGTTCTGCAAA 2884585
                             APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REPERENCE: 24366-20007.00

TUDERCULOSIS

FILE REPERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 1998-C NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                       Sequence 1, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 51.3%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA SEQUENCES FO TITLE OF INVENTION: TUBERCULOSIS FOR THE REFERENCE: 24366-2007.00 CURRENT APPLICATION NUMBER: US/09/10 CURRENT FILING DATE: 198-06-24 NUMBER OF SEQ ID NOS: 2 COPTENDED DATE: 198-06-24 COPTENDED DATE: 198-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
                                                                                                                                                                                                                                                                                                              202 AAAATCGGTCAGAGCATGGACCAGCAGGATAA 233
                                                                                                                                                                                                                                                                                                                                                             142 GGCTCTGGTCGTGTGTCGATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGCTCT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                  82 GAAGTTGGCGCGGCCACCGGTGCGGTTGTGGGGCGGTGTTGCCGGCCAGCTGTTCGGTAAA 141
PatentIn Ver.
                  1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33.6; DE Pred. No. 18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DВ
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US-08-403-852D-10/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08403852D Patent No. 5891695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application US/08765907A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 63528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: THIBAUT,
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TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
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APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Inv
TITLE OF INVENTION: Bigsynthesis Of
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                     COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                              STATE:
                                                                                                                                                                                                     STREET:
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                                                                                                                                                                   Washington
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DUTRUC-ROSSET, Gilles
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DEBUSSCHE, Laurent
FAMECHON, Alain
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BAMAS-JACQUES, Nathalie
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                                                                                                                                                                                                     3: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W., Suite 700
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                                                                                                                                                                                                                                                                                                                               Polypeptides Involved In The Biosynthesis Of Streptogramins, Nucleotide Sequences Coding For These Polypeptides And Their Use
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Best Local Similarity
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INFORMATION FOR SEQ
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELECOMMUNICATION INFORMATION:
                                                                                       APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins,
TITLE OF INVENTION: Coding For These Polypeptides A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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ATTORNEY/AGENT INFORMATION:
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ANTI-SENSE: NO
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                                                            CORRESPONDENCE
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                                                                              NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
           CITY: Washington
                              STREET:
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FILING DATE: 25-SEP-1993
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                                             ADDRESSEE:
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D.C
                              1300 I Street,
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                            Finnegan, Henderson, Farabow, 00 I Street, N.W., Suite 700
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                                                             ADDRESS:
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55.7%;
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Patricia
Denis
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                                             Garrett & Dunner
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                                                                                          And Their Use
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ZIP: 20005-3315
MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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RESULT 8
US-09-231-818-10/c
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                                                                                                                                                                                                    Sequence 10
Patent No.
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                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
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Best Local S
                               TITLE OF
TITLE OF
TITLE OF
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SEQUENCE CHARACTERISTICS:
TYPE:

1052 has:
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LOCATION: 84..962
OTHER INFORMATION:
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REFERENCE/DOCKET NUMBER: 031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYPOTHETICAL:
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APPLICATION NUMBER: FR 9
FILING DATE: 25-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: S.pristinaespiralis
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
                                                                                                                                                                                             10, Application US/09231818
5. 6171846
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FILING DATE: 25-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                               6.9%;
64; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 03-AUG
                                                     INVENTION:
Thibaut, Denis
Zagorec, Monique
Debussche, Laurent
De Crecy-Lagard, Valerie
VENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
                                                                                                                            Jacques, Nathalie
                                                                                                              Lacroix, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Gene PapM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FR 92/11441
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GENERAL INFORMATION
APPLICANT: BLANC,
APPLICANT: THIBAL
                                                                                                                             RESULT 9
US-08-765-907A-1/c
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                                         APPLICANT:
APPLICANT:
                                                                                               Sequence 1, Application US/08765907A
Patent No. 6352839
                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS

LOCATION: 84..962

OTHER INFORMATION: /Product= "Gene Papm"
                             APPLICANT:
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                        Query Match
Best Local ;
                                                                                                                                                           183 GEGTETCGECCCGEGCGCGTCGGCGGTGATCCCGGCCGGTCAGCTGCCCGGT 129
                                                                                                                                                                                  135 cggtaaaggcrcrggrcgrgrgrcgarggccarcggcggrgcggrrcrgggcggr 189
                                                                                                                                                                                                          243 CGGCCAGGCAGGTGTCGAGGTCCCCCGGGGGGGACCTGGCAGGCGTGGGGGGGCGGCCAGCAGCC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1052 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA.
APPLICATION NUMBER: US/08/403,852
EILING DATE: 10-MAY-1995
EILING DATE: 10-MAY-1995
EILING DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PEILING DATE: 25-SEP-PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20003-3-1.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FIRE PC-DOS/MS-DOS
PC-TOS/MS-DOS
PC-TOS/MS-DOS
PC-TOS/MS-DOS
                                                                                        INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FR 9 FILING DATE: 25-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                 BLANC, Veronique
THIBAUT, Denis
BAMAS-JACQUES, Nathalie
BLANCHE, Francis
COUZET, Joel
BARRIERE, J
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         NO
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        Jean-Claude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
                                                                                                                                                                                                                                                                                   6.9%; Score 33.4; DB 55.7%; Pred. No. 0.71;
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                                                                                                                                                                                                                                                                         Mismatches
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TITLE OF INVENTION: Streptogramins and Method For Preparing Same:
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 2888
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-1
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US-09-773-816-1
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                        ORGANISM: Human
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(23623)
OTHER INFORMATION: n = A.
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/773,816
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/243,458
PRIOR FILING DATE: 2000-10-25
PRIOR APPLICATION NUMBER: US 60/179,305
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stanford University
APPLICANT: Khosla, Chaitan
TITLE OF INVENTION: NON-STEROIDAL ESTROGEN-RECEPTOR
TITLE OF INVENTION: ANTAGONISTS
FILE REFERENCE: 28600-20210.00
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
 8386
                                                                                                                                       8266 GGGTTCGGCGATGACGTCGCACAGGGTCGCGAAGGACGCCGCGACGCCGTAGGT 8325
                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 GGTTGCGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGCCCACCGGTGCGGTTGTGGGC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                    GGTGTTGCCGGCCAGCTGTTCGGTAAAAGGCTCTGGTCGTGTGTCGATGGCCATCGGCGGT 174
GCTGGTCTTGGCCATCTGCATG 8407
                                 GCGGTTCTGGGCGGTCTGATTG 196
                                                                   GGGGTCGGTGACCAGCGAGATGGTCAACACGCCGGCCTCGTCCAGTTGCCCGAGGGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                23673
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DUTRUC-ROSSET, Gilles
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                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                        6.9%;
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55.7%;
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Pred. No. 3.1;
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Pred. No. 1.1;
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                                                                                                                                                                                                                                        DB 4;
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                                                                   8385
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APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: WHITE, OWEN R.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-24007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DAFE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 1
SEQ ID NO 1
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                                                                                                                                     ; ORGANISM: Mycobacterium tuberculosis ; OTHER INFORMATION: H37Rv US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Applicat Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Applicat
Patent No. 6294328
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      835557 GGGCCGGCGATTGTTCTTCGGCAACGGCGCGCGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C.
                                                                                                                                                                                           LENGTH: 4411529
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 TTGCCGGCCAGCTGTTCGGTAAAGGCTCTCGGTCGTGTCGATGGCCATCGGCGGTGCGG 178
59 GCGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGGGGCGCCACCGGTGCGGTTGTGGGCGGTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 GCGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGGCCACCGGTGCGGTTGTGGGCGGTG 118
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                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGC
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                                                           l Similarity
80; Conserv
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                                                           Conservative
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                                                                         50.6%;
                                                       Score 33.2; D
Pred. No. 23;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR STRAIN ANALYSIS
                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
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                                                                                             Length 4411529;
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                                                         Indels
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                                                         Gaps
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Db 833319 TGGGGCGCCCGCTGATCGGTAACGGCGCCGACGGGGCGCCGGGGACCGGGGGCCGCCGGCG 833378

TTCTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGC 216

TTGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGTCGATGGCCATCGGCGGTGCGG 178

833259 GCGCCGCGTCCATAACCAGTCCGCTGCTCGACGCGATCAACGCGCCCTTCCTGGCGGCGT 833318

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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saln
US-08-332-747-1
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                                                         δÃ
                                                                          Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                     INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1295 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: DE 43 37 295
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1628
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-332-747-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, \
CURRENT APPLICATION DATA.
942 TTGGCGCTATCGGCGGCGCGCTGTTGGGCGGATTCCTCGGCAACACTATCGGCGGCGGCGTA 883
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                                                                                                                                                                                   TOPOLOGIC TYPE: DN
                86 TTGGCGCGGCCACCGGTGCGGGTTGTGGGGGGGTGTTGCCGGCCAGCTGTTCGGTAAAGGCT 145
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APPLICANT: Neumann, Siegfried
TITLE OF INVENTION: Oligonucleotides for the detection of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: ADDRESSEE MILLEN, WHITE, ZELANO & BRANIGAN
STREET: 2200 CLARENDON BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
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CITY: ARLINGTON
STATE: VA
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ZIP: 22201
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FILING DATE: 01-NOV-1994
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                                                                        Conservative
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5427925 3/c
;Patent No. 5427925
;APPLICANT: GEARING, DAVID P.;GOUGH, NICHOLAS M.;HILTON, INCOLA, NICOS A.;SIMPSON, RICHARD J.;WILLSON, TRACY A.

TITLE OF INVENTION: RECOMBNIANT METHOD FOR MAKING
NUMBER OF SEQUENCES: 38
CURRENT APPLICATION.DATA:
"NETTON MILLSON, TRACY A.
CURRENT APPLICATION.DATA:
"NETTON MILLSON, DATA:
"NETTON MILL
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5187077-4/c
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NUMBER OF INVENTION: LEUKEMIA INHIBITORY FACTOR A.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/294,514

FILING DATE: 09-DEC-1988
422 CACAGACGCAAAAGCACATTGCTGAGGAGGCCCCTCATGACGTCTATAGTAGCATTGAGC
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                                                                                                                                                32 TCATTATCTCTGTTTTCCTGGTGGGTTGCGCCCAGAACTTCAGCCGCCAGGAAGTTGGCG 91
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FILING DATE: 22-SEP-1992
APPLICATION NUMBER: 667,159
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FILING DATE: 06-MAY-1993
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                                              CGGCCACCGGTGCGGTTGTGGGCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTC 151
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93; Conservative
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
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DNA sequence of E.
DNA sequence of cl
OSPA 17kD antigen
Piscirickettsia sa
PCR primer #4 used
PCR primer #2 used
PCR primer #3 used
PCR primer #3 used
PCR primer #1 used
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AAX61355 AAD17186 AAD17186 AAD17186 AAD17186 AAA51609 AAA14651 AAA59606 AAA23386 AAA23386 AAX23386 AAX351625 AAX68532 AAX199683 ABL03846 AAL37335 AAA45539 AAX90448 AAS59277 ABA90946 AAF86256 AAC45883 AAT18913 AAT59268 AAS08693 AAC75679 AAT18912 AAT31799 Human Delta7-stero
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ALIGNMENTS

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                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of ospa in the form of a vaccine remed Ospa, or an immunogenic amount of particularly polkilothermic fish, against the bacterial pathogen partickettsial septicaemia (SRS) and other rickettsial diseases. The method is suffer the bacterial pathogen sequence represents DNA which has been optimised for expression in Escherichia coli to encode the P. salmonis Ospa protein. An Ospa protein anni-osna antibody resonnes
                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                    Sequence 483 BP; 108
                                                                                                                                                                                                                                                                                                                                           61
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                    AAA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                        GAAATCTACGGCACGGGTGCCCTCAGCCGGATGGCCGGTGGCAGGTGATTAGCACCGAA
                                    GAAATCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAA
                                                                                    CGCCGTCAGCAGTACTGCCGCGAATTTCAGCAGAAAGCCATGATCGCAGGTCAGAAACAG
                                                                                                                                                                                                                                                                                                                                                                              1 ATGCGTGGTTGCCTGCAGGGCAGCTCTCTGATCATTATCTCTGTTTTTCCTGGTGGGTTGC 60
                                                                       CGCCGTCAGCAGTACTGCCGCGAATTTCAGCAGAAAGCCATGATCGCAGGTCAGAAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAYW/)
(BURI/)
                                                                                                                                                                                                                                   CTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGAGATAAAATCAAA
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                                                                                                                                                                                                                     CTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGATAAAATCAAA
                                                                                                                                                                                                                                                                                                                   GCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGCCGCCACCGGTGCGGTTGTGGGCGGTGTT
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PSDB; AAB81127.
                                                                                                                                                                                                                                                                                                                                                                  ATGCGTGGTTGCCTGCAGGCAGCTCTCTGATCATTATCTCTGTTTTTCCTGGTGGGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Fig 4C; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAY W W.
BURIAN J.
KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 483; DB 22; 100.0%; Pred. No. 3.9e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 127 C; 148 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 2

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1 ATGCGTGGTTGCCTGCAGGGCAGCTCTCTGATCATTATCTCTGTTTTCCTGGTGGGTTGC

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                                                    This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of oppa in the form of a vaccine. The method is used for protecting animals, rickettsial septicaemia (SRS) and other rickettsial gaginst salmonid expression in Escherichia coli fused to DNA encoding animals, rickettsial septicaemia (SRS) and other rickettsial diseases. The present P. salmonis OspA DNA termed (17E2 optimised for expression in Escherichia coli fused to DNA encoding an undefined is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                         Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                               Example 4; Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                                                                        Kay ww,
                                                                                                                                                                                                                                                                                                                                           (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A
                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence of c17e2 ospA
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                    Similarity
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                                                                                                                                                                                                                                                                                                                    Burian J,
       100.0%;
ilarity 100.0%;
Conservative
                                         220 A; 183 C; 190 G; 175 T; 0 other;
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Score 483; DB 22;
Pred. No. 4.7e-136;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding
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(BURI/)
(KUZY/)
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                                                           KAY W W.
BURIAN J.
KUZYK M A.
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                       Burian J,
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                                                                                                                                                                                      99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fish; Piscirickettsia salmonis; rickettsial pathogen; salmonid rickettsial septicaemia; rickettsial disease;
                                                                                                                                                 99CA-2281913
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/parduct= "OspA"
/note= "Genus specific 17kDa antigen, the sequence
/note= "Genus specific 27kDa antigen, the sequence
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This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen p. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents DNA encoding the P. salmonis OspA protein. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                     Method for protecting poikilothermic fish against salmonid rickett septicaemia and other rickettsial diseases comprises administering vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2B; 35pp; English.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-316844/34.
DB; AAB81126.
486 BP; 137 A; 79 C; 144 G; 126
T; 0 other;
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Query Best L Matches 125 83 Local 65 8 S Match GTGGTTGCCTGCAGGGCAGCTCTCTGATCATTATCTCTGTTTTTCCTGGTGGGTTGCGCCC AGAACTTCAGCCGCCAGGAAGTTGGGCGCGCGCCACCGGTGCGGTTGTGGGGCGGTGTTGCCG GAGGATGTTTGCAAGGTAGTAGTCTAATTATTATCAGTGTGTTTTTAGTTGGCTGTGCCC 364; Similarity Conservative 61.1%; 76.0%; 0; Score 295; DB 22 Pred. No. 2.9e-79 0; Mismatches 11 115; 22; Length Indels 0; Gaps 184 127 124 67 64 0

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425 TCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAAAAA 483

TTTACGGCACTGCATGCCGGCAACCGGATGGTCGTTGGCAAGTCATTTCAACAGAAAAA

RESULT 4 AAH79040

AAH79040 standard; cDNA; 489 ВP

AAH79040

15-JAN-2002 (first entry;

Piscirickettsia salmonis polynucleotide P10.6.

septicaemia; :
ATCC VR-1361; Piscirickettsia salmonis; SRS; almonis; piscirickettsiosis; salmonid rickettsial; surface antigen; vaccine; antibacterial; fish;

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Matches
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                   425
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                                                                                                                                                                                          125 GCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGTCGATGGCCATCGGCGGTGCGGTTCTGG 184
                                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 4; 25pp; English.
                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids encoding an amino acid sequence homologous to surface antigen present on Piscirickettsia salmonis are useful to protect fish against piscirickettsiosis
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Burzio
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01-JUL-2000; 2
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29-JUL-2000; 2
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TCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAAAAA 483
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                    GCCAGCAATATTGTGGAGAATTTCAGCAAAAGGGGGATGATTGCAGGGGCAGAAGCAAGAGA
                               GTCAGCAGTACTGCCGCGGAATTTCAGCAGAAAGCCATGATCGCAGGTCAGAAACAGGAAA 424
                                                                     GTAACAGCTACTCTGTGGAACCGGTTCGCACCTACCAGCGTTACAACAACAGGAACGCC
                                                           GCAATAGTTATAGTGTTGAGCCAGTGCGTACTTACCAGCGTTACAATAAGCAAGAGCGTC
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                                                                                                 ACCAGAGTTTGGAÁÁÁGGTAÁAAGCAGGGCÁAGTGÁCACGTTGGCGTÁATCCAGATÁCAG
                                                                                                             ACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGTAATCCGGACACCG
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                                                                                                                                         GTGGATTAATTGGTTCTAAAATCGGTCAATCGATGGATCAGCAGGATAAAATAAAGCTAA
                                                                                                                                                    GCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGATAAAATCAAACTGA
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                                                                                                                                                                                                                                                           AGAACTTCAGCCGCCAGGAAGTTGGCGCGCCGCCACCGGTGCGGTTGTGGGCGGTGTTGCCG 124
                                                                                                                                                                                                                      GTGGTTGCCTGCAGGGCAGCTCTCTGATCATTATCTCTGTTTTCCTGGTGGGTTGCGCCC
                                                                                                                                                                                                                                                                                                                   364;
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DB; AAG78025.
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Conservative
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; 2000GB-0016082.
; 2000GB-0018599.
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0; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                   DB 22;
.9e-79;
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                                                                                                                                                                                                                                                                                                                         Length 489;
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Best Local Similarity
Matches 118; Conserv
                    AAF86252
                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a OspA in the form of a vaccine. The method ospA, or an immunogenic fragment of particularly poikilothermic fish, against the bacterial pathogen salmonis. The method is also useful for protecting animals, rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of invention
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                                                                                                                                                                                                         208 GGTCAGAGCATGGACCAGGAGAGAAAATCAAACTGAACCAGTCTCTGGAAAAAGTGAAA 267
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
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                                                                                       GCCGGCCAGGTTACTCGTTGGCGTAATCCGGACACCGGTAACAGCTACTCTGTGGAAC 325
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                                                                                                                                                                                  GGTCAGAGCATGGACCAGCAGGATAAAATCAAACTGAACCAGTCTCTGGAAAAAGTGAAA 59
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            standard;
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) BURIAN J.
) KUZYK M A
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salmonid rickettsial septicaemia; rickettsial disease;
ion construct; PCR primer; ss.
                                                                                                                                                                                                                                                                                      24.4%; Score 118; DB 22; 100.0%; Pred. No. 5.5e-26; 0;
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       110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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                                                                                                                                                                                                                                                                                                                                                                                 28 G; 37 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                 Length 118;
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Best Local :
                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of the P. salmonis OspA gene. The OspA gene is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct; PCR primer; ss.
 Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; Ospa; salmonid rickettsial septicaemia; rickettsial disease
                                                                      11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                            Sequence 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              septicaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piscirickettsia
                                                                                                 AAF86255;
                                                                                                                          AAF86255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer
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                                         PCR primer #5 used in cloning an optimisation of OspA gene
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                                                                                                                                                                                                                                              TGGGTTGCGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGGCCACCGGTGCGGTTGTGG
                                                                                                                                                                                                          GCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGTCGATG
                                                                                                                                                                                            GCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGGCGATG
                                                                                                                                                                                                                                                                                                       109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for protecting poikilothermic fish against salmonid rickettsial aemia and other rickettsial diseases comprises administering a containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                      Similarity 99.:
)9; Conservative
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                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                   22.4%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                            28 C;
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                                                                                                                          BP
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Pred. No. 4.2e-23;
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4.2e-23;
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                                                                                                                                                                                       Poikilothermic fit
vaccine; OspA; sa
SRS; 17E2; fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a
                                                                                                                                                                                                                                                                                                  PCR primer
                                                                                                                                                                                                                                                                                                                                                        11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF86253 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAYW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 ANAGCCATGATCGCAGGTCAGAAACAGGAAATCTACGGCACC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 ACCTACCAGCGTTACAACAAACAGGAACGCCGTCAGCAGTACTGCCGCGAATTTCAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAY W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 BP; 14 A; 23 C;
                                                                                                                                                                                                                                                                                                     #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                     used
                                                                                                                                                                                                                   fish; Piscirickettsia salmonis; rickettsial pathogen; salmonid rickettsial septicaemia; rickettsial disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99CA-2281913
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                                                                                                                                                                                          construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                  in cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuzyk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 102;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 G;
                                                                                                                                                                                                                                                                                                  an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                       primer;
                                                                                                                                                                                                                                                                                                  optimisation of OspA gene
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CA2281913-A1 Piscirickettsia

Kay WW,

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(KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                Piscirickettsia
                                                                                                                                                                                                                                                       Poikilothermic fish; Piscirickettsia salmonis; rickettsial pavaccine; OspA; salmonid rickettsial septicaemia; rickettsial SRS; 17E2; fusion construct; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                        PCR primer #1 used in cloning an optimisation
                                                                                                                                                                                                                                                                                                                                                                 11-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                          AAF86251 standard; DNA; 111 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a OspA in the form of a vaccine. The method ospA, or an immunogenic fragment of particularly poikilothermic fish, against the bacterial pathogen particularly poikilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial diseases. The method is also useful for protecting against salmonid sequence represents a PCR primer used in the cloning and optimisation of invention. The salmonis OspA gene. The OspA gene is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 AAAGGCTCTGGTCGTGTGTCGATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 94 BP; 18 A; 20 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Fig 4B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTAAAATCGGTCAGAGCATGGACCAGCAGGATA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTAAAATCGGTCAGAGCATGGACCAGCAGGATA 232
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93; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) KAY W W.
) BURIAN J.
) KUZYK M A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                  99CA-2281913.
                                                                                                                                                                                                                                             salmonis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 92.4; DB 22;
Pred. No. 2.7e-18;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                 of OspA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                       pathogen;
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                  RESULT 10
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ID AAF862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis .
                                                                                                                                           (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                      CA2281913-A1
                                                                                                                                                                                                                                                                                                                                                Polkilothermic fish; Piscirickettsia salmonis; rickettsial vaccine; OspA; salmonid rickettsial septicaemia; rickettsial SRS; 17E2; fusion construct; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                  Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer #6 used in cloning an optimisation of OspA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF86256 standard; DNA; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF86256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, piscirickettsia salmonis. The method comprises administering an immunogenic amount of a particularly poikilothermic firmed OspA, or an immunogenic fragment of particularly poikilothermic fish, against the bacterial pathogen particularly poikilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial disasses. The present sequence represents a PCR primer used in the cloning and optimisation of sequence represents a PCR primer used in the cloning and optimisation of invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 111 BP; 16 A; 32 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis .
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74; Conserv
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rickettsial disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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23-JUL-1999; 23-JUL-1999; 26-JUL-1999; 27-JUL-1999; 27-JUL-1999;

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RESULT 12
AAT18913
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Best Local S
Matches 67
                                                                    Claim 5; Page 122; 168pp; English.
                                                                              New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                          P-PSDB;
                                                                                                                                                Fahnestock SR;
                                                                                                                                                             (DUPO ) DU
                                                                                                                                                                               15-JUN-1993;
                                                                                                                                                                                             15-JUN-1994;
                                                                                                                                                                                                                                               Spider; dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothin; rope; surgical suture; implant; reinforcement; film; coating; ss.
                                                                                                                                                                                                              22-DEC-1994.
                                                                                                                                                                                                                              W09429450-A2.
                                                                                                                                                                                                                                                                                                 DNA encoding
                                                                                                                                                                                                                                                                                                                                              AAT18913 standard;
                                                                                                                                                                                                                                                                                                                   17-JAN-1997
                                                                                                                                                                                                                                                                                                                                  AAT18913;
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DB; AAR99054.
                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                                                        th 8.2%; Similarity 59.3%; 67; Conservative
                                                                                                                                                               PONT
                                                                                                                                                                                                                                                                                         spider dragline variant, DP-1B.9 monomer.
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                            93US-0077600.
                                                                                                                                                                                           94WO-US06689.
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99US-0161404
99US-0161405
99US-0161406
99US-0161359
99US-0161350
99US-0161360
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99US-0161992
99US-0161993
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                                                                                                                                                           NEMOURS &
                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                              303
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; Pred. No. 0.11;
0; Mismatches ;
                                                                                                                                                                                                                                                                                                                                             ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                        clothing;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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This sequence encodes a synthetic spider dragline variant monomer, DP-1B.9. The sequence of the DP-1B.9 polymer is given in AAR99055. The polypeptide monomer is a variant based on a consensus sequence derived from the fibre forming regions of spider dragline protein. The natural protein 1 (Spidroin 1) from Nephila clavipes. This sequence may be used in the recombinant production of the subtilis. Synthetic analogues of DP1 were designed to mimic the repeating consensus sequence of the natural protein and the pattern

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC of variation among individual repeats. DP-1B analogues were designed CC by reordering the four repeats within the monomer of DP1A. This CC monomer exhibits all of the regularities of (1)-(5) below. In addition, CC it exhibits a regularity of the natural sequence which is not shared by CC DP-1A, namely that a repeat in which both GYG and GRG are deleted is CC generally preceded by a repeat lacking the entire poly-alanine repeat, CC with one intervening repeat. The sequence of DP-1B matches the natural CC sequence more closely over a more extended segment than does DP-1A. The CC individual repeats differ from the consensus according to the pattern: CC (1) the poly-alanine sequence varies in length from 0-7 cC (2) when the entire poly-alanine sequence is deleted, CC (3) aside from the poly-alanine sequence and gARGGLGGQAGANGG; CC (3) aside from the poly-alanine sequence consecutive residues; (4) deletion of GYG is generally accompanied by deletion of GRG in the same asonuence. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                          Spider: dragline protein; variant; monomer; polymer; fibre forming region; Spidroin 1; Nephila clavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothir rope; surgical suture; implant; reinforcement; film; coating; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The proteins may be used to produce fibres of high tensile strength elasticity, suitable for clothing, rope, surgical sutures, biomater
                                                                   WPI; 1995-036479/05
P-PSDB; AAR99052.
                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT18912 standard; DNA; 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 303 BP; 43 A; 69 C; 138 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the same
New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells
                                                                                                                     Fahnestock
                                                                                                                                                                                      15-JUN-1993;
                                                                                                                                                                                                                        15-JUN-1994;
                                                                                                                                                                                                                                                          22-DEC-1994
                                                                                                                                                                                                                                                                                           W09429450-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residues
                                                                                                                                                     (DUPO ) DU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 TCTGGTCGTGTGTCGATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 GCTGGTGCAGCAGCTGCCGCTGCGGGGTGCAGGCCAAGGTGGATATGGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 GTTGGCGGGCCACCGGTGCGGTGTTGTGGGGCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              implants, plastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGCGGCAGCTGGTGGTGGTCAGGGCCGGTCTTGGCTCACAAGGGGCCCGGTCAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e sequence; and
) a repeat in which the entire poly-alanine sequence
generally preceded by a repeat containing six alanin
                                                                                                                                                     PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                      93US-0077600
                                                                                                                                                                                                                        94WO-US06689
                                                                                                                                                                                                                                                                                                                                                                                                                                                 dragline variant, DP-1A.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.6%;
57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reinforcements,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36.6; DB Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                     m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rope, surgical sutures, biomaterials its, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 six alanine
                                                                                                                                                                                                                                                                                                                                                                           clothing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
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В QΥ

멍 20

198 145

TCTGGTCGTGTCGATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGCT

199

GCTGGTGCAGCAGCAGCTGCCGCTGGCGGTGCAGGCCAAGGTGGATATGGTGGCT

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CC DP-1A.9. The sequence of the DP-1A.9 polymer is given in ARP9053.

CC The polypeptide monomer is a variant based on a consensus sequence CC derived from the fibre forming regions of spider dragline protein, CC esp. the natural protein 1 (Spidroin 1) from Nephila clavipes. This CC DNA sequence may be used in the recombinant production of the CC variant protein in a recombinant host, e.g. E. coli or Bacillus CC subtilis. Synthetic analogues of DP1 were designed to minic the CC repeating consensus sequence of the natural protein and the pattern CC of variation among individual repeats. DP-1A analogues are composed CC of atandemly repeated 101 amino acid monomer which comprises four crepeats which differ from the consensus sequence given in AAW06201, CC according to the pattern (1)-(5) given below. This 101 amino acid CC monomer is repeated 1-16 times in a series of analogue proteins. The CC individual repeats differ from the consensus according to the pattern. CC (1) the poly-alanine sequence varies in length from 0-7 creating is the surrounding sequence according to the pattern.
                                                                                                                                            Query Match
Best Local :
                                                                                                                Matches
                                                                                                                                                                                                                                                                                           The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films, coatings, etc.
                                                                                                                                                                                                                                                                                                                                                                                                        in the same sequence; and (5) a repeat in which the entire poly-alanine deleted is generally preceded by a repeat containing s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes a synthetic spider dragline variant monomer, DP-1A.9. The sequence of the DP-1A.9 polymer is given in AAR99053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2;
                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encompass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  so also
                                                                                                                                                                                                                                                                                                                                                                                        residues
138
                                                        85
GCTGCGGCAGCTGGTGGTGCTGGTCAGGGCGGTCTTGGCTCACAAGGGGCCCGGTCAAGGC 197
                                  GTTGGCGGCCACCGGTGCGGTTGTTGGGCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGC
                                                                                                            l Similarity
66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is the surrounding sequence encompassing AGRGGLGGQGAGANGG;
(3) aside from the poly-alanine sequence, deletions usually
ss integral multiples of three consecutive residues;
(4) deletion of GYG is generally accompanied by deletion of
                                                                                                                                                                                                                                      303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 121; 168pp; English
                                                                                                                Conservative
                                                                                                                                                                                                                                   B₽;
                                                                                                                                                                                                                                      43
                                                                                                                                                                                                                                      A;
                                                                                                                                            7.6%;
57.4%;
                                                                                                                                                                                                                                      69
                                                                                                                                                                                                                                      Ç
                                                                                                                0;
                                                                                                                                            Score 36.6;
Pred. No. 0
                                                                                                                                                                                                                                   138 G;
                                                                                                                Mismatches
                                                                                                                                                                                                                                      53 T;
                                                                                                                                        0.34;
                                                                                                                                                                                                                                      0 other;
                                                                                                                                                                           DB 16;
                                                                                                                49;
                                                                                                                Indels
                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                    six alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                           303;
                                                                                                                0
                                                                                                            Gaps
                                                    144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRG
                                                                                                                0
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RESULT 14
                                                                                                                                                                                                                                       AAT31799,
                                                                                                                          Phytoene dehydrogenase; Erythrobacter longus; Erwinia hebicola; open reading frame; lycopene cyclase; Rhodobacter sphaeroides; beta-carotine; food colourant; additive; anti-cancer; ds.
                                                                                                                                                                                                                             AAT31799 standard; DNA; 1305
                            30-SEP-1994;
                                                                   09-APR-1996
                                                                                     JР08089241-A
                                                                                                        Erythrobacter
                                                                                                                                                                   Erythrobacter
                                                                                                                                                                                      20-SEP-1996 (first entry)
                                               30-SEP-1994;
                                                                                                                                                                   longus lycopene cyclase gene
                                                                                                        Longus
                            94JP-0236621.
                                               94JP-0236621
                                                                                                                                                                                                                              ВP
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(ASAH) ASAHI

KASEI KOGYO KK

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RESULT 15
ABL03846
ID ABL03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                      New isolated nucleic a
genes from Drosophila
interactions -
                                                                                P-PSDB;
                                                                                                                 Venter
                                                                                                                                                         23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                    (PEKE ) PE CORP NY.
                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide SEQ ID NO 6020.
                                                                                                                                                                                                                  27-SEP-2001.
                                                                                                                                                                                                                                       WO200171042-A2
                                                                                                                                                                                                                                                                                  pharmaceutical;
                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                 ABL03846;
                                                                                                                                                                                                                                                                                                                                                                                   ABL03846 standard; cDNA; 3251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence encoding the lycopene cyclase enzyme from Erythrobacter longus ATCC 14126. The gene was isolated from an E.longus genomic DNA library using a 1 kb fragment of the phytoene dehydrogenase gene from Erwinia hebicola as a probe. The probe isolated once 1578 bp) encodes the phytoene dehydrogenase (AAT31798) whereas ORF1 (1302 bp) encodes the phytoene dehydrogenase (AAT31798) whereas ORF1 plasmid probes lycopene cyclase. The two ORFs were inserted into the Rhodobacter sphaeroides for prodn. of the proteins. The phytoene dehydrogenase and lycopene cyclase can be used to produce beta-carotine effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1305 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 6-7; 7pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erythrobacter sp. phytoene dehydrogenase and lycopene cyclase genes for the prodn. of beta-carotine useful as a food colourant
                                                                                                                                                                                                                                                                                                                                                                                                                                             840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                            2001-656860/75.
DB; ABB59743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGTTCTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGTTGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGTCGATGGCCATCGGCGGT 174
                                                                                                               JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1996-233337/24
DB; AAR95698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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cal; gene; ss.
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                                        acid detection reagent and for elucidating ce
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Search completed: October Job time: 129.627 secs

27, 2002, 16:40:46

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Claim 1;

IJ

NO 6020; 21pp + Sequence Listing; English

interactions

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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CTGCGGGCGACC
                                                         GTGGACCTCTTGAGCCTGCAATTGGGAAGGGGAAAATATCAGTTCTGGAAGAGATTAGCCT 1518
                                   AATCCGGACACC
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                                                                                      AAAATCAAACTGAACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGT
                                                                                                                          GCGCAGGCTGGCGGACACCTCCTTGGAGATGTTGTCGCTCAGCCACTGGCGCAGGAAGGC 1458
                                                                                                                                                        GGTGCGGTTCTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGAT 231
                                                                                                                                                                                           GTCGGGCTTCTTGGCCAGCTCCTTGGCGTTGGCGGCGGTCACGGATCCACCGTACTGGAT 1398
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                                                                                                                       Fish vaccine against piscirickettsia Patent: WO 016865-A 5 20-SEP-2001; Aqua Health (Burpe) Limited (GB)
Location/Qualifiers
                                                                                                                                                                                                                       Burzio, L.
                                                                                                                                                                                                                                     Simard, N., Brouwers, H., Jones, S.F.,
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M284490 R.conorii 1
M28479 R.rickettsi
AE008675 Rickettsi
AE008675 Rickettsi
AE008675 Rrabidops
JED08675 Arabidops
JED08675 Ara
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AC100687 Mus muscu
AP004589 Oryza sat
AC025524 Homo sapi
AC092934 Homo sapi
AC025802 Homo sapi
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AF184152 Piscirick
D16515 Rickettsia
AJ235273 Rickettsi
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                                                                                                                                                                                                                                            Valenzuela,P.
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05-OCT-2001

group;

Database

Result

Minimum

Maximum

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JOURNAL
REFERENCE
AUTHORS
TITLE
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ORGANISM
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                                                                                                                                                                                                                      Submitted (10-SEP-1999) Biochemistry & Microbiology, Victoria, Petch Building, PO Box 3055, Victoria, BC v Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      Kuzyk,M.A., Burian,J., Thornton,J.C. and Kay, Identification of a genus-common Rickettsial salmonid pathogen Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piscirickettsia salmonis alanine racemase (alr) gene, partial cds; and BAX (bax), DNA repair enzyme RadA (radA), 17 kDa antigen (ospA), and transposase (tnpA) genes, complete cds.
                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                             2 (bases 1 to 4983)
Kuzyk, M.A. and Kay, W.W.
                                                                                                                                                                                                                                                                                                                                          Unpublished
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Pred. No. 1
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repeat_region
BASE COUNT 1362
ORIGIN
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AUTHORS
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ORGANISM
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                                                                        specimens
J. Clin.
95229950
                                                                                                                                                        Submitted (05-JUL-1993) Yoshiya Yoshida, Kanagawa Prefectural Pabulic Health Laboratoty; 52-2 Nakao-cho, Asahi-ku, Yokohama, Kanagawa 241, Japan (Tel:045-363-1030, Fax:045-363-1037) (bases 1 to 537)
                                                                                                                                                                                                                                                                                                                          17K genus-common antigen; 17k dalton protein. Rickettsia japonica (sub_species:YH) DNA. Rickettsia japonica
                                                                                                          Furuya,Y., Katayama,T., Yoshida,Y. and Kaiho,I. Specific amplification of Rickettsia japonica DNA specimens by PCR
                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia; spotted fever group.
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/sub_species="YH"
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Andersson,S.G.E.
Direct Submission
Submitted (11-NOY-1998) S.G.E. Andersson,
Siv.Andersson@molbio.uu.se, Dept. of Molecular Biology, University
of Uppsala, Husargatan 3, Uppsala, S-751 24, SWEDEN
                                                                                                                                               Rickettsiaceae; Rickettsiae; typhus q
1 (bases 1 to 237523)
Andersson,S.G., Zomorodipour,A., Andersson,J.O.,
Sicheritz-Ponten,T., Alsmark,U.C., Podowski,R.M.,
Eriksson,A.S., Winkler,H.H. and Kurland,C.G.
The genome sequence of Rickettsia prowazekii and t
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Rickettsiaceae; Rickettsieae; Rickettsia; typhus
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/db_xref="GI:1435056"
/translation="MKLLSKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLG
/translation="MKLLSKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLG
SQPFGKGTGQLVGYGYGALLGAVLGGQLGAGMDEQDRRLAELTSQRALETAPSGSNVEW
RNPDNGNYGYVTPNKTYRNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN"
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2074...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="
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                                                                                                                                                                                                                                                                                                                                                                                                 complement(7264.
                                                                                                                                                                                                                                                                                                                                                                                                                                 YAVLSNIDGKIIHAKIYYKPMMSFIWIGVILTTAGFVIALIRKNSY"
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                                                                                                                     translation="MAQKPNFLKKIISAGLVTASTATIVAGFSGVAMGAAMQYNRTTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3348
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DYNAMPNYLYTPMAGLSYLKSSNENYKETGTTVANKRINSKFSDRYDLIVGAKVAGST
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                                                                                                                                                                                                                    APGVSQNISRCLESTNTAAYNNMLLAKDPSDVATFVGAIATDTSAAVTTVNLNDTQKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVHGIAANSISFENASLGTSLFLPSGTPLDVLTIKSTVGNGTVDNENAPIVVVSGIDS
MINNGQIIGDKKNIIALSLGSONSITVBANTLYSGIRTYKNGGTVTLSGGMPNRPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNTNTTLADGTNLGSAENPLSTIHFATKAANADSILNVGKGVNLYANNITTNDANVGS
LHFRSGGTSIVSGTVGGQQGHKLNNLILDNGTTVKFLGDTTFNGGTKIEGKSILQISN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QANGGTIKLTNTQNNIVVNFDLDITTDKTGVVDASSLTNNQTLTINGSIGTVVANTKT
LAQLNIGSSKTILNAGDVAINELVIENNGSVQLNHNTYLITKTINAANQGQIIVAADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAAGSIQLDGSAIITGDIGNGGVNAALQHITLANDASKILALDGANIIGANVGGAIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSNEGSTNEGNLDTQIVVPDTKILKGNEIGDVKNNGNTAGVITENANGALVSASTDPN
IAVTNINAIEAEGAGVVELSGIHIAELRLGNGGSIEKLADGTVINGPVNQNALMNNNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSVDNGNAATISGQVYAKNMVIQSANAGGQVTFEHIVDVGLGGTTNFKTADSKVIITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKNGAATEFNVTGTLGGNLKGIIELNTAAVAGKLISQGGAANAVIGTDNGAGRAAGFI
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ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                           RESULT 5
AL646071
                                                                                                                                                                   DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGCGTTACAACAAACAGGAACGCCGTCAGCAGTACTGCCGCGAATTTCAGCAGAAAGCC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTAGCGGTAGTAACATAGAATGGCGCAATCCAGATAACGGCAATCATGGTTACGTCACA 172881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTCGTTGGCGTAATCCGGACACCGGTAACAGCTACTCTGTGGAACCGGTTCGCACCTAC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACCAGCAGGATAAAATCAAACTGAACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGTAGGTGTAGGCGCATTACTTGGGGCAGTTCTTGGTGGACAAATCGGCGCAAGTATG 172764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGGCGCAGGAGGTGCATTACTTGGTTCTCAATTCGGTCAAGGTAAAGGACAACTTGTC 172704
                                                                                                                                                                                                                                                                                                                                                             TGGCAAGTTGTGA 173014
                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCAGGTGATTA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGATCGCAGGTCAGAAACAGGAAATCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTAATAAAACTTATAGGAACAGTGCAGGTCAATATTGCCGTGAATACACTCAAACAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGAGCAGGATAGAAGACTTCTAGAACTAACATCACAAAGAGCTTTA---GAATCTGCA 172821
                                                                  segment 15/19.
AL646071 AL646
AL646071.1 GI
                                                                                                                                                               AL646071 : Ralstonia solanacearum
         Ralstonia solanacearum.
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/note="Pseudogene with one
to resolvase"
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/gene="RP711"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA15144.1"
/db_xref="GI:3861245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MSIEKEKFWASHKQVVKEIGGTNLINGKHDLFKAVAYTSDDIEA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA15145.1"
/db_xref="GI:3861246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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Pred. No. 1.4;
0; Mismatches 195; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ralstonia solanacearum
Bacteria; Proteobacteria; beta subdivision; Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INRA, BP27, F31326 Castanet-Tolosan Cedex
Christian.Boucher@toulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://sequence.toulouse.inra.fr/R.solanacearum.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boucher, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="elements of external origin; functions on bacterial functions" /note="product confidence: putative Gene name confidence: hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSCRIPTION REPRESSOR PROTEIN"
/protein_id="CAD16313.1"
/db_xref="GI:17429628"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RSc2606"
                                                                                                                                                                                                                                                                                                                                                   complement(1052. .1327)
/gene="RSc2607"
                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1052. .1327)
/gene="RSc2607"
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/gene="RSc2606"
/evidence-not_experimental profess."
product="HyPOTHETICAL PROTESS."
/protein_id="CAD16314.1"
/db_xref="GI:17429629"
                                                                                                                                                                                                                           predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYEILRFIGRSTSLNDYQRLKAALDRLQSTSIATSIRETTGRRLHRFSWINEWRELAD
ASGKPLGIELILPDWFYAGVLDAALVLTIDPAYFRLKGGIERWLYRLVRKHGGRQEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mssppgqalpqreqLDLfralpgDmaprdsqDLmafpffslaks
RRTAPIDfraggITIRVEGTAEHGIATIWDADVLIWAASQIVEARDAGIRPSRWIRAT
                                                                                                                           /transl_table=11
                                                                                                                                                                                          predicted by FrameD"
                                                                                                                                                                                                                                               /function="miscellaneous: hypothetical/partial homology"
/note="product confidence : hypothetical
Gene name confidence : hypothetical
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/product="HYPOTHETICAL REPLICATION INITIATOR AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="GMI1000"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTERPLSCFYGNPHLRIPTEPGNRIRVFPASDNSASVLPFFCGC
DGLH RASTRWHRYGSTVLCFGTRAHPRIVGFVRRLPMTLPLVTADERAFLLAHGAAL
AAGGRLDPLPVVRLFTPDAHYTMLIVSLDPADGDTAYGLIDLGIGLPSLGTVKLSDLA
GIVGPRKLPVRRDRYFQAAHLLSEYVRLAQENGAITD"
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/gene="RSc2608"
predicted
                                                                                                                                                                                        TLHKLTELCEVMDVHPLTLLTLAFAGDSTRKADELLAQVRQELEAVLNSDGD
                                                                                                                                                                                                                                                                                                                                                             predicted by Codon_usage predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                  /function="miscellaneous; not classified regulator"
/note="Product confidence : putative
Gene_name_confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
/evidence=not_experimental
/product= PROBABLE LIPOPROTEIN"
/protein_id="CAD16316.1"
/db_xref="GI:17429631"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene name confidence : hypothetical predicted by Codon_usage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2557. .3150)
/gene="RSc2609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRKQLIHDGKRLVLVSHWPGCCLRLALAPGLEDGMAYLYATRACATPCARYRTLTAEL
DALATATVAAPTAAARSRPTLAAVLELHTLQALDATLAGASLREVAVGLFSADAVAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTDRSAEHWYPTAAYLYVLHLDGPALAWEYLRRNPDYRRDWLRR
RRRPDAAQVWGLRLLEDPALDARDAHPAWFPDHDAVVQLYPDADPPPEAHAFEFWRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="HYPOTHETICAL/UNKNOWN PROTEIN"
/protein_id="CAD16315.1"
/db_xref="GI:17429630"
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GPKERKEGRRVMYAVSDLDAWADQRSYEATSDPEYAERHAGDYRDGR"
                                                                                                                                                                                                                                /evidence=not_experimental
/product="PUTATIVE TRANSCRIPTION REGULATOR PROTEIN"
/protein_id="QAD16317.1"
/db_xref="G1:17429632"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predicted by FrameD"
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                                       /function="miscellaneous; unknown"
/note="Product confidence : hypothetical
                                                                                                                                              /gene="RSc2611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="RSc2610"
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/note="Product_confidence : probable
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                                                                                                                                                                                                                translation="MAAKYSLAKALKTVRKARGLSQEAFSDVSSRTYMSTLERDLKSP"
                                                                                                                                                                                                                                                                                                                     transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="RSc2610"
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'note="Product confidence : hypothetical
                                                                                                                           note="RS00860"
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             confidence : hypothetical
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  Rickettsia
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327 GGTTCGCACCTACCAGCGTTACAACAAACAGGAACGCCGTCAGCAGTACTGCCGCGAATT 386
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Rickettsia sp. 17kDa
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tfpfydshdktysvrdgsdweytlkprlrerlrsskniilllssittnsralreeidy
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/evidence=not_experimental
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LKAGLAFLAILALTYVVIWLWSNNLNSIDINVEGSDVAIKTGDIFQQPGLKAIAFNEY
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Ying, Z. and Davis, M.J.
Direct Submission
Submitted (01-NOV-1996) Tropical Research and Education Center,
University of Florida, 18905 SW 280 Street, Homestead, FL 33031,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis,M.J., Ying,Z., Brunner,B.R., Pantoja,A. and Ferwerda,F.H. Rickettsial relative associated with papaya bunchy top disease Curr. Microbiol. 36 (2), 80-84 (1998) 98087556
                                  Ralstonia solanacearum (
segment 5/19.
AL646061 AL646052
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AAVGAGALLGAILGNQIGAGMDEQDRKLAELTSQRALEAAPSGSSVQWRNPDNGNYGT
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47.7%;
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Pred. No. 8.3;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evdex, France, LMGM CNRS Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire INRA, BP27, F31326 Castanet-Tolosan Cedex
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Direct Submission
Submitted (05-DEC-2001)
Cremieux, CP5706, 91057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Christian.Boucher@toulouse.inra.fr
http://sequence.toulouse.inra.fr/R.solanacearum.html
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                                                                                                                                      predicted by Codon_usage
predicted by Homology
predicted by FrameD"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="putATIVE TRAISMEMBRANE DEHYDROGENASE (SMALL
SUBUNIT) OXIDOREDUCTASE PROTEIN*
/protein_id="CAD14472.1"
/db_xref="GI:17427782"
/translation="MHTRPPSSDGDDPAGLTRROWLOSALAATAASLVGSVTLYAVAQ
APGEPLDAFMGLSQALTARSALDRAVGARLLAALQASAGFAAQLRPLAQSLAAGTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Product confidence : putative Gene name confidence : hypothetical
/evidence=not_experimental
/product="PUTATIVE TRANSMEMBRANE DEHYDROGENASE (LARGE SUBUNIT) OXIDOREDUCTASE PROTEIN"
/protein_id="CAD14473.1"
                                                                                                                                                                                                                                                                   /note="Product confidence : putativ Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLQQETALRILQAWYTGVVDGTVVTYEQALMYGVVSDILVIRTYCPNRPGFWAEPPVE
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predicted by FrameD"
                                                                                                                                                                                                                                                                                                                        /gene="RSc0771"
/EC_number="1.-.-"
/function="small molecule metabolism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="RS05083"
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/transl_table=11
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/EC_number="1.-
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151. .642
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/strain="GMI1000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="RSc0771"
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                                                                                                                   transl_table=11
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CDS

gene

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NLAFLKRAPYLEKGDMPTWNIGAY LAGCLAIGTCHTPRGFAMQEKAMBERGKGYLAGGEAGGTCHTPRGFAMQEKAMBERGKGYLAGGEAGHGTCHTPRGFAMQEKAMBERGKGYLAGGEAGHGTCHTPRGFAMGEAVQHSFSRM TERDVRAIAEYLETVPAVSTGAQRARIGWGTPATDVIALRGKPIETTIDAARLYLGNC ATCHQADGRGTPDGYYPPLLHNSAYGARDTRNILVQVMLHGIERRAGDRHIGMPAFGRQ LSDAQLAALANYVTRQFGDPATPALTADEIAKRRMPQ"

complement (3559. .5781)
/gene="RSC0773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/product="putative Oxidoreductase Dehydrogenase
/product="putative Oxidoreductase Dehydrogenase
(CYTOCHROME C SUBUNIT) SIGNAL PEPTIDE PROTEIN"
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DGENLYPAMPYPSYAKINDADMRDLYAYFRYGVAAVQYAPPPGTIRWPLNMRWPLKLW
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predicted
                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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/db_xref="GI:17427785"
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1AFSKGSVQLDDEVKRIHLAATLDTVDNQALYTAASCTAIRGSEPAAPSGAAASTA
PAAPDPQQYVGIAWTVGTYNNAAIRGSGKAGGVLRLQDARRPYPLQADTVGKTRI)
LAGTLTNPSSLTALDLRLHLSGASMAHLYPLTGVVLPDTPPPDTRGRLIGELRRQGSS
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                                                                                                                                                               WRYEOFTGRVGGSDLGGTLTFAMRPEPPGQRPQLTGELVSHQLLFADLAPIIGADŚNAS KQRRDAPVRQPADKVLPVEPERTDRWALDAVKTTGERIVETADLPIDHLVTHIKLQ KQRRDAPVRQPADKVLLPVEPERTDRWALDAVKTTGERIVETENLESMHASI GELVELDFLAVATURA KRIPQLFPNIESMHASI GELNGDARLSATGNEVAALLGASNGELKILVEGGTVSKFILBAMGLNVGNVILTKLFG DKQVSINCAAGDFAVSDGLAQARTFVVDTQDAVIDVTGATSEKHESLDFTIHPDSKGL RVFSLRTPLYVKGTYKHPDVSVNPAVVALRAGGAVALAFAAPVAAVLPVLELQPAPDS
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/gene="RSc0773"
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/note="Product confidence : putative
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                                                                     5883.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="miscellaneous; hypothetical/global homology"
/note="Product confidence : probable
Gene name confidence : hypothetical
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                                                                                                                                  PCGKLLADVRQRPTAPPPGKVYRSGQTGRAADGSPKDPAAAPARQPALPLRDPTTAGG
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/note="RS05080"
                         /gene="RSc0774"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="RSc0772"
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                                                                 .6785
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by Codon_usage
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CDS

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RESULT 8
AL646079
LOCUS
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      VERSION
                                    ACCESSION
                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGTCGATGGCCATCGGCGGTGCGGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGGCCACCGGTGCGGTTGTGGGCGGTGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCCGGCCAACAGCCCCGGTATTCTCGGCACCATCATCGGCGGCGTGGCGGGTGGCGTG 135978
                                                                                                                                                                                                                                                                    CTGGGTGCCCTGGCGGCCAATCAGGTGGAGCGG 136071
                                                                                                                                                                                                                                                                                                                           CTGGGCGGTCTGATTGGCTCTAAAATCGGTCAG 213
                                                                                                                                                                                                                                                                                                                                                                                       Ralstonia solanacearum GMI1000
segment 4/11.
AL646079 AL646053
AL646079.1 GI:17430956
                                                                                                                      AL646079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/note="Product confidence: hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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DPAVEXISRFYEHPEGFADAFAARWFKLTHADAETIPGAARYLGFEVPAEALHWQDDFTA
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VDHKLIDTQDIAALKARILASGLSVSQLVSTAWASASTFRGSDMRGGANGARIRLAPQ
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PLRYPEPEQQACAVEVPAESSHAGIDDLAAAGAIEVVNAPPAPQPSRGPQGLACAGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene name confidence : predicted by Codon_usag predicted by Homology predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="katGb"
/note="RSC0775; RS05079"
complement(6890 8257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDWEANQPAQLAKVLETLES IQGAFNGAQSGGKKVSLADL IVLAGCAGVEQAAKNAGH
AVEVPFTPGRMDAAQAQTDVESFAVLEP IADGFRNYQKGKYTLPAEALLVDKAQLLTL
TAPEMTVLVGGLRVLDTN IGQTRHGVFTQRPESLTNDFFVNLLDMGTEWKATDGRDVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6890. .8257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="cell processes; protection responses;
detoxification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSVCVTAVFGMVAASTALRAIAAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGRDRATGALKWTGTRVDLVFGSHSQLRALAEVYGSADAQAKFVRDFVAAWDKVMNLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="PROBABLE PEROXIDASE/CATALASE (CATA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Product confidence :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="katGb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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sequence;
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TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INRA, BP27, F31326 Castanet-Tolosan Cedex Christian.Boucher@toulouse.inra.fr http://sequence.coulouse.inra.fr/R.solanacearum.html.Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 213050)
Boucher, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia solanacearum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene name confidence : hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD"
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/note="Product_confidence : hypothetical
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                                                                                                                                                                                                                                                                                                                                                      KSRGEQLAFVIDEGLLITEGVVPGLTKPAALIGVTEKGFLSVALKLSATPGHSSMPPA
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/note="Product confidence : probable
Gene name confidence : probable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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HISTIDINE KINASE FOR COBALT ZINC CADMIUM RESISTANCE
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GEPVAAPAAVPEDVLASSSALHTWWSRTGIASRAIAAQARLGHRDTVTVLVAQDGDS
                                               predicted predicted
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complement(3145. .3819)
/gene="czcR"
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/note="Product confidence : probable
Gene name confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIAVRNPGPGIPAASLPLLFDRFYRGDPARANSERSAGLGLAIVOTIMDLHGGTAQAS
SPPGGLTEFRLIFPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAALMASYRRHIFLAVIAGVAAVALLSLMLVRSTLKGLARIGRQAASVVPSQLDTRLT
LEGAPRELSDLLAALMAMLTRLQDGFARLSQFSADLAHDFRTPLAVLIGQTEVTLAHP
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                                                                                                                                                                                              /function="cell processes; protection responses"
/note="Product confidence : probable
Gene_name_confidence : probable
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predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="RSp0490"
/function="miscellaneous; hypothetical/global homology"
/note="Product confidence: putative
/note="name confidence: hypothetical
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/codon_start=1
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/productc="PUTATIVE SIGNAL PEPTIDE PROTEIN"
/protein_id="CADJ7641.1"
/db_xref="GI:17430960"
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/transl_table=11
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/codon_start=1
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/product="probable cobalt-zinc-cadmium resistance (CATION
/product="probable cobalt-zinc-cadmium resistance (CATION
/product="probable cobalt-zinc-cadmium resistance (CATION
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/protein_id="CAD17643.1"
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EAHAREKRLWEQGIAAAQDYQQARTALQEARIADNARQLAVIGAAPAGTALNFEI
RAPPDGVVVARHLSQGEAVQAEAAVTLADLRTVWADFAVTAKDLEAVTTHATATVRA
TATGTAYQGKVSYVGALLGEQTRSAPARVTLDNPKRAWRFGMEVSVSYSGSRVPVPVA
TATGTAYQGKVSYVGALLGEQTRSAPARVTLDNPKRAWRFGMEVSVSYSGSRVPVPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="cell processes; transport of small molecules"
/note="Product confidence: probable
Gene name confidence: probable
predicted by Codon_usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="cell processes; protection responses"
/note="Product confidence : probable
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ADLLVAQRALSAFWGGAVAVÞEADGSAETLÞAVÞÞEAHRVLAAATAAEÞVALASTÞRA
LRARLEIEHRQALVNVERSKRVÞDVTLSVGAKRDSGANANMAVVGIAVÞLÞLFDRNQG
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apasvpgaahermtlqqaidralathpalaaagyavrasegavDqasrlanpeaarlt
eDvrrdratyraqlniplelggkraarrraaelardaaggdavlaaelradprafe
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/db_xref="GI:17430961"
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/product-"PROBABLE COBALT-ZINC-CADMIUM OUTER MEMBRANE
RESISTANCE PROTEIN"
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-10_signal
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                                                                              TGGCAAGTTGTGA 534
                                                                                                             TGGCAGGTGATTA 472
                                                                                                                                            ATGATCGCAGGTCAGAAACAGGAAATCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGC 459
                                                                                                                                                                                                         CCTAATAAAACTTATAGAAATAGCACTGGTCAATATTGCCGTGAGTACACTCAAACAGTT 461
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Rickettsia conorii
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia; spotted fever gro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson, B.E. and Tzianabos, T. Comparative sequence analysis of a
RIRANT17KD
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RNDDNGNYGYVTPNKTYRNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN"
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93 c 125 g 14
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                                                                                     ATGATCGCAGGTCAGAAACAGGAAATCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGC
                                                                                                                                                                    CAGCGTTACAACAACAGGAACGCCGTCAGCAGTACTGCCGCGGAATTTCAGCAGAAAGCC
                                                                                                                                                                                                                     CCTAGTGGTAGTAACGTAGAATGGCGTAATCCGGATAACGGCAATTACGGTTACGTAACA 401
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                 TGGCAAGTTGTGA 534
                                                  TGGCAGGTGATTA 472
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by B.A
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mkilskimiialatsmiqacngpggmnkqgtgtliggaggalig
sqfgkgkgqlvgvgvgkgllgavlggqigagmdeqdrrlaeltsqraletapsgsnvew
RNPDNGNYGYVTPNKTYRNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120.
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92 c 125 g 143 t
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/db_xref="taxon:783"
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/db_xref="GI:152464"
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Ogata, H., Audic, S., Renesto-Audiffren, P., Fournier, P.-E., Barb, Samson, D., Roux, V., Cossart, P., Weissenbach, J., Claverie, J.-M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ogata, H., Audic, S. and Claverie, J.-M Selfish DNA and the origin of genes Science 291 (5502), 252-253 (2001)
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20485642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A public version of R. conorii genome database is accessible at http://igs-server.cnrs-mrs.fr/. The database intends to provide updated data. Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful. Comments to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-APR-2001) Unite des Rickettsies, Faculte de Medecine, CNRS UMR 6020, Universite de la Mediterranee, 27 boulevard Jean Moulin, Marseille Cedex 05 13385, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mechanisms of Evolution in Rickettsia Science. 293 (5537), 2093-2098 (2001) 11557893
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AE008675.1 GI:15
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                                                                                  complement(1064. .1087./note="perc"
                                                                                                                                                                                                    /gene="RC1277"
1141. .1452
                                                                                                                                                                    WYGDTSRMYYVGDVAIKPKRLIQVTYDAMMKGIEVVRPGAKLGDIGHAIQSYAEKHNY
SVVRDYTGHGIGRVFHDEPSILNYGRSGTGLTLEEGMFFTVEPMINAGNYDTILSKLD
                                                                                                                                     complement (977.
                                                                                /note="REP02, RS3-like
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                                                                                                                                                                                                                                                                                                                                                         /note="RC1276"
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J.-M. and
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repeat_region
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                                                                                                                                        complement (4505.
                                                                                                                                                    /note="REP03, repeated element"
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                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3509. .4258)
/gene="RC1281"
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/note="REP02, RS3-like repeat"
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2792. .3115
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="mray2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="mray2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="similarity to DNA repair protein (Radc)"
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LEVMLFSAIPRKDIKPLAKKLLDHFDITDLINLDKERLLSIKGTNENLYINFALRELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1457.
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1457. .1825
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/gene="RC1278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeated element"
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Best Local
8359 GATGAACAGGATAGA---AGACTTGCAGAGCTTACCTCACAGAGAGCTTTAGAAACAGCT 8415
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                                      220 GACCAGCAGGATAAAATCAAACTGAACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTT 279
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                                                                                   GGAGTAGGTGTAGGTGCATTACTTGGAGCAGTTCTTGGTGGACAAATCGGTGCAGGTATG
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                                                                                                                       ATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATG 219
                                                                                                                                                               GGCGGTGCTGGCGGCGCATTACTTGGTTCTCAATTCGGTAAGGGCAAAGGACAGCTTGTT 8298
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                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                       complement(7027. .7947)
/gene="p34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="cytosine deaminase [EC:3.5.4.1]"
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SRLKRLFYGASDSKHGVVESNLRYFNSSACFHRPEIYSGILAEDSGLLMKEFFKRIRT
                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="p34"
                                                                                                                                                                                                                                                                                                                                                                                                /note="RC1286"
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/gene="RC1285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Product="heme exporter protein C"
/product="heme exporter protein C"
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SLVTGSLWGKPIWGYWWWDDARLTSMLILFLYLSYIIIVNSADNIRKAQWPSSIIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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/gene="RC1285"
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RTAILIDKIKNR"
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/gene="ccmC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MTYVVTDECVKCKYTDCVEVCPVDCFYEGEREDDFMLVINPDECIDCGVCVPDCP1GAIKPESPGLIEWVERAKDFIENKGWKNITKKKTALPDADKFKDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="REP06, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="unknown"
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TNISASHKPTITRLLINGYVDLTNFDMFDVFAGAGVUSALVKEKITYNGITGLSSNYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ferredoxin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="fdxA"
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/gene="fdxA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="RC1283"
                                                                                                                                                                                                                                                                                        8.38;
                                                                                                                                                                                                                                                           Score 40.2; DB
Pred. No. 19;
0; Mismatches
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and T rich
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 40
20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Washington Genome Box 352145, Seattle, WA 98195,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-MAY-2000) Department of Medicine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hancock, R.E.W., Lory, S. and Olson, M.V.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H., Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
Pseudomonas aeruginosa
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406 (6799), 959
                                                                                                                                                                                                                                                                                     /gene="PA1047"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                      /gene="69. .12
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                                                   VAHYWPEFAAAGKAAISVRQLLCHRAGLPALREOMPPEALYDWOAMTTALAAEEPWWT
PGEAHGYAPITYGWLLGEVIRRVDGREPEGAIYARTAAPLGLDEDFUYGLDDSOFGRVAH
MARSKGSLGDAAAQRMLKTMMSEPLALTTRAFTNPPSILTSTMKPEWRRAWQOPAANGH
GNARALAGFYSGLLOGRLLEDELLGQLAHEHAVGEDRTLLTRTRFGLGTMLDQPGVAN
                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:287"
69. .1247
                ATYGLGPKAFGHPGAGGSIGFADPERDLAFSFVSNALGPYVLMDPRAQQLARVAGECI
"
                                                                                                                                                                                                          /product="probable esterase"
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                                                                                                                                                            /translation="mprplshrnlpmtpQGHCDSrfaplaEAfArlfDnpQErGAALC
LEVGGETVVDLWGGVADKDGEQPWQRDTILnLfSCTKTFTAVAVLQLVAEGKLELDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="PAO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pseudomonas
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Center, University Of Washington,
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98 of 529 of the complete
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                                                                                                                                                      /gene="PA1052"
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LGSTLSALGIGLFMFFVVAAALKTAQGSTTVALVTTSALVAPLLPQLGLDSEMGRVLT
                                                                                                                                                                                                                                                                                                                                                                 PIAAAGNLGLDASLGLVIVVGLVVAFVTAMAGMWWANRFVGKDIPLVDDGQVVQTEED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRQAVFLELPEHADPLPCQARLLAALGGRAEHWSAALGERLVFWCRPVAHADTLEHWL
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1453. .2334
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10907. 117--
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Best Local
                                                                                                                                                                                                                                             AL Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, On Aug 18, 1999 this sequence version replaced gi:3892698.

Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thail/.urce 1.106702
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les 75; Conserv
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bevan, M., Robben, J., Grymonprez, B., Mewes, H.W., Lemcke, K. and Mayer, K.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 92830 to 92989)
Bevan, M., Volckaert, G., Grymonprez, B., Voet, M., Robben, J., Bancroft, I., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
3 (bases 1 to 1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
4 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1570 to 106702)
Bevan,M., Wedler,H., Wambutt,R., Bancroft,I., Mewes,H.W., Lemcke,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases
                                              /note="strong similarity to NHP2/RS6 FAMILY PROTEIN, sapiens, PID:94826860 Contains Ribosomal protein L7Ae signature AA73-90
                                         contains EST gb:F13981"
                                                                                                          complement(join(<3 .98,594 .821))
/gene="AT4g22380"</pre>
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/product="Ribosomal protein L7Ae-like (fragment)"
                                                                                                                                         /note="basepairs 1-15769 are not integral part of BAC clone F7K2"
                                                                                                                                                                                             Organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/chromosome="4"
                                                                                                                                                                                      1. .15769
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No. 27;
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e 4, BAC clone F7K2
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snRNP assembly	/number=1 complement(join(61126297,66756812,69087075, 7168 7353 7429 7513 7775 8034)\	complement(61126297) /gene="AT4g22410"	Complement(Join(6112. 629/6675. 6812,6908. 7075, 7168. 7353,7429. 7513,7775. 8034)) /gene="AT4672410"	61128034 /gene="AT4922410"	IESISPSPDKISIEIWPKRYDFTFQTQEWNVSNFIPVDPIQWDPFHDQSLYHVKHRLQ LPENPSTLAIIIGTSTDRTRVRNKIIGDQSDDDDPRASDHIIDGVWVEVRP"	GSTLGWLVMSESLDLNPRKTHQTFLYNPFISELQQLPELTLDSPYPTGVLRYGVLTGN PSDNNTYACLITDYLHEIGNRRDTYTLLIYYVAKTSGRWEQNWSYASMLVYGIFDTWY	/translation="MLSSHLSQICFSCRDPLGNLPADLIRKCTDLMDLNFAEGQRLRT LNKNWKLALPSFRKGAYREERPWLLYRERGSGETRFFDPVRERVHRGNDPRLADARFL	/protein_id="CAB52814.1" /db_xref="GI:5738371"	/codon_start=1 /product="putative protein"	ana 17595"	<pre>/gene="A149224U0" /note="similarity to various predicted proteins,</pre>	47285711	47285711 /appa="##4422400"	/gene="A14g22400" /number=1	47285711	WFDLESQSLTTAGIECDSSFTADILVSSLVLGCKGDPTQAQRSKDQKYMPKSTKRWYA	HWILPRRQGVIAFNAIIKYDLASDDIGVLSFPQELYIEDNMDIGVLDGCVCLMCYDEY SHVDVWVLKEYEDYKSWTKLYRVPKPESVESVEFIRPLICSKDRSKILLEINNAANLM	LKEGKKKFPCPVEVKVFSLKKNSWKRVCLMFEFQILWISYYYHLLPRRGYGVVVNNHL	/ CTAIRS LA CLOID = "MARCLYTULLINEME UKLWA IT LYKOVILSKYLESVELSPERYSSH LRRRLETGEHLMI LLRGPRILLRTVELDSPENVSD IT PHPLQAGGETEVFGSFNGVIGLC NGDUYS LTENGGEN VIGT TENGGEN TO THE TOTAL TOT	/db_xref="GI:5738370"	/protein_id="cAB52813.1"	Arabidopsis thaliana" /codon start=1	<pre>/gene="Alf4922390" /note="similarity to various predicted proteins,</pre>	/number 1 Complement (1789 2973)	/gene="AT4g22390"	/gene="AT4g22390" Complement/1789, 2973)	/gene="AT4g22390" complement(17892973)	1789 2973	Comptement (394. 621) /gene="AT4922380"	/number=1	complement(99593)	complement(join(398,594821)) /gene="AT4g22380"	3821 /qene="AT4q22380"	/yene= 1 /number=1	Complement(398)	/translation="mTGEVVNPKAYPLADSQLSITIMDLVQQATNYKQLKKGANEATK TLNRGISEVVMAADAEPLEILLHLPLLAEDKNVPYVFVPSKQALGRACGVTRPVIAC	/protein_id="CAB52812.1" /db_xref="GI:5738369"
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. exon	intron						CDS	gene	gene		exon	LTR	misc_feature	LTR		exon		intron	exon		intron		exon	intron	•	exon		intron	exon		intron						
/ Humber - 1 complement (1370114033) /gene="AT4g22420"	complement(1361913700) /gene="AT4922420" /number=1	EEVDDEEDDDDDASKGRGKHSRHVEVRRDCPYLDTVNRQVIIIDQFLMLRVPLATMRK RMRTGGRKAKAMEKYLKKVLKKSG"	/db_xret="G1:5/38373" /translation="waecPyDoINEMFLRLRATTLKKCRVLSKPCFSLIDSPEKRVIE PSDAGDDDIGFNUHI DI AMAYDDDDFFFGNEIKKSGARBNGVAKCFGNGWYVNGFAO	<pre>/product="putative protein" /protein_id="CAB52816.1"</pre>	<pre>contains EST gb:T44427" /codon_start=1</pre>	<pre>/note="similarity to predicted protein, Arabidopsis thaliana</pre>	complement(join(1351313618,1370114033,1421614331)) /gene="AT4g22420"	1351314331 /qene="AT4q22420"	complement(join(1351313618,1370114033,1421614331)) /gene="AT4g22420"		<pre>/note="389bp LTR" complement(1351313618)</pre>	13234. 13624	8450 13234	/note="389bp I.TR"	/number=6	complement(77758034)	/gene="AT4g22410" /number=5	/number=5 complement(75147774)	complement(429/513) /gene="AT4g22410"		complement(73547428) /gene="AT4g22410"	/gene="AT4g22410" /number=4	/number=3 complement(71687353)	complement(/0/6/16/) /gene="AT4922410"		complement(69087075)	/gene="AT4g22410" /number=2	/number=2 complement(68136907)	/gene="AT4g22410"		complement (62986674)	IPQVALEDLLKKEDGETVTEVVRPKLARMRYRVIKSPRYLMFHMVREKKNNFFKEKNP TIGESV"	FGELTRKIWHARNFKGQVSPHEFLQAVMKASKKRFRIGQQSDPVEFMSWLLNTLHMDL RTSKDASSIIHKCFOGELEVVKEFOGNENKEISRMSFLMLGLDLPPPPLFKDVMEKNI	THSUEAGHHYYLNLLTERYYCLPUSYELNUPSLUULKHYLNEFHIPENYQHCKSPLVHC SRALDGSDYLPGMYGLNNIQKTEFVNYTIQSLMRVTPLRNEFHIPENYQHCKSPLVHC	/translation="MVEFQVLDFHFERFCSVSLSNLNVYACLVCGKYFQGRSQKSHAY	/product="putative protein" /protein_id="CAB52815.1"	Homo sapiens, PID:g5730025" /codon_start=1

/number=2

- 다음 - 다음 - 다음 - 다음 - 다음 - 다음 - 다음 - 다음	/note="similarity to alternative oxidase, Mangifera indica, PIR2:S45035 contains EST gb:T42793, AI994896.1, AI997645.1, R30022, AA395166"
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Query Match
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14209 ...14314,14995 ...15111))
/gene="AT4g22280"
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                                 complement(13379.
/gene="AT4g22280"
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AYLEYSDLVPRHFPFVNLESLVEAKLALDLCSDSNPTNLIKGLRNVEVLELSSGYTSQ
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FGVVDAGDLLFRLITPERFIRIWQRMDRINEATSTSVLSMRWRYLFAFRPNLCLDDQE
VGGGDSFIDFVDRVLVVTGNEPIRRISIKCRMSIDTGHVTRWMVDVLEHGVSYLDIDI
                                                                                                                                                                                                                                                                                                                                                                                            /product="putative protein"
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ALLTTTRASVAVNIYEVGELALCSLSLVTGVEICLRSATKITHKAQSVTSLAAKMIVC
ATVDSFDHLDGETPFGSIIESOVSLAGNAIETSDDEBEGEDDDLDNTKIHPIYANTIS
YQKRQALVTYLENNKAGITVYGFLVDRSWLNTIFGIELALLLWLLNKTIGILA"
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   112 GGCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGTCGATGGCCATCGGC 171
                                   927 GTTGATGATGTCCACGAACTCGGGCTTCAGGGAGGCGCCTCCGACCAGGAAGCCATCGAT 868
                                                                   52 GTGGGTTGCGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGGGCCACCGGTGCGGTTGTG 111
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Best Local Similarity Matches 67; Conserv
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins.
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1070)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-JUN-1996) Ecology & Evolution, Stance York at Stony Brook, Stony Brook, NY 11794,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1070)
Hasson, E., Wang, I.W., Zeng, L.W.,
Direct Submission
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LAKKPDIDGFLYGGASLKPEFVDIINARQ"
3 345 c 301 g 186 t
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/translation="MSRKFCVGGNWKMNGDQKSIAEIAKTLSSAALDPNTEVVIGCPA
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/gene="Tpi"
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/strain="DPF-46"
/db_xref="taxon:7227"
/chromosome="3R"
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                                            Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library PRCI-11. For BAC
Library availability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 666 row: K column: 15
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Class: BAC ends
                                                                                                                                                              401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 516)

Mahaliras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Mahaliras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. au
                                                                                                                                                                                                                                                                                                                                                                                      AQ518147 516 bp DNA linear GSS 05-MAY-HS_5090_Al_F08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=666 Col=15 Row=K, DNA sequence.

AQ518147 AQ518147.1 GI:4743329
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B1326875 AR070H081
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Department of Animal Science
University of Nebraska, Lincol
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: dpomp@unl.edu oligo-dT track not found, Not I si is likely internal to the message.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caetano, A.R., Johnson, R.K. and Pomp, D. Generation and sequence characterization of a normalized cDNA recent from swine ovarian follicles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 823)
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI186311 823 bp mRNA linear EST JUNL-P-EN-cf-b-07-0-UNL.s2 UNL-P-FN Sus Scrofa cDNA clone
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//Ab_host="Union in the life Technologies"
//Ab_host="Union in the lif
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                       TAG_SEQ=None found"
272 c 231 g
                                                                                           by Bonaldo,
, 1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9823"
/clone="UNL-P-FN-cf-b-07-0-UNL"
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="University of Nebraska, Lincoln Swine Selection Lines"
                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
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156 c 129 g 104 t 5 others
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/clone="Plate=666 Col=15 Row=K"
/clone_lib="RPPCI-11 Human Male BAC Library"
/sex="male"
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REFERENCE
AUTHORS
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Best Local Similarity 100.0%; n
Matches 19; Conservative 0;
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FR0011976
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Best Local S
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 348)

Hillier L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., More Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          730
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348 bp mRNA linear EST 06-FEB yb28d01.r1 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:72481 5', mRNA sequence.
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Direct Submission
Submitted (09-SEP-1997) MRC Human Genome
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1 (bases 1 to 190)
Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S.
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Takifugu rubripes
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AL003232
AL003232.1 GI:2448802
GSS; genome survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clome_lib="cosmid 072L05"
/clone="072L05aE5"
/clone="072L05aE5"
38 c 40 g 56 t
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Email: biohelp@hgmp.mrc.ac.uk
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AV763598 MDS I
AV763598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High qality sequence stops: 262 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image_llnl.gov) for further information.
                                                                                                                      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,Y., Gao,G., Zhang,Q., Chen,S., Han,Z. and Chen,Z. Homo sapiens cDNA MDS clones
                                                                                                                                                                                                                                                                                                                                                                      EST
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97044478
                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                         Gu, J., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y.,
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert Length: 502
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                                                          l: hanzg@chgc.sh.cn
clone is available at CHGC
Location/Qualifiers
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314 286 1810
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/db_xref="taxon:9606"
/clone="MDSAOD07"
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/tissue_type="fetal spleen"
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                                                                                                                                                                                                                                         Y., Song,H., Xiao,H.
Cheng,Z., Xu,Z., Ze
S., Zhong,M., Lu,G.,
                                                                                                                                                     Pudong, Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                EST 19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                         Xiao, H.
                                                                                                                                                                                                                                                            Zeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
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ORGANISM
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BM381932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                source
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GGTTCTGGGCGGTCTGATT 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Individual basecall and confidence value were assigned using the phred software(http://www.phrap.org/). Overall sequence quality assessment and vector trimming was conducted using the Lucy software (version 1.16s, http://www.tlgr.org/softlab/). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers using a Perl program (est_process.pl), written by Dr. Hui-Hsien
                                                                                                                                                                                                                                                                                                                                                                      FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer Sp6 (ATT TAG GTG ACA CTA TAG)
Seq primer: universal (GTA AAA CGA CGG CCA GT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEST542-A12.univ ISUM6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Patrick S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clade; Panicoideae; Andropogoneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM381932.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iowa State University
                                                                                                                                                                                                                                                                                                                                                    POLYA=Yes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agronomy, Io 515-294-0975
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/note="Vector: pTriplEx2;
146 c 144 g 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/lab_host="BM25.8"
                                                                                                                                                                                                   /clone="MEST542-A12"
/clone_lib="ISUM6"
                                                                                                                                                                                                                                           /cultivar="B73"
/db_xref="taxon:4577"
                                                                                                                                                     /tissue_type="mixed"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                       /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="MDS"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 459
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167 TCGGCGGTGCGGTTCTGGG 185
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Single pass sequencing. Bases called and alt_trimmed with phred
                                                                                                       Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                              Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle 21180013
                                                                                                                                                                                                                                                                                          1 (bases 1 to 528)
Smith, T.P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94440 MARC 1BOV Bos taurus
AW658421
AW658421.1 GI:7424247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                         402 762 4366
402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 separate first-strand cDNA synthesis. Hence, these bar code tags can be used to identify the mRNA pool from which associated with specific tissue sources are: ACTGGC-Mixed mature tissues (17, 21, 38, 69, 77 DAG); CACAGC-Kernels (3, 5, 10, 15, 20, 25, 30, DAP); CACAGC-Kernels (3, 5, 10, 15, 20, 25, 30, DAP); CM, Saraccc-Adventious roots (65 DAG); CAGGGC-Mixed mature tissues (17, 21, 38, 69, 77 DAG); CM, Saraccc-Adventious roots (65 DAG); CAGGGC-Miss (0.2-3.0 cm, 53, 54, 59 DAG); TGAGGC-Husks (73 DAG); GACCAC-Silks; GAGGAG-entiolated seedlings; CAGGGC-Miss (17, 21, 38, 69, 77 DAG); CM, Saraccc-Cyclohexinide-treated callus; GTCACC-Anaerobic reated seedlings; CGTCAC-NAA (a-Naphthalene acetic acid AAGACC-Cyclohexinide-treated callus; GTCACC-Anaerobic reated seedlings; CGTCAC-NAA (a-Naphthalene acetic acid AAGACC-ACPC (1-aminocyclopropane-1-carboxylix acid seedlings; CTAGCC-ABA (Abscisic acid)-treated seedlings; GCTGA-Brassinolide-treated seedlings; GTGAGC-ABA (Abscisic acid)-treated seedlings; GCGGA-GA (Gibberellic acid)-treated seedlings; GCGGA-GA (Gibberellic acid)-treated seedlings; GCGGA-GA (Gibberellic acid)-treated seedlings; amounts of first-strand cDNA from each reaction were strand synthesis. After the addition of EcoRI adaptors, and 2.0 kb were directionally cloned into the EcoRI and disolated from the library was digested with NotI to remove purified and ligated at low concentration to promote transformed into DH10B host cells. The complexity of the resulting library was 1.2 x 10x6. The complexity of the palipa to the complexity of the creation and stated at low concentration to promote
                                       smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
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Pred. No.
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                                                                                                                                                                                                                                                                                                          Stone,
Bennett
"own,C.G.,
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                                                                                            ORIGIN
                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
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AI637152
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JOURNAL MEDLINE COMMENT

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Gaps

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TITLE

REFERENCE AUTHORS

RESULT 7 AW658421/c

DЬ Qy

BASE COUNT ORIGIN

Query Match Best Local Matches

Local

KEYWORDS SOURCE VERSION DEFINITION

ORGANISM

ACCESSION

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Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 CAGAGCATGGACCAGCAGG 229
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               l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                    Email: walbot@stanford.edu
Plate: 603001 row: D column:
                                                                                                                                                                                                                                                                                                                                                              Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize ESTs from various cDNA libraries sequenced at Stanford University Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                          855 California Ave,
                                                                                                                                                                                                                                                                                                                                                                                                             Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Walbot, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1637152 536 bp mRNA linear EST 26-APR-1999 603001D08.x1 603 - stressed root cDNA library from Wang/Bohnert lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI637152.1 GI:4688482
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays cDNA, mRNA sequence.
AI637152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 100.
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 62 row: P column: 3
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRimers
         Conservative
                                                                                                 95
                                                                                    /tissue_type="seedling"
/tissue_type="seedling"
/dev_stage="salt stress"
/lab_host="E. coli XL Gold"
/note="organ: root; Vector: pl
Seedling stressed root cDNA 1.
a 150 c 195 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                  /db_xref="taxon:4577"
/Clone_lib="603 - stressed root cDNA library from
Wang/Bohnert lab" . . . .
                                                                                                                                                                                                                                                        /organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

164 c 150 g 117 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
 100.0%; 14
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                    Score 19; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                Palo Alto, CA 94304, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19;
Pred. No.
Mismatches
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                                                                                                                                                                                                                                                                                                                        80
                                     DB 9;
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41;
                                                                               pBluescriptII SK(+) xR;
library from Wang/Bohnert lab*
2 others
 0,:
                                 Length 536;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phred software, (<a href="http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b">http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b">http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b">http://www.tipr.org/softlab/>).</a>

The conducted using the Lucy software (<a href="http://www.tigr.org/softlab/>).

Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORMARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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BM335231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 515-294-2299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1
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/db_xref="taxon:4577"
/clone="MEST147-F07"
/clone_lib="ISUM5-RN"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                             /tissue_type="mixed"
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Best Local :
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                        252 TCTGGAAAAAGTGAAAGCC 270
                                                           l Similarity
19; Conserv
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167 TCGGCGGTGCGGTTCTGGG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bilottusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
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1 (bases 1 to 648)

1 (bases 1 to 648)

Shetty,J., Malek,J., Koo,H., Collins,F., Gardner,M. and Loftus

Direct Submission of BAC-end sequences from Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     partial digest.
Seq primer: M13 For
Class: BAC ends.
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Other_GSSs: AG-ND-132N21.TR
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Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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          Conservative
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                                                                                                                                                                                                                                                 /clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
132 c 114 g 234 t
                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:7165"
/clone="AG-ND-132N21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Anopheles gambiae"
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Pred. No. 42;
Score 19; DB 12; Length 648; Pred. No. 42; 0; Mismatches 0; Indels
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BM350333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (<a href="//depts.washington.edu/ventures/collabtr/direct/index.htm>#b overall sequence quality assessment and vector trimming were conducted using the Lucy software (<a href="http://www.tigr.org/softlab/">http://www.tigr.org/softlab/</a>)). The start of the sure an overall trimmed quality of parameters were set to ensure an overall trimmed quality of high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schnable Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM350333 697 bp mRNA linear EST 16-JAN-2002
MEST264-C11.T3 ISUM5-RN Zea mays cDNA clone MEST264-C11 3', mRNA
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BM350333.1
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//ortea-Tvector: pT773PAC; Site_1: EcoRI; Site_2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissures (17, 21, 38, 69, 77 DAG), Kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventious roots (65 DAG),
Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 first ear, ear shank, etiolated seedlings, callus,
Cycloheximide-treated callus, Anaerobic treated seedlings,
NAA (a-Naphthalene acetic acid)-treated seedlings,
Kinetin-treated seedlings, ACPC
(1-aminocyclopropane-1-carboxyllx acid)-treated seedlings,
mrassinclida-treated seedlings, ARA (a-Naphthalene acetic acid)-treated seedlings,
ACPC
(1-aminocyclopropane-1-carboxyllx acid)-treated seedlings,
mrassinclida-treated seedlings, ARA (a-Naphthalene acetic acid)-treated seedlings,
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Agronomy, Iowa State University, Ames, IA 50011-1010, USA 515-294-0975
515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="ISUM5-RN"
/tissue_type="mixed"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="MEST264-C11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAC TAA AG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and tissues
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VERSION
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BI764273
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Best Local
           348 AAAGTGAAAGCCGGCCAGG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                         19;
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Query Match
Best Local Similarity
259 AAAGTGAAAGCCGGCCAGG 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11465 row: a column: 17
High quality sequence stop: 692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 744)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         603045965F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5186200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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                                                                                                                                                         147
                                             Conservative
                                                                                                                           /note="Octyan: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 citomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. 023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118
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                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:5186200"
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
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                                    100.08; +4
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                                                               Score 19;
Pred. No
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42;
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                                                                            Length 744;
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                             Gaps
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BASE COUNT
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BG715056/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
; Anopheles.
1 (bases 1 to 372)
Shetty, J., Malek, J.,
                                        Eukaryota; Metazoa; Pterygota; Neoptera;
                                                                                                                                      DNA sequence.
BH395820
                                                                                                                                                                BH395820 372 bp
AG-ND-119B5.TF ND-TAM Anopheles
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL http://lmage.llnl.gov plate: LLAM10679 row: b column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG715056.1 GI:13993987
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                                                                         Anopheles gambiae
                                                                                         African malaria mosquito
                                                                                                                        BH395820.1 GI:17341961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4795701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="hypothalamus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NIH_MGC_96"
                                                           Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                 3.9%;
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Primates;
Koo, H.,
                                                                                                                                                                                                                                                                                                                     0
                                             Endopterygota;
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Pred. No.
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 Collins, F.,
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                                                                                                                                                                o DNA
gambiae
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CDNA clone IMAGE:4795701
                                             Diptera;
                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                  linear GSS 11-DEC-20 genomic clone AG-ND-119B5
                                                                                                                                                                                                                                                                                                                                               Length 2405;
 Gardner, M. and Loftus, B.
                                              Nematocera;
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                                             Culicoidea
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 CTGGAAAAAGTGAAAGCC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 CTGGAAAAAGTGAAAGCC 270
                                                                                                                                                                                  Unpublished (1999)
Contact: Ralph Quatrano
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                   Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Punaridae; Funariales; Funariaceae; Physcomitrella.

1 (bases 1 to 386)
Quatrano,R., Bashiardes,S., Cove,D., Cuming,A., Knight,C., Clifton
(S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood
(K., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T.,
Steptoe,M., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashiardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Physcomitrella patens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW145423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW145423 386 bp mRNA line ga20h03.yl Moss EST library PPU Physcomitrella PEP_SOURCE_ID:PPU021606 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13 For Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_GSSs: AG-ND-119B5.TR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission of BAC-end sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW145423.1 GI:6167159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: bjloftus@tigr.org
                                                                                                                                              314 286 1800
314 286 1810
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.3e+02;
                                                                                                 Stavros Bashiardes as part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from
                                                                                                                                                                                             Louis,
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Search completed: October 27, 2002, 22:36:41 Job time: 972.668 secs
                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                       В
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                                                                                                                                                                                                    Query Match 3.7%; So Best Local Similarity 100.0%; I Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                    187 GTTGCCTGCAGGGCAGCT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                     8 GTTGCCTGCAGGGCAGCT 25
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High quality sequence stop: 373.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            104 a
                                                                                                                                                                                                                                                                                                                    //Octes*Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhOI; Construction of the cDNA library was carried out using Stratagenes 'UnizAp - cDNA synthesis kit'. cDNA contains a XhOI site within it. Following ds cDNA and sample was digested with XhOI. The result is cDNA and sample was digested with XhOI. The result is cDNA with an EcoRI sticky end on one side and a XhOI sticky end on one side and a XhOI sticky UnizAp arms. The vector is designed containing the cloned within this pBluescript sequence as well as lambda DNA and cDNA is then packaged using Gold gigapackaging extracts. Library was grown in XLIBlue MRF cells and amplified. The library was excised by mass excision using Stratagens 'Mass excised by mass excision using Stratagens 'Mass releases the pBluescript sequence and circularises it as plage) and secreted out of the host cell as phageinds. Splage) and secreted out of the host cell as phageinds. Was plated out on LB-amp plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered by using Qulagen Midi prep kit. 2 micro grams of electroporation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ammonium-grown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Organism="Physcomitrella patens"
/db_wref="taxon:3218"
/clone="pep_SOURCE_ID:PPU021606"
/clone_lib="Moss_EST_library_PPU"
/tissue_type="protonemata: 7 day old tissue
                                                                                                                                                                           3.7%; Score 18; DB 9; Lengtn 300.0%; Pred. No. 1.3e+02; '''ematches 0; Indels
                                                                                                                                                                                                                                               Length 386;
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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq
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length: 2000000000
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    October 27, 2002, 20:42:44; Search time 248.035 Seconds (without alignments) 7028.450 Million cell updates/sec
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483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pending_Patents_NA_New: *
                                                                                                                                                         atgcgtggttgcctgcaggg.....aggtgattagcaccgaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3:*
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3:*
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3:*
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                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                 48908
58175
91772
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          PCT-US02-2632-47
US-10-219-999-30827
US-10-108-2608-2343
US-10-108-260-2343
US-10-221-279-4847
US-09-918-995-8784
US-10-027-632-276565
US-10-027-632-276566
US-10-027-632-276566
US-10-027-632-276566
US-10-027-632-173497
US-10-027-632-173498
US-10-027-632-173498
US-10-027-632-22462
PCT-US02-25766-2948
                                                                                                                                                                                                                               US-10-114-170-79
US-10-53-853A-876
US-10-053-853A-484
US-10-114-170-137
US-10-153-853A-37
US-10-053-853A-37
US-10-053-853A-3
US-09-918-995-216
                                                                                                                                                                                                   US-09-919-002-8373
US-10-211-818-27
                                                                                                                                                                                                                                                                                                                                    US-10-114-170-252
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276567,
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173498,
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2343, Ap
24847, Ap
8784, Ap
                                                                                                                                                                       27, Appl
47, Appl
30827, A
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876, App
484, App
137, App
337, App
1, Appli
216, App
8373, Ap
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US-10-114-170-252/c
(S-10-114-170-252/c); Sequence 252, Application US/10114170
; GENERAL INFORMATION:
GENERAL INFORMATION:
Hattner, Frederick R.
Publicant: Burland, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0000
                                                                                 TELEFAX: (608) 251-91
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 53701-2113
                                                                      LENGTH: 12848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plunkett,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rod
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ALIGNMENTS

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COMPUTER: DISkette, 3.50 inch.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
/CURRENT APPLICATION DATA:
APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Novel Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                             REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/114,170 FILING DATE: 01-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Quarles & Brady STREET: 1 South Pinckney Street CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burland,
Burland,
Porna, Nicole T.
                                                                                                                                                                           251-9166
    NO::
                                                                                                                                                                                                                                              960296.95017
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US-10-114-170-252

Local

Similarity

1larity 100.0%; Score 22; Conservative 0; Mismatc

Mismatches

0;

DB 8;

Length 12848;

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RESULT 3
US-10-053-853A-876
Sequence 876, Application US/10053853A; GENERAL INFORMATION:
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                                                                                                                                                   Qy
                                                                                                                                                         Query Match
Best Local Similarity
Tatches 22; Conserve
                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-10-114-170-79
; Sequence 79, Application US/10114170
; GENERAL INFORMATION:
GENERAL INFORMATION:
Frederic
                                                                                                         31926 TAATCCGGACACCGGTAACAGC 31947
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                                                                                                                                                                                                                                                                                                                                 TELEFAX: (608) 251-9
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                         291 TAATCCGGACACCGGTAACAGC 312
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44M
COMPUTER: END COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
SOFTWARE: Word Perfect 8.0
SOFTWARE: Word Perfect 8.0
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION UMBER: 09/453,702
APPLICATION NUMBER: 09/453,702
APPLICATION NUMBER: 09/110,955
FILING DATE: 04-DEC-1998
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Novel Sequences of E. coli 0157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                    LENGTH: 38155
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Madison
                                                                                                                                                              ilarity 100.0%; Pred. No. 0...
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burland,
Burland,
Perna, Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perna,
Plunkett, ba,
Rod
                                                                                                                                                                                 4.6%; Score 22;
00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valerie
                                                                                                                                                                                                                                             79:
                                                                                                                                                                                DB 8;
0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.44Mb storage
                                                                                                                                                                 0,
                                                                                                                                                                                        Length 38155;
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                                                                                                                                                           0;
                                                                                                                                                       Gaps
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RESULT 5

US-10-114-170-137/c

Sequence 137, Application US/10114170
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R
Valerie
Valerie
                                                                                                                                                                                          DЬ
                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Escherichia coli O157:H7
US-10-053-853A-484
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
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Sequence 484, Application US/10053853A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/053,853A CURRENT FILING DATE: 2002-05-28 PRIOR APPLICATION NUMBER: UP2001-112010 PRIOR FILING DATE: 2001-01-24 SEQ ID NOS: 1866
LENGTH: 48423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Escherichia coli 0157:H7
US-10-053-853A-876
                                                                                                                                                                          28594 TAATCCGGACACCGGTAACAGC 28615
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MAKINO, KOZO
APPLICANT: HAYASHI, Tetsuya
APPLICANT: OHNISHI, Makoto
APPLICANT: HATTORI, Masahira
APPLICANT: KUROKAWA, Ken
TITLE OF INVENTION: Polynucleotide molecules and polypeptides specific to Enterohe
FILE REFERENCE: 2002-0060A/WMC/01704
CTIDEDENTM ADDITION: MINIMPER. NE /10/082 0523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HAYASHI, Hideo
APPLICANT: SHINAGAWA, Hideo
APPLICANT: MAKINO, KOZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: JP2001-112010 PRIOR FILING DATE: 2001-01-24 NUMBER OF SEQ ID NOS: 1866 SEQ ID NO 876 LENGTH: 39824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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APPLICANT: HAYASHI, Tetsuya
APPLICANT: OHNISHI, Makoto
APPLICANT: HATTORI, Masahira
APPLICANT: HOMENTORI, Masahira
APPLICANT: KUROKAWA, Ken
TITLE OF INVENTION: Escherichia coli 0157:H7 and use thereof
CURRENT APPLICATION NUMBER: US/10/053,853A
CURRENT FILING DATE: 2002-05-28
CURRENT FILING DATE: 2002-05-28
DEFFOR ADDITION NUMBER: US/10/053,853A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HAYASHI, Hideo
APPLICANT: SHINAGAWA, Hi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHINAGAWA, Hideo
               Burland,
Burna, Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHINAGAWA, Hideo
Plunkett, Guy
Welch, Rod
                                                      Blattner, Frederick R
                                                                                                                                                                                                                                      4.0°;
100.0%; PI
                                                                                                                                                                                                                                                         Score 22;
; Pred. No.
                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                DB_8; Length 48423;
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. 0.11;
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CORRESPONDENCE ADDRESS:

OF SEQUENCES:

TITLE OF INVENTION: Novel Sequences of E.

coli 0157

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APPLICANT: MAKINO, KOZO
APPLICANT: HAYASHI, Tetsuya
APPLICANT: OHNISHI, Makotto
APPLICANT: HATORI, Masahira
APPLICANT: HATORI, Masahira
APPLICANT: KUROKAWA, Ken
TITLE OF INVENTION: Bolynucleotide molecules and polypeptides specific to Enterohemor
TITLE OF INVENTION: Escherichia coli 0157:H7 and use thereof
FILE REFERENCE: 2002-0050A/WMC/01704
CURRENT APPLICATION NUMBER: US/10/053,853A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: JP2001-112010
PRIOR FILING DATE: 2001-01-24
NUMBER OF SEQ ID NO 337
LENGTH: 58175
TYPE: DNA
ORGANISM: Escherichia coli 0157:H7
US-10-053-853A-337
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-053-853A-337; Sequence 337, Application US/10053853A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: 137: US-10-114-170-137
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HAYASHI, Hideo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15032 TAATCCGGACACCGGTAACAGC 15011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 TAATCCGGACACCGGTAACAGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,170

FILING DATE: 01-Apr-2002

CLASSIFICATION: CUNKnown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/453,702

FILING DATE: 03-DEC-1999

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-198

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 22; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 incl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Madison
STATE: WI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                           SHINAGAWA, Hideo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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100.0%; Pred. No.
14ve 0; Mismatches
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259 AAAGTGAAAGCCGGCCAGG 277

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Query Match
Best Local Similarity
Watches 22; Conserve
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; ORGANISM: Escherichia coli O157:H7
US-10-053-853A-1
                                                                     US-09-918-995-216
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-918-995-216
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 216, Application US/09918995
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10053853A GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1866 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Polynucleotide molecules and polypeptides specific to Enterohe TITLE OF INVENTION: Escherichia coli 0157:H7 and use thereof FILE REFERENCE: 2002-0060A/MMC/01704 CURRENT APPLICATION NUMBER: US/10/053,853A CURRENT FILING DATE: 2002-05-28 PRIOR APPLICATION NUMBER: UF2001-112010 PRIOR FILING DATE: J0201-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(453)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                            TYPE: DNA
                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                            LENGTH: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 TAATCCGGACACCGGTAACAGC 312
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OHNISHI, Makoto
HATTORI, Masahira
KUROKAWA, Ken
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 Conservative
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                3.9%;
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00.0%; Pred. No.
 0;
                                                                                        or G
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                  Score 19;
Pred. No.
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 Mismatches
                  DB 5;
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0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 91772;
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                                  Length 453;
 Indels
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Gaps
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 0;
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100 AAAGTGAAAGCCGGCCAGG 118

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APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PM030C1N
CURRENT APPLICATION UNMBER: US/10/211,818
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: 09/758,470
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
INUMBER OF SEQ 1D NOS: 722
SOFTWARF: DATE: 2000-02-04
SOFTWARF: DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-211-818-27
; Sequence 27, A
                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 27
LENGTH: 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-919-002-8373
OTHER INFORMATION: n equals a,t,g, or
                                                                NAME/KEY: misc_feature
LOCATION: (793)
OTHER INFORMATION: n equals
                                                                                                                             NAME/KEY: misc_feature
LOCATION: (717)
OTHER INFORMATION: n equals a,t,g, or
                                      NAME/KEY: misc_feature
                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(455)
OTHER INFORMATION: n = A,T,C or
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GENERAL INFORMATION
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
PRIOR FILING DATE: FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
NUMBER OF SEQ ID NOS: 13203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 AAAGTGAAAGCCGGCCAGG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AAAGTGAAAGCCGGCCAGG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10211818
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100.0%; Pred. No.
                                                                a,t,g,
                                                                  or
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APPLICANT: TRAN, UYEN K.
TITLE OF INVENTION: INTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: FF-1145 PCT
CURRENT APPLICATION NUMBER: PCT/US02/26322
PRIOR APPLICATION NUMBER: US 60/313,245
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/314,751
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-31
PRIOR PILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/316,752
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/316,847
PRIOR APPLICATION NUMBER: US 60/322,188
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APPLICANT:
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PCT-US02-26322-47
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APPLICANT:
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Best Local :
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LOCATION: (833)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (812)
OTHER INFORMATION: n equals a,t,g, or
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les 19; Conserv
                                                                                                                                                                                             MARQUIS, Joseph
JACKSON, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BECHA, Shanya D.
LEE, Ernestine A.
WARREN, Bridget A.
LEHR-MASON, Patricia M.
                                                                                                                                                                                                                                                 NGUYEN, Danniel B.
HONCHELL, Cynthia D.
                                                                                                                                                                                                                                            LUO, Wen
                                                                                                                                                                                                                                                                                           HAFALIA, April J.A.
                                                                                                                                                                                                                                                                                                                   ELLIOTT, Vicki S. SPRAGUE, William W.
                                                                                                                                                                                                                                                                                                                                                                                                     GIETZEN, Kimberly J.
LAL, Preeti G.
BOROWSKY, Mark L.
                                                                                                                                                                                                                                                                                        DING,
                                                                                                                                                                                                                                                                                                                                                                             THANGAVELU, Kavitha
                                                                                                                                                                                                                                                                                                                                                                                           ISON, Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                DUGGAN, Brendan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAUGHN, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAO, Monique G.
RAMKUMAR, Jayalaxmi
RICHARDSON, Thomas W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMERLING, Brooke M. FORSYTHE, Ian J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRIFFIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWARNAKAR,
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Conservative 0;
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                                                                                                                                                                                                                        Narinder K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENOMICS, INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aina M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.98,
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Pred. No
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FILING DATE: 2001-09-14

APPLICATION NUMBER: US 60/326,390

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RESULT 13
US-10-108-260A-2343
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 3744219CB1
PCT-US02-26322-47
                                                                                                                                                                                                                                                                                                                  US-10-219-999-30827
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PRIOR APPLICATION NUMBER: US 60/328,952
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/345,468
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/372,499
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PERL Program
Sequence 2343, Application US/10108260A
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; F
Matches 19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J
APPLICANT: Hinkle, Gregory J
APPLICANT: Kovallo, David K
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
LOCATION: (1571)..(2227)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2322
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                        912 AAAGTGAAAGCCGGCCAGG 930
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100.0%; Pred. No
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pred. No. 5.2
n; Mismatches
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                                                                                                                                                                                                                                     0;
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RESULT 14
US-10-108-260-2343
; Sequence 2343, Application US/10108260
; GENERAL INFORMATION:
              Qy
                                                                                                                  ; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-279-4847
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-221-279-4847/c
; Sequence 4847, Application US/10221279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/108,260
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2343
LENGTH: 2329
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2343
LENGTH: 2329
TYPE: DNA
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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SEQ ID NO 4847
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Best Local
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CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hyseq, Inc
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length cDNA FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/519,705 PRIOR FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 12360
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14 TGCAGGGCAGCTCTCTGA 31
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Local Similarity 100.0%;
es 19; Conservation
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18; Conserv
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                                              3.7%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%; Score 19; DB 8; 100.0%; Pred. No. 5.2;
                                                ; Score 18; DB
; Pred. No. 18;
0; Mismatches
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Pred. No. 5.2;
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                                                              DB 8;
18;
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Db 128 TGCAGGGCAGCTCTCTGA 111

Search completed: October 28, 2002, 00:39:40 Job time: 373.035 secs

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Sequence Sequence Sequence

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3, Appli 6, Appli 6, Appli 1, Appli 6, Appli 6, Appli 6, Appli 5, Appli 5, Appli 57, Appl

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Minimum
Maximum
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length: 2000000000
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/packfiles1.seq:*
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2 US-08-972-631-3

2 US-08-972-629-3

2 US-08-972-630-3

2 US-08-672-211-3

3 US-09-225-170-3

4 US-09-103-840A-1
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US-09-541-941B-26
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US-08-510-646B-6
US-08-510-646B-6
US-09-232-201-68
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                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,917
FILING DATE: 15-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/672,211
FILING DATE: 27-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application Patent No. 5856132
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 1036-2811
COUNTRY: USA
                                              Query Match
Best Local Similarity
                          Matches
                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 3808 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                         NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                        18;
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                     Conservative
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                                              3.7%;
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US-09-232-191-6
US-09-232-197-6
US-09-232-201-6
US-09-232-201-6
US-09-232-201-6
US-09-63-950-1
US-08-468-8568-1
US-08-468-8568-6
US-08-468-858-6
US-08-468-859A-6
US-08-468-859A-6
US-08-468-859A-6
US-08-468-859A-6
US-08-468-537A-106
US-08-468-537A-106
US-08-468-537A-57
US-08-486-273A-57
US-08-940-035A-57
US-08-940-035A-57
US-08-940-035A-57
US-08-940-035A-57
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Pred. No.
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MANE: Halluin Albert P.
REGISTRATION NUMBER: 25.277
REFERENCE/DOCKET NUMBER: 8549-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
INFORMATION FOR SEQ ID NO: 3:
EQUIENCE CHARACTERISTICS:
LENGTH: 3808 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
US-08-972-631-3
                                                                                                                                                                   RESULT 3
US-08-972-629-3
                                                                                                                                                                                                                                     Вb
                                                GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
                                                                                                                                      Sequence 3, Application US/08972629
Patent No. 5859201
                                                                                                                                                                                                                                                                                         Matches
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Best Local 9
                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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US-08-972-631-3
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               STREET:
                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION UNBER: US/08/972,631
FILING DATE:
CTASCTOTE:
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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18; Conservative
Menlo Park
               2730
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       Pennie & Edmonds
30 Sand Hill Road
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Stephens, Len

L: Hawkins, Phillip T.
INVENTION: G-BETA-GAMMA REGULATED
PHOSPHATIDYLINOSITOL-3' KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
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US-08-972-630-3
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                                                                         FILING DATE:
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CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
APPLICATION NUMBER: 27-JUN-196
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REGISTRATION NUMBER: 25,277
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08972630
Patent No. 5869271
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
INTERD OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: CDNA

US-08-972-629-3
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Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 8549
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
TELEPACE: (415)854-3694
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
ADDITION DATA:
                                                                                                                                                                                                                                                                                                 STREET: 2/J
STREET: 2/J
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2951 TCAGAAACAGGAAATCTA 2968
                                                                                                                                                            APPLICATION NUMBER:
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LENGTH: 3808 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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2730 Sand Hill Road
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     NUMBER:
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8549-0005-999
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Pred. No. 3.5;
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US-08-672-211-3
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Best Local Similarity 100.0%;
                                                        Matches
                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                              TELEPHONE: (415)854-3660
TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                        REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 85-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2951 TCAGAAACAGGAAATCTA 2968
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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 2951 TCAGAAACAGGAAATCTA 2968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 TCAGAAACAGGAAATCTA 428
                            411 TCAGAAACAGGAAATCTA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2730 Sunc
CITY: Menlo Park
                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/672,211
FILING DATE: 27-JUN-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                     Similarity
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VENTION: G-BETA-GAMMA REGULATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                  3.7%; Sur
100.0%; Pr
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                                                      Score 18; DB; Pred. No. 3.5
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Pred. No
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                                                                     DB 2;
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RESULT 6

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              NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09225170 Patent No. 6017763
                                                                                                                                                                                                                        Sequence 1, Applicat Patent No. 6294328 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                              APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, JOHN C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-2007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24
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                                                                                                                                                                                      APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/9: FILING DATE: 15-AUG-1997 ATTORNEY/AGENT INFORMATION:
LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3808 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 85-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEPEAX: 650-493-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US.
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                                                                                                                                                                                                                                                                                                                                              2951 TCAGAAACAGGAAATCTA 2968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                411 TCAGAAACAGGAAATCTA 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                          Application US/09103840A
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                                                                                                                                                                                    WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3808 base pairs
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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Pred. No.
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Matches

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RESULT 9
US-08-553-888A-1/c
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GENERAL INFORMATION:
APPLICANT: Huang
TITLE OF INVENTION: DETERMINING I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Tulipa Edulis
US-09-541-941B-26
                                       SOFTWARE: WOTGHER FOR THE SOFTWARE: WOTGHER FOR THE SOFTWARE TO NUMBER: US/08/55.

FILING DATE: 11/06/95

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: 0'Dea, Sean W.
REGISTRATION NUMBER: 37690
REFERENCE MOTORE WINDER: 37690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Jun
APPLICANT: Shaw, Pang Chui
APPLICANT: Shaw, Pang Chui
APPLICANT: Shaw, Pang Chui
APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPH
FILE REFERENCE: 2913/52188-ZA
CURRENT APPLICATION NUMBER: US/09/541,941B
CURRENT APPLICATION NUMBER: US/09/541,941B
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.1
LENGTH: 754
TYDE: NNA
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mycobacterium tuberculosis; OTHER IMPORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
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                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: ADDRESSE: Hoffmann & Baron, LLP STREET: 350 Jericho Turnpike CITY: Jericho STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                               REFERENCE/DOCKET NUMBER:
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                 New York
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                                                                                                                                                                IBM compatible SYSTEM: MS-DOS
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100.0%; Pr
100.0%; O;
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                                                                                                                  US/08/553,888A
                               454-5
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RESULT 11
US-09-032-742-1/c
; Sequence 1, Application US/09032742
; Patent No. 6255089
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                                                                                                                                                        Query Match
Best Local S
Matches 17
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SEQUENCE CHARACTERISTICS:
LENGTH: 1466 nucleotides
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
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US-08-553-888A-2/c
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                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: O'Dea, Sean W.
REGISTRATION NUMBER: 37690
REFERENCE/DOCKET NUMBER: 454-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-553-888A-1
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GENERAL INFORMATION:
APPLICANT: Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: IBM compatible
COMPUTER: CYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.5%; Score 17; Best Local Similarity 100.0%; Pred. No. Matches 17; Conservative 0; Mismatc
                                                                                      649 GCTCTCTGATCATTATC 633
                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERSTECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,888A
FILING DATE: 11/06/95
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TELEPAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                        23 GCTCTCTGATCATTATC 39
                                                                                                                                                                   Local Similarity
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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STREET: 350 Jes
CITY: Jericho
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COUNTRY:
ZIP: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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350 Jericho Turnpike
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                                                                                                                                            100.08; +1
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                                                                                                                                                                Score 17;
Pred. No
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                                                                                                                                              Mismatches
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В Q

COUNTRY:

GENERAL INFORMATION:

Egan, Christina C. Herrick-Davis, Katharine

Teitler, Milt

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RESULT 12
US-09-032-742-12/c
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                                                                                                                                                                                                                                                                                                                                                            Patent No. 6255089
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09032742 Patent No. 6255089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,742
FILING DATE: 27-FEB-1998
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Herrick-D
APPLICANT: Egan, Chr
TITLE OF INVENTION:
TITLE OF INVENTION:
ZIP: 19380-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1566 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Laurence Weinberger
STREET: 882 S. Matlack Street, Suite 103
STREET: P.O. Box 1663
                                                                                                                                                                                                                                                   TITLE OF INVENTION: Constitutively Activated Serotonin TITLE OF INVENTION: Receptors NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                       APPLICANT: Teitler, Milt
APPLICANT: Herrick-Davis,
APPLICANT: Egan, Christin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1062 TTACAACAACAGGAA 1047
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STREET: 882 S. Matlack Street, Suite 103
STREET: P.O. Box 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 301
                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.0%; I les 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Weinberger, Laurence REGISTRATION NUMBER: 27,96
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                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                         Christina C.
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39;
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RESULT 13
US-09-032-742-13/c
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                                                                              TELEFAX: (610) 431-418
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (610) 431-41 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Laurence Weinberger
STREET: 882 S. Matlack Street, Suite 103
STREET: P.O. Box 1663
CITY: West Chester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Teitler, Milt
APPLICANT: Herrick-Davis, Katharine
APPLICANT: Egan, Christina C.
TITLE OF INVENTION: Constitutively &
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1062 TTACAACAAACAGGAA 1047
 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (610) 431-1703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                             TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 TTACAACAAACAGGAA 360
                                                                                                                                                              NAME: Weinberger, Laurence REGISTRATION NUMBER: 27,96 REFERENCE/DOCKET NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.3%;
Local Similarity 100.0%;
es 16; Conservation
                              STRANDEDNESS:
                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 27-FEB-1998
                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2 CLASSIFICATION:
                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                               : 1566 base pairs
nucleic acid
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DNA (genomic)
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) 431-4181
~ NO: 12:
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US-09-032-742-16/c
; Sequence 16, Application US/09032742
; Patent No. 6255089
; Patent No. 6255089
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NAME: Weinberger, Laurence
REGISTRATION NUMBER: 27,965
REFERENCE/DOCKET NUMBER: 3086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 431-1703
TELEPAX: (610) 431-4181
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1566 base pairs
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                             Query Match
Best Local (
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                                                                                                GENERAL INFORMATION:
   APPLICANT: Teitler, Milt
APPLICANT: Herrick-Davis, Katharine
APPLICANT: Egan, Christina C,
TITLE OF INVENTION: Constitutively Activated Serotonin
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09032742 Patent No. 6255089
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 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                         345 TTACAACAAACAGGAA 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Herrick-Davis, Katharine
APPLICANT: Egan, Christina C.
TITLE OF INVENTION: Constitutively &
TITLE OF INVENTION: Receptors
NUMBER OF SEQUENCES: 25
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CORRESPONDENCE ADDRESS:
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les 16; Conserv
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STRANDEDNESS: single
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FILING DATE: 27-FEB-1998
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Laurence Weinberger
STREET: 882 S. Matlack Street, Suite 103
STREET: P.O. Box 1663
CITY: West Chester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                345 TTACAACAAACAGGAA 360
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Receptors
25
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100.0%; Pred. No.
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Pred. No.
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39;
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STRANDEDNESS:
TOPOLOGY: lin.
MOLECULE TYPE: 1
US-09-032-742-16
                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 3086
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 431-1703
TELEPAX: (610) 431-4181
INFORMATION FOR SEQ ID NO: 16;
SEQUENCE CHARACTERISTICS:
                                                                 Matches
                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/032
FILING DATE: 27-FEB-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weinberger, Laurence
REGISTRATION NUMBER: 27,965
1062 TTACAACAAACAGGAA 1047
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                            345 TTACAACAAACAGGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Laurence Weinberger
STREET: 882 S. Matlack Street, Suite 103
STREET: P.O. Box 1663
CLIT: West Chester
                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                    LENGTH:
                                                                16;
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19380-0053
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                                                                                                                                                                                               1566 base pairs
                                                             Conservative
                                                                                                                                                      linear
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                                                    3.3%; 5c,
100.0%; Pr
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                                                      Score 16; DB. Pred. No. 39; 0; Mismatches
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                                                                          DB 4;
                                                                                    Length 1566;
                                                      Indels
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Search completed: October 27, 2002, 23:22:22 Job time: 1738.87 secs

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Human polynucleoti
Mycobacterium tube
Asialoglycoprotein

DNA encoding novel Propionibacterium

Propionibacterium Mycobacterium tube

Human map-related

Pig p120 regulator DNA encoding novel Porcine G-protein

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Perfect score:
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   118
104
102
75
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40
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1: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

6: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*

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11: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*

12: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*

13: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

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18: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                                                                                                                                                                                Query
Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          satisfying chosen
                                                                                                                                                                                 Length
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102
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                                                                                                                                                                                                                                        SUMMARIES
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             DNA sequence of E.
DNA sequence of Cl
PCR primer #4 used
PCR primer #2 used
PCR primer #5 used
PCR primer #1 used
PCR primer #1 used
PCR primer #6 used
Description
 melanog
RESULT 1
AAF86247
ID AAF8
XX AAF8
AC AAF8
XX DA AAF8
XX DA DA AAF8
XX DA DA AXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; ds.
   17-SEP-1999;
                                     17-SEP-1999;
                                                                       17-MAR-2001.
                                                                                                            CA2281913-A1
                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                           Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence of E. coli optimised ospA gene 17E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF86247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF86247 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99CA-2281913
                                     99CA-2281913
                                                                                                        /partial
/product= "OspA"
/note= "Genus specific 17kDa antigen, the sequence does
/note= not include a stop codon"
                                                                                                                                                                                                                                                                                                             salmonis
                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                        L..483
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AAS 29545

AAS 199682

AAS 68405

ABA48015

ABA65900

ABA3298

AAK40045

AAI 20825

AAI 20825

AAI 46064

AAI 06540

AAI 6664

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AAH652010
AAH66951
AAS59780
AAS84339
AAV74103
AAV74103
AAV74103
AAV74103
AAX868250
AAS68250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human breast cell
Human foetal liver
Probe #11452 for g
Human brain expres
Human bone marrow
Probe #10762 for g
Probe #14750 used t
Human DNA for an
Novel human polynu
Human breast cell
Human foetal liver
Probe #1547 for ge
Human brain expres
Human bone marrow
Human brain expres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #1548 for ge
Probe #1597 used t
Probe #1533 used t
Tulipa edulis ITS1
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Probe
Human
Human
Probe
Probe
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Ripening banana pu Human olfactory re Human olfactory re

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481
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                     481
                                       421
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                      361 GGCGTCAGCAGTACTGCCGCGAATTTCAGCAGAAAGCCATGATCGCAGGTCAGAAACAG
                                                                                               361
                                                                                                                 301
                                                                                                                                   301
                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis The method comprises administering an immunogenic amount of a particularly polkilothermic fish, against the bacterial pathogen for protecting animals. The method is used for protecting animals sequence represents DNA with a News) and other rickettsial septicaemia (SRS) and other rickettsial diseases. The period is also useful for protecting against salmonid sequence represents DNA with has been optimised for expression in Escherichia coli to encode the p. salmonis ospa protein. An ospa protein anti-ospa antibody resnonse.
                                                                                                                                                                                                                               121
 AAA
                                                                                                                                                                                                                                                                                                                                                                                Sequence 483
                AAA 483
                         GAAATCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAA 480
                GAAATCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAA
                                                                                                                                                                                                                                                                                CGCCGTCAGCAGTACTGCCGCGAATTTCAGCAGAAAGCCATGATCGCAGGTCAGAAACAG
                                                                                                    Example 3; Fig 4C; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                           ACCGGTAACAGCTACTCTGTGGAACCGGTTCGCACCTACCAGCGTTACAACAACAACAGGAA
                                                                                                                               CTGAACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGTAATCCGGAC
                                                                                                                                          CTGAACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGTAATCCGGAC
                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                GCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTGTCGATGGCCATCGGCGGTGCGGTT
                                                                                                                                                                                                                                             GCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGGGCCACCGGTGCGGTTGTGGGCCGTGTT
                                                                                                                                                                                                                                                       483
                                                                                                                                                                                                                                                                                                                                    Similarity 100.
183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-316844/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB81127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burian J,
                                                                                                                                                                                                                                                                                                                                                                BP; 108 A; 127 C; 148 G; 100 T; 0 other;
                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kuzyk MA;
                                                                                                                                                                                                                                                                                                                          Score 483; DB 22; I
; Pred. No. 7.1e-243;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                             Length 483;
                480
                                                                                            360
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                                                                                                                                                                                                                                                               120
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        FT FT FT FT FT FT FT FT FT XX XX PD PD XX XX PD PD XX
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RESULT

Qγ

В Ş В ρ В Qγ Дb Qγ В γQ Ъ δδ Дb δÃ В Ş В ρy

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Query Match
Best Local
                                                                               Matches
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AAF8
AC AAF8
XX
AC AAF8
XX
DT 11-J
XX
DF DNA
XX
POIK
KW POIK
KW POIK
KW SRS;
XX
OS PISC
XX
PIT CDS
FT CDS
FT CDS
FT TT
FT misc
                                                                                                                            This invention relates to a method for the protection against infection of a poskilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a OspA in the form of a vaccine. The method is used for protecting animals, particularly poskilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial pathogen sequence represents P. salmonis OspA DNA termed (JPE2 optimised for N-terminal fusion partner. The protein one mended by this fusion construct is used in a vaccine to create an anti-OspA antibody response.
1 ATGCGTGGTTGCCTGCAGGGCAGCTCTCTGATCATTATCTCTGTTTTTCCTGGTGGGTTGC 60
                                                                                                                                                                                                                                                                                                                                                  Example 4; Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                        Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay WW, Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA2281913-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poikilothermic fish, Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease SRS; 17E2; fusion construct; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF86248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-316844/34.
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB81128.
                                                                     Conservative
                                                                                                                        220 A; 183 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99CA-2281913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of c17e2 ospa construct with N-terminal fusion partner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "DNA ,
286..768
                                                                                 100.0%;
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1..285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "C17E2 OspA with N-terminal fusion
/note= "No stop codon is given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                        Score 483; DB 22;
Pred. No. 7.1e-243;
Mismatches 0;
                                                                                                               190 G; 175 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           undefined N-terminal
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                                                                                                             (KAYW/)
(BURI/)
                                                                                                                                                                                                                                     Poikilothermic fish; Piscirickettsia salmonis; rickettsial paccine; OSpA; salmonid rickettsial septicaemia; rickettsial SRS; 17E2; fusion construct; PCR primer; ss.
                                                                                                                                                             17-SEP-1999;
                                                                                                                                                                                17-MAR-2001.
                                                                                                                                                                                                   CA2281913-A1
                                                                                                                                                                                                                      Piscirickettsia
                                                                                                                                                                                                                                                                              PCR primer
                                                                                                                                                                                                                                                                                                                     AAF86254;
        Example
                           vaccine
                                    septicaemia
                                             Method
                                                                                 Kay ww,
                                                                                                                                           17-SEP-1999;
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                                                                                                      (KUZY/)
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                                                                                                                                                                                                                                                                                                                                                                                                        AAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCCGTCAGCAGTACTGCCGCGAATTTCAGCAGAAAGCCATGATCGCAGGTCAGAAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGTAATCCGGAC
                                                                2001-316844/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCGTCAGCAGTACTGCCGCGAATTTCAGCAGAAAGCCATGATCGCAGGTCAGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGTAATCCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGCCGCCACCGGTGCGGTTGTGGGCGGTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                          GAAATCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCGGTAACAGCTACTCTGTGGAACCGGTTCGCACCTACCAGCGTTACAACAACAACAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCGTGGTTGCCTGCAGGGCAGCTCTCTGATCATTATCTCTGTTTTCCTGGTGGGTTGC
                         for protecting poikilothermic fish against salmonid rickettsial aemia and other rickettsial diseases comprises administering a e containing the OspA protein of Piscirickettsia salmonis
                                                                                                    ) KAY W W.
) BURIAN J.
) KUZYK M A.
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                                                                                                                                                                                                                                                                                                                                                                                                         483
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                                                                                  Burian J,
       Fig
                                                                                                                                                                                                                                                                              #4 used in cloning
                                                                                                                                                                                                                                                                                                (first entry)
         4B;
                                                                                                                                          99CA-2281913
                                                                                                                                                             99CA-2281913
                                                                                                                                                                                                                      salmonis.
       35pp;
                                                                                  Kuzyk
        English
                                                                                   MA;
                                                                                                                                                                                                                                                                                                                                        ВÞ
                                                                                                                                                                                                                                                                              an
                                                                                                                                                                                                                                                                              optimisation
                                                                                                                                                                                                                                                                             of OspA
                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                           pathogen;
                                                                                                                                                                                                                                                  disease
                                                                                                                                                                                                                                                                                                                                                                                                                                            480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465
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RESULT 4
AAF86252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of the P. salmonis OspA gene. The OspA gene is used in the method of the
                                                                                                                      Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                      WPI; 2001-316844/34
                                                                                                                                                                                             Kay WW,
                                                                                                                                                                                                                                                                17-SEP-1999;
                                                                                                                                                                                                                                                                                       17-SEP-1999;
                                                                                                                                                                                                                                                                                                              17-MAR-2001
                                                                                                                                                                                                                                                                                                                                     CA2281913-A1
                                                                                                                                                                                                                                                                                                                                                           Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                 vaccine; O
SRS; 17E2;
                                                                                                                                                                                                                                                                                                                                                                                                       Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer #2 used in cloning an optimisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF86252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF86252
                                                                                                                                                                                                                   (KUZY/)
                                                                                                                                                                                                                               (BURI/)
                                                                                                                                                                                                                                         (KAYW/) KAY W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 GCCGGCCAGGTTACTCGTTGGCGTAATCCGGACACCGGTAACAGCTACTCTGTGGAAC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGGCCAGGTTACTCGTTGGCGTAATCCGGACACCGGTAACAGCTACTCTGTGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
118; Conserv
                                                                                                                                                                                                                   KUZYK M
                                                                                                                                                                                                                               BURIAN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118
                                                                                                                                                                                            Burian
                                                                                                                                                                                                                                                                                                                                                                                             OspA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                  fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                         Σ
                                                                                                                                                                                                                                                                                                                                                                                             salmonid rickettsial septicaemia;
                                                                                                                                                                                                                                                                99CA-2281913
                                                                                                                                                                                                                                                                                       99CA-2281913
                                                                                                                                                                                            Ġ,
                                                                                                                                                                                                                                                                                                                                                           salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                  construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α;
                                                                                                                                                                                             Kuzyk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
                                                                                                                                                                                             MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                  PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 118;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .<del>.</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                               of OspA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                             rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present

animals,

Example

3; Fig 4B; 35pp; English.

SSSSS

sequence represents a PCR primer used in the P. Salmonis OspA gene. The OspA gene

Sequence 110 BP;

13 A; 28 C; 45 G; 100.0%; 21.5%;

24 T; 0 other;

the cloning and optimisation is used in the method of the

of

Q В δÃ

53 TGGGTTGCGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGGCCACCGGTGGGGTTGTGG 112 1 TGGGTTGCGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGGCCACCGGTGCGGTTGTGG

60

Matches Query Match

104;

Conservative

0;

Mismatches

0,

0

Score 104; DB 22; Pred. No. 2.2e-44;

Length 110; Indels

Jocal

Similarity

0;

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Query Match
Best Local Similarity
                                                    This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a OspA in the form of a vaccine. The method is used for protecting fragment of particularly polkilothermic fish, against the bacterial pathogen animals. The method is also useful for protecting animals, rickettsial septicaemia (SRS) and other ricketting against salmonid the P. salmonis OspA gene. The OspA gene is used in the method of the present invention.
                                              Sequence 102 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                                                                                                                                                                        (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                    Example 3; Fig 4B; 35pp; English.
                                                                                                                                                                                                           Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                            WPI; 2001-316844/34.
                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             CA2281913-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial pathogen; SRS; 17E2; fusion construct; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF86255 standard; DNA; 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #5 used in cloning an optimisation of OspA gene.
                                      14 A; 23 C; 30 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        99CA-2281913.
                                                                                                                                                                                                                                                                                                                                                                    99CA-2281913
         21.1%;
100.0%;
                                                                                                                                                                                                                                                                                                 Kuzyk MA;
Score 102; DB 22;
Pred. No. 2.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВÞ
                                      35 T;
                                 0 other;
       Length 102;
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Ω

218

TGGACCAGCAGGATA

COATGOCCATCOGCGGTGCGGTTCTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCA 79

DЬ Qy

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Matches
                                                                     Query Match
Best Local
                                                                                                  This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a particularly poikilothermic fish, against the bacterial pathogen animals. The method is also useful for protecting animals, rickettsial septicaemia (SRS) and other rickettsial gazinst salmonis sequence represents a PCR primer used in the cloning and optimisation of the P. salmonis OspA gene. The OspA gene is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
AAF86253
158 CGATGGCCATCGGCGGTGCGGTTCTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCA 217
                                                                                               Sequence 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ДЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                      Example 3; Fig 4B; 35pp; English.
                                                                                                                                                                                                                                             Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                          WPI; 2001-316844/34.
                                                     es 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                (KAYW/) KAY W W.
(BURI/) BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA2281913-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poikilothermic fish; piscirickettsia salmonis; rickettsial vaccine; OspA; salmonid rickettsial septicaemia; rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer #3 used in cloning an optimisation of OspA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF86253 standard; DNA; 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 AAAGCCATGATCGCAGGTCAGAAACAGGAAATCTACGGCACC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGCCATGATCGCAGGTCAGAAACAGGAAATCTACGGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTACCAGCGTTACAACAACAAGAACGCCGTCAGCAGTACTGCCGCGAATTTCAGCAG 393
                                                                                                                                                                                                                                                                                                                                                     KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTACCAGCGTTACAACAAACAGGAACGCCGTCAGCAGTACTGCCGCGAATTTCAGCAG
                                                                                                                                                                                                                                                                                                                                Burian J,
                                               Conservative
                                                                                       BP; 18 A; 20 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                           99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                99CA-2281913.
                                                         15.5%;
                                                                                                                                                                                                                                                                                                                            Kuzyk MA;
                                              0;
                                                       Score 75; Pred. No.
                                                                                  35 G; 21 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВÞ
                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                     DB 22;
3.4e-29
                                                                                0 other;
                                                   .4e-29;
                                        0,
                                                        Length 94;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rickettsial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathogen;
                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43
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В

80

TGGACCAGCAGGATA

94

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RESULT 8
AAF86256/C
ID AAF86256 standard; DNA; 110
XX
AC AAF86256;
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                                                                                                              δÃ
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                                                                                           밁
                                                                                                                                                                                                Query Match
Best Local S
Matches 74
                                                                                                                                                                                                                                                                                  salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of the P. salmonis OspA gene. The OspA gene is used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA2281913-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay ww,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piscirickettsia
                                                                                                                                                                                                                                                    Sequence 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAYW/) KAY W W.
(BURI/) BURIAN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer #1
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF86251 standard; DNA; 111
                                                                                                                                             38
                                                                                                                    61
                                                                                           86
                                                                                                                                                                      1 ATGCGTGGTTGCCTGCAGGGCAGCTCTCTGATCATTATCTCTGTTTTTCCTGGTGGGTTGC
                                                                                          1 GCCCAGAACTTCAG :
                                                                                                                                             ATGCGTGGTTGCCTGCAGGGCAGCTCTCTGATCATTATCTCTGTTTTCCTGGTGGGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-316844/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BURIAN J.
KUZYK M A.
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Fig 4B; 35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burian J,
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99CA-2281913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 salmonis
                                                                                                                                                                                                                                                    16
                                                                                                                    74
                                                                                                                                                                                                                                                  ?
                                                                                                                                                                                                            15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloning
                                                                                                                                                                                                                                                  32 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                           Score 74;
Fred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                  30 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            optimisation
                                                                                                                                                                                                                                                  33 T; 0 other;
                                                                                                                                                                                                 1.1e-28;
hes 0;
                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of
                                                                                                                                                                                                                          Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OspA
                                                                                                                                                                                                 Indels
                                                                                                                                                                                                0;
                                                                                                                                                                                               Gaps
                                                                                                                                                97
                                                                                                                                                                                                 0;
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RESULT 9
ABL02577
ID ABLC
XX
AC ABLC
XX
DT 26-M
DT Dros
XX
DE Dros
XX
EW Dros
XX
DROS
DROS
XX
DROS
DROS
XX
DROS
XX
DROS
XX
PN WO20
                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of the P. salmonis OspA gene. The OspA gene is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAYW/)
(BURI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay ww,
                                           Drosophila melanogaster
                                                                      pharmaceutical;
                                                                                      Drosophila;
                                                                                                                                                                          ABL02577;
                                                                                                                                                                                                     ABL02577 standard; cDNA; 3833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 4B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piscirickettsia
                                                                                                                Drosophila melanogaster expressed polynucleotide SEQ ID NO 2213.
                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                       444 TCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAAAAA 483
                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                           TCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-316844/34
                                                                                                                                                                                                                                                                                                                                ch 8.3%; So l Similarity 100.0%; F 40; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAY W W.
BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUZYK M A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burian J,
                                                                                     developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                          ВP;
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99CA-2281913.
                                                                      gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    salmonis.
                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                         A; 34 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuzyk MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rickettsial septiruct; PCR primer;
                                                                                                                                                                                                                                                                                                                                 Score 40; DB; Pred. No. 7.3
                                                                                                                                                                                                                                                                                                                                                                                         27 G;
                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      optimisation
                                                                                                                                                                                                                                                                                                                                                                                         32 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  DB 22;
7.3e-1
                                                                                                                                                                                                                                                                                                                                               .3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of.
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                                                                                                                                                                                                                                                                                                                                                            Length 110;
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                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                   Gaps
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WO200171042-A2

23-MAR-2000; 11-JUL-2000;

23-MAR-2001; 27-SEP-2001.

2001WO-US09231.

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RESULT 10
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                       26-DEC-2000;
                                                                                                                                                                                                                        WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                    26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; cancer; alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic;
                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 1357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI59154 standard; cDNA; 2562 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 GATGGCCATCGGCGGTGCGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in developmental biology and in elucidating cell-cell interactions in higher eukaryotes for the development in the invent insecticides, therapeutics and pharmaceutical drugs. The invent discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA The sequences (ABL72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 2213; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGGCCATCGGCGGTGCGG 1447
); 2000US-0488725.
); 2000US-0552317.
); 2000US-0598042.
); 2000US-0620312.
); 2000US-0653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JC,
                                                                                                                           2000WO-US34263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 1094 A; 1030 C; 858 G; 851 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-191637P.
2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection reagent for detecting 1000 for elucidating cell signalling and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 23; Pred. No. 2.2; 0; Mismatches (
                                                                                                                                                                                                                                                                                        screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                     CC The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM38642-AAM42213) with nootropic, CC immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide CC system, such as peripheral nervous injuries, peripheral neuropathies and central nervous system diseases. CC lateral sclerosis, and shy-Drager Syndrome. Other uses include the CC lateral sclerosis, and shy-Drager Syndrome. Other uses include the activity, chamcatchic/chemokinetic activity, haemostatic/chemokinetic activity, haemostatic/c and thrombolytic activity, cancer diagnosis and therapy, drug screening, CC c.N.S disorders.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 19
   Eisenberg D,
                      (REGC ) UNIV
                                                    12-NOV-1999;
12-NOV-1999;
                                                                         13-NOV-2000; 2000WO-US31152.
                                                                                                   17-MAY-2001
                                                                                                                    WO200135317-A1
                                                                                                                                 Mycobacterium tuberculosis
                                                                                                                                                         Drug target;
                                                                                                                                                          Mycobacterium tuberculosis potential drug target gene SEQ ID
                                                                                                                                                                                                04-SEP-2001
                                                                                                                                                                                                                                  AAH52010 standard; DNA;
                                                                                                                                                                                                                     ААН52010;
                                                                                                                                                                                                                                                                                1197 AAAGTGAAAGCCGGCCAGG 1215
                                                                                                                                                                                                                                                                                                                                                      Sequence 2562 BP; 524 A; 794 C; 791 G;
                                                                                                                                                                                                                                                                                            259 AAAGTGAAAGCCGGCCAGG 277
                                                                                                                                                                                                                                                                                                                                                                                    specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1357; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-2000; 2000US-0662191
19-CCT-2000; 2000US-0693036
29-NOV-2000; 2000US-0727344
                                                                                                                                                                                                                                                                                                                             l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QA,
                                  99US-0165086.
99US-0165124.
2000US-0179531.
                   CALIFORNIA.
Rotstein SH,
                                                                                                                                                       growth;
                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                    Conservative 0;
                                                                                                                                         organism viability; characterisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asundi V, Che
Wehrman T, X:
, Goodrich R,
                                                                                                                                                                                                                                                                                                                                           3.9%;
                                                                                                                                                                                                                                  1029
                                                                                                                                                                                                                                                                                                                                                                        for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                            Score 19; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen R, Ma Y, Xu C, Xue AJ, R, Drmanac RT,
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                               450 T; 3 other;
                                                                                                                                                                                                                                                                                                                          7.2;
                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for treating disorders
                                                                                                                                                                                                                                                                                                                              Length 2562;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                           ds.
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Zhang J;
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                        Gaps
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Marcotte EM;

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RESULT 1
AAT66951
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                 Asialoglycoprotein receptor L-H2; autoantibody; diagnosis; liver; ds
                                                                                                                                                                                                                                                                                                                                                                                                                               AAT66951 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying nucleotide or polypeptide sequence for use as drug involves providing algorithm that analyzes a functional relation between nucleotide or polypeptide sequences, and comparing the
Asialoglycoprotein receptor H1 and L-H2 soluble comprise extracellular domains, optionally also
                                                                                                                                       21-AUG-1995;
                                                                                                                                                                20-AUG-1996;
                                                                                                                                                                                         14-MAY-1997
                                                                                                                                                                                                               EP773289-A2
                                                                                                                                                                                                                                                                                                                                                     Asialoglycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1029 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide sequence that may be a drug targ
or viability of an organism. Polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 91; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences
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P-PSDB; AAG81159.
                                                                                                              (TOFU ) TONEN CORP
                                                                                      Hasegawa A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 CAGGAACGCCGTCAGCAG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 CAGGAACGCCGTCAGCAG
                                       1997-261316/24.
DB; AAW15246.
                                                                                                                                                                                                                                                                                         sapiens
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                                                                                      Kiyosawa
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                       95JP-0212118
                                                                                                                                                                96EP-0113349
                                                                                                                                                                                                                                                   Location/Qualifiers 191..1054
                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169
                                                                                                                                                                                                                                                                                                                                                     receptor L-H2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA; 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that may be a drug target,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 338 C; 341 G;
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                                                                                       Ohue
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Pred. No.
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                                                                                                                                                                                                                                                                                                                  ds
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                                                                                                                                                                                                                                                                                                                            AGPR; autoimmune hepatitis;
                                                                                       Tanida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for identifying a nucleotide
drug target, or essential fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tifying a nucleotide or growth sequences AAH51947 - AAH52092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1029;
derivatives - with cytoplasmic
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone for AGPR L-H2 was isolated from human liver cDNA by PCR amplification (see AAT66956-61). Subregions coding for the extracellular domain, optionally also with the cytoplasmic domain, can be amplified by PCR (see AAT66966-69), cloned into appropriate vectors and used for large-scale prodn. of AGPR derivatives (see AAW165251-52), free of contaminating liver antigens, in bacterial (pref. E. coli) or animal (pref. mammalian) host cells. Such AGPR (L-H2 derivatives can be used in a claimed method for detecting or measuring anti-AGPR antibody. AGPR H12 cDNA has also been cloned (see AAT66950).
                                                                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
                                                                                                                                                           Skeiky YAW, Pers
L'maisonneuve J,
                                                                                                                                                                                                                              21-APR-2000; 2000US-199047P
02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This cDNA clone codes for human asialoglycoprotein receptor (ACL-12 (AAW15246), a membrane protein expressed specifically by hepatocytes. The appearance of autoantibodies against AGPR caused as an indicator for autoimmune hepatitis (AIH). The cDNA
                                                                                                                                                                                                                                                                                                                                           WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                dermatological; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                             uveitis; endophthalmitis; bone; joint; central ner inflammatory lesion; acne vulgaris; enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS59780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS59780 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1300 BP; 302 A; 395 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 35-34; 40pp; English
                                                                                                                                                                                                                                                                                      20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                 01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domains, useful for autoimmune hepatitis diagnosis
                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         962 CAGCCGGATGGCCGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 CAGCCGGATGGCCGCTGG 462
                                                                                                                                   2001-616774/71.
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                                                                                                                                                                           Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                         synovitis;
                                                                                                                                                              Zhang
                                                                                                                                                                                                                                                                                                                                                                        acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 1356
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100.0%;
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                                                                                                                                                      Mitcham JL, wu...
                                                                                                                                                                                                                                                                                                                                                                                                                                        acne; pustulosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                neuroprotectant; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 G;
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                                                                                                                                                                           Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         hypertosis; osteomyelitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                             nervous system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1300;
                                                                                                                                                                            Bhatia
                                                                                                                                                                                                                                                                                                                                                                                                              immunosorbent assay;
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Sequences AAS59506-AAS59804 represent DNA molecules encoding Propionibacterium acnes immunogenic polypeptides. The proteins associated DNA sequences are used in the treatment, prevention

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their

Claim

SEQ ID

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275;

1069pp;

English.

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RESULT 14
AAS84339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC diagnosis of medical conditions caused by P. acnes. The disorders include CC SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and conditions caused the context of the province of the profit of the infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne context of the proteins of the invention and determining the amount of bound protein comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein context of the sample. The polypeptides may be used as antigens in the production context of the sample activity of particularly of particularly context of therefore treat P. acnes infections. The antibodies and the production context of the sequence of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of particularly of p
                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
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                                                                                                                                                            Claim 1;
                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                              Drmanac
                                                                                                                                                                                                                                                                                                               P-PSDB; ABG20152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W0200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #20143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GCCATCGGCGGTGCGGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1356 BP;
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                                                                                                                                       SEQ ID No 20143; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0540217.
2000US-0649167.
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           also used in diagnostics
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Pred. No.
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24;
as expressed sequence tags
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Matches
Claim 54; Fig 3A-C; 151pp; English.
                     DNA encoding G-beta-gamma regulated phosphatidyl-inositol-3' kinase, pl01 and p120 subunits - useful for diagnosis, drug screening, clinical trial monitoring and treatment of inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                              XXNO (-XXNO)
                                                                                                                                                                                                          27-JUN-1996;
                                                                                                                                                                                                                                          26-JUN-1997;
                                                                                                                                                                                                                                                                         31-DEC-1997
                                                                                                                                                                                                                                                                                                     W09749818-A2
                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-beta-gamma regulated phosphatidylinositol-3' kinase; phosphoinositide 30H-kinase; PI3K; signal transduction; phosphatidylinositol (3,4,5)-triphosphate; G-protein; rtransgenic animal; knockout animal; inflammation; arthr
                                                                                                                                                                                                                                                                                                                                                                                                                                           septic shock; adult respiratory distress syndrome; pno asthma; allergy; reperfusion injury; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's disease; cancer; antisense; ribozyme; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porcine phosphoinositide 30H-kinase p120 subunit cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (II) (II) is useful for generating antibodies against it, detecting or a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences. AAS4197-AAS94564 represent novel human Note: The sequence data for this patent dia not appear in the printed are the wine intermed and in electronic format directly from WIPO are the intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermed and interesting intermediation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for identifying expressed genes. (1) is useful to restore normal activity of (II) or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 TGCAGGGCAGCTCTCTGA 31
                                                                                               1998-077181/07.
DB; AAW23948.
                                                                                                                                                                                                                                                                                                                                                                                                scrofa.
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                                                                                                                                            Hawkins
                                                                                                                                                                                                       96US-0672211
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                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 89..3397
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                                                                                                                                                                                                                                                                                                                                                                                                                         ss.
                                                                                                                                        Stephens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation; arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                743 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in gene therapy techniques disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumonia;
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CC This cDNA sequence codes for the p120 catalytic subunit (see CC ahw22948) of pig G-protein regulated phosphatidylinositol-3' kinase, CC a heterodimeric enzyme which produces the intracellular messenger CC phosphatidylinositol (3,4,5)-triphosphate in response to activation CC of trimeric G protein-linked receptors. This novel protein, which CC also contains a regulatory subunit, p101 (see AAV04633), is found in CC cells of haematopoietic origin and is involved in immune system CC pig neutrophil cDNA library using a degenerate oligonucleotide protein (see AAT99713) based on an isolated p120 tryptic peptide. The CC probe (see AAT99713) based on an isolated p120 nucleotides, CC invention encompasses pig and human p101 and p120 nucleotides, CC (invention encompasses pig and human p101 and p120 nucleotides, CC (awa23946-49), fusion proteins, p0101 and p120 proteins (see CC disorders can be identified by screening assays using a G protein CC compounds which are useful for treating inflammatory response CC disorders can be identified by screening assays using a G protein CC gene. Antagonists of G protein stimulated p13K (acting through the CC p101 subunit, especially by disrupting the interaction between the CC p101 subunit, especially by disrupting the interaction between the CC shock, adult respiratory distress syndrome (ARDS), pneumonia, CC asthman, allergies, reperfusion injury, atherosclerosis, cancer and CC Alzheimer's disease. The nucleic acids and their products can also be used for diagnosis, drug screening and clinical trial monitoring CC of inflammatory diseases.
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Sequence 3808 BP; 1010 A; 965 C; 953 G; 880 T; 0 other;

Query Match Best Local Similarity Matches Conservative 3.7%; Score 18; DB 19; Length 3808; 100.0%; Pred. No. 24; tive 0; Mismatches 0; Indels 0; Gaps 0

Search completed: October 27, 2002, 20:42:30 Job time: 130.349 secs

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Blattner,F.R. and Kadereit,J.W.
Morphological evolution and ecological diversification of the
forest-dwelling poppies (Papaveraceae: Chelidonioideae) as ded
from a molecular phylogeny of the ITS region
Plant Syst. Evol. 219, 181-197 (1999)
2 (bases 1 to 589)
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Hylomecon japonica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papayeraceae; Hylomecon
Direct Submission Submitted (02-OCT-1997) Blattner F.R.,
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AF229747 Delarbrea
AF465874 Milleria
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5.85 ribosomal RNA; 5.85
ITS1, ITS2
Chelidonium majus.
Chelidonium majus
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Submitted (02-OCT-1997) Blattner F.R., Dept.
for Plant Genetics and Crop Plant Research,
                                                                                                                                                                                                                                                                                                                                                                                             Blattner, F.R. and Kadereit, J.W.
Morphological evolution and ecological diversification of torest-dwelling poppies (Papaveraceae: Chelidonioideae) as from a molecular phylogeny of the ITS region
Plant Syst. Evol. 219, 181-197 (1999)
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Papaveraceae; Chelidonium.
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Blattner,F.R. and Kadereit,J.W.
**Arrhological evolution and ecological diversification (
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Blattner, F.R.
Direct Submission
Submitted (02-OCT-1997) Blattner F.R., Dept.
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/product="5.8s ribosomal RNA
230. .391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="internal transcribed spacer 1" 230. .391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Chelidonium majus"
/sub_species="asiaticum Hara"
/db_xref="taxon:71251"
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                                                                                                                                                                                                                                                                                                                                    4.6%;
100.0%;
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mal RNA; 5.8S
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                                                                                                                                                                                                                                                                    354
                                                                                                                                                                                                                                                                                                                       0;
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rRNA gene.
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                                                                                                                                                                                              DNA
                                                                                                                               internal transcribed spacer;
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                                                               Embryophyta; Tracheophyta;
edons; Ranunculales;
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Rahn,A.B. and Horne,F.
The Molecular Phylogeny of Z.
Based on nrDNA
Unpublishod
                                                                                                                                                                                                                                                                                                                                                                                                          648 bp DNA linear PLN 21-NOV-19. Zizania texana 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 25S ribosomal RNA gene, partial sequence.

AF169233
                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                      Zizania texana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-OCT-1997) Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 forest-dwelling poppies (Papaveraceae: Chelidonioideae) as deduced from a molecular phylogeny of the ITS region Plant Syst. Evol. 219, 181-197 (1999)
2 (bases 1 to 596)
                                                                                                                                                                                 Submitted (14-JUL-1999) Biology,
                                                                                                                                                                                                            2 (bases 1 to 648)
Kahn, A.B. and Horne, F.
                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                     Zizania texana.
                                                                                                                                                                                                                                                                                                                                                                                                 AF169233.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Plant Genetics and
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391. .596
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/strain="Neustadt/W."
/sub_species="majus"
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/product="5.8S ribosomal RNA"
                          /product="internal transcribed spacer 1"
                                          /note="ITS1"
                                                                  /product="18S
                                                                                               country-"USA"
                                                                                                              /organism="Zizania texana"
/db_xref="taxon:34180"
                                                                                                                                                      s, TX 78666, USA
Location/Qualifiers
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/product="5.8s ribosomal
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Pred. No.
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                                                                     ribosomal
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376 GCGTGCCCTCAGCCGGATGGCC 355
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2 (bases 1 to 7286)
2 (bases 1) to 7286)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirk, Ha., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A., Posfal,G., Hackett,J., Kilnk,S., Boutin,A., Shao,Y., Miller,L., Grotbeck,E.J., Davis,N.W., Lim,A., Dimalanta,E., Potamousis,K., Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C., Welch,R.A. and Blattner,F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-OCT-2000) Laboratory of Genetics, Un
Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of enterohaemorrhagic Escherichia coli O157:H7
Nature 409 (6819), 529-533 (2001)
21074935
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Escherichia coli 0157:H7
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AE005332.1 GI:12514830.
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                                                                                                                                                                                                            /gene="Z1901"
316. .642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="25S ribosomal RNA"
211 c 192 g 109 t
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                 /trans1_table=11
/product="unknown protein
/protein_id="AAG55994.1"
/db_xref="GI:12514831"
                                                                                                                                               Related)
                                                                                                                                                                                                                                                       homologous to E. 316. .642
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/note="ITS2"
                                                                                                                                                                                                                                                                         /note="0-island #52; Region of the EDL933 chromosome homologous to E. coli K-12 MG1655"
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Escherichia
/strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .7286
                                                                                                    /codon_start=
                                                                                                                                                                                                                                                                                                                                 /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:155864"
translation="MTALLTLEEIKAHLRYDHDADDEMLMDKVRQATAVLLAYIQGSR"
                                                                                                                         'note="No significant matches"
                                                                                                                                                                     function-"orf;
                                                                                                                                                                                        /gene="Z1901"
                                                                                                                                                                                                                                                                                                                                                                               /serotype="0157:H7"
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EDL933
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3, section 1 of
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•	gene		CDS	gene				CDS	gene				CDS	gene				CDS	gene
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			CDS				CDS	gene				CDS	gene					CDS	_

gen

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2978. 3259
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2978. 3259
...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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/function="orf; Other or unknown (Phage or Prophage Related)"
/function="forf; Other or unknown (Phage or Prophage Rote="Residues 1 to 77 of 80 are 62.33 pct identical to residues 1 to 76 of 224 from GenPept 118:
gil6901601|gb|AAF31104.1| (AF069529) Gp14 [Bacteriophage HK97]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Z1910"
2578. .2820
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TREVSYVVPLAFVKNDEKTLTVNTGALLTMSVSVNGGTPPYKYAWKKDGQPVEGQTT
DTFSKANAQSGDKGAYTCMVMDSAEQPQSITSDACTVTVNGAGG"
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or Prophage Related)"

note="Residues 25 to 258 of 262 are 67.09 pct identical to residues 1 to 234 of 234 from GenPept 118:

gi|6901588|gb|AAF31091.1|AF069529_4 (AF069529) major tail

subunit [Bacteriophage HK97]"
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REFERENCE
AUTHORS
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AE005325
LOCUS
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpattick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Melch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfal, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
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Escherichia coli 0157:H7 EDL9
of 155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-OCT-2000) Laboratory of Genetics, University Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli 0157:H7 EDL933.
Escherichia coli 0157:H7 EDL933
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AE005325.1 GI:12514723
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                                                                                                                                                                                                                                                                                                               /gene="
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Related)"
                                                                                                                                                                                                                                                                                                                                                      109
                                                                                                                                                                                                                                                                                                                                                                       homologous to
                                                                                                                                                                                                                                                                                                                                                                       /note="O-island #50; Region of the EDL933 chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                         /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:155864"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                              /gene="Z1808"
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100.0%;
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0.47;
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                                                                                                                            CP-933N"
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Related)"
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1093. 1878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or Prophage Related)"
/note="Residues 24 to 257 of 261 are 67.09 pct identical to residues 1 to 234 of 234 from GenPept 118 : gi|6901588|gb|AAF31091.1|AF069529_4 (AF069529) major tail subunit [Bacteriophage HK97]"
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                                                                                                                                                                                                                                                    HK97
                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Z1812"
1845. .2267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AETMDKAEYLRLDCTIKEVQFTAGQKQDIDVTTLCSTEQENINGLGASSEISMSGNFY
LNQAQNALRDAYDNDALYAFKVLFPSGKGFKFLAEVRQHTWSSGTNGVVAATFSLRLK
GKPVSFVVPLAFVKNPDKTLTVNTGALLTMSVSVNGGTPPYKHAWKKDGQPVEGQTTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="orf;
Related)"
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residues 1 to 149 of 149 from GenPept 118 :
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                                                                                                                                         /product--"putative
prophage CP-933N"
                                                                                                                                                                                                                                                                       Prophage Related)"

Note="Residues 17 to 140 of 140 are 62.90 pct identical to residues 1 to 123 of 224 from GenPept 118: gi[6901601]gb[AAF31104.1] (AF069529) Gp14 [Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFSKPGAQSADAGKYTCVVTDSAEKAQSVTSVECTVTVSAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1093.
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VVSRAPVRRGKLRRNVVVLSRRSRDGGMESGVHIRGVNPDTGNSDNTMKADNPRNAFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="unknown protein
/protein_id="AAG55909.1"
/db_xref="GI:12514725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAG55911.1"
/db_xref="GI:12514727"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Residues 1 to 113 of 114 are 49.12 pct identical to
residues 1 to 114 of 115 from GenPept 118 :
gi|6901599|gb|AAF31102.1| (AF069529) Gp11 [Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Z1812"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Z1810"
                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                               /function="putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MTFSFFYKTHTPPRAGFLLSGGRMSALYERSQLTQVMISSAPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="putative structure; Structural component (Phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_
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                                                                                                                                                                 tail assembly
                                                                                                                                                                                                                                                                                                                                                                               factor; Structural component (Phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or unknown (Phage or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded
                                                                                                                                                                 chaperone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or
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Matches
291 TAATCCGGACACCGGTAACAGC 312
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                                                                                            Similarity 100.
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
/product="putative tail component L homolog encoded by prophage CP-933N"
protein_id="AAG55915.1"
/db_xref="G1:12514731"
/translation="MQNIHEESLNESVKSEQSPRVVIWEIDLTVQGGERYFFCNELNE KGEAVTWQGTQTVQFTIDGSGTEMNGKGSSARPSLTVSNLFGLYTGMAEDLQSLVGAT WARRYVARFILDAVNFVAGNPEADPEQELKDRWVVEQMSELTAMTASFVLATPTETING WARRYVARFILDAVNFVAGNPEADPEQELKDRWVEQMSELTAMTASFVLATPTETING TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE 
                                                                                                                                                                        4911...5069
/gene="Z1816"
/function="orf; Other or unknown (Phage or Prophage
                                                                                                                                                                                                                                                                                      /gene="Z1816"
4911. .5069
                                                                                                                                                                                                                                                                                                                                                                  ANFGGFLSINKLSQ"
                                                                                                                                                                                                                                                                                                                                                           ALFPGRIMLANTCMWDYRGDECGYHGFAVADEFDNPTTDIRKDRCSKCMRGCEMRGMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-Residues 1 to 232 of 232 are 76.72 pct identical residues 1 to 232 of 232 from GenPept 118 : [bacteriophage lambda]" (J02459) L (tail component;232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Product="unknown protein encoded by prophage CP-933N"
/protein_id="AAG55914.1"
/protein_id="AAG55914.1"
/db_xref="GI:12514730"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="putative structure: Structural component (Phage
or Prophage Related)"
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/gene="Z1815"
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                                                                               4.b.,
100.08; Fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tape measure protein [Bacteriophage HK97]" /codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Z1814"
2624. .3817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mrlalrugrtlselrhslsaseammmefdryspigdergdirn
AQIVKAVEGAQGMNVALKDAMLCWGEDEDKPEVDPFAALEDALSLAAMS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="unknown protein encoded by prophage CP-933N"
/protein_id="AA655913.1"
/db.xref="GI:12514729"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Residues 1 to 90 of 93 are 61.11 pct identical to residues 133 to 222 of 224 from GenPept 118 : 9i|6901601|gb|AAF31104.1| (AF069529) Gp14 [Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Z1813"
2291. .2572
/gene="Z1813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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Related)"
                                                                                                         Score 22; DB 1;
Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2572
                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or unknown (Phage or Prophage
                                                                               0,
                                                                                                                          Length 10029;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pct identical to
                                                                  0;
                                                           Gaps
                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
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AUTHORS
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KEYWORDS
SOURCE
                                       CDS
                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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AE005290
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    멍
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l (bases 1 to 11809)

Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Sosfal, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Apodaca, J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Mpodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAATCCGGACACCGGTAACAGC 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 11809)
Perna, N.T., Plunkett,
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Escherichia coli 0157:H7 EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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AE005290.1 GI:12
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Related)"
                                                                             /gene='
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                                                                                                                                                                                                                                        /product="unknown protein CP-933M"
                                                                                                                                                                                                                                                                                               /note="Ŕesidues 1 to 67 of 67 are 56.71 pct identical to residues 48 to 112 of 112 from GenPept 118 : gil6901597|gb|AAF31100.1| (AF069529) putative head-tail
                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                             /function="orf; Other or unknown (Phage or Prophage Related)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Z1367"
109. .312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Cryptic prophage CP-933M; includes one copy of the 60 bp direct repeat that flanks the prophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="0-island #44; Region of the EDL933 chromosome not
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Z1367"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="EScherichia coli 0157:H7 EDL933"
/strain="EDL933"
/serotype="0157:H7"
/db_xref="taxon:155864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="enterohemorrhagic"
                                                                                              "Z1368"
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    Other or unknown (Phage
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                                                                                                                                                                                                                                by cryptic
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or Prophage
                                                                                                                                                                                                                              prophage
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prophage

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/transl_table=11
/product="putative tail assembly chaperone encoded by /product="putative tail assembly chaperone encoded by cryptic prophage CP-933M" /protein_id="AAG55504.1" /protein_id="AAG55504.1" /Ab_xref="Gi:1251/215" /translation="MAKDLKTLALARLSGFRHKTVKVPEWRNVSVVLREPSAEAWYLW QEVLNGOGEDDDTLSVVAKTRRULEADVTLFCDVLCDTDLQRVFAPDDREQVLAVYGP VHARLLRQALELIADAESARKK" 2276...2557
                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Z1371".
1878. .2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative tail component encoded by cryptic prophage CP-933M"
/protein_id="nac55503.1"
/db_xref="GI:12514214"
/translation="MMFENRTHINPPRAGFILSGGRMSALYERSOLTQWISSAPATAE THERAPYLRIDGTIKEVQFTAGGKQDIDVTTLCSTEQENINGLGASSEISMSGHFYLN QAQNALRDAYDNDTVKAFKVQFPSGKGFKFLAEVRQHFWSSGTNGVVAATFSLRLKGK PVSYVVPLAFVKNLDKTLTUNTGALLTMSVSVNGGTPPYKHAMKKDGQPVEGQTTDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Residues 22 to 255 of 259 are 66.66 pct identical
to residues 1 to 234 of 234 from GenPept 118 :
g1|6901588|g9|Ap$31091.1|ApF069529_4 (AF069529) major tail
subunit [Bacteriophage HK97]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Z1370"
1093. .1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mTEADLYPHLAHLAGGQVYPYVVPLLDGRPSVALPWVVFSLISS VSADVMGGQAESSVSVQIBVYAGTVTQARQIRQDAREXIMLLAPGSVSEMQDYIPENR CYRATLEFQYTV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="unknown protein CP-933M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown CP-933M"
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                                                                                                                                                                                                                                                              /note="Residues 1 to 124 of 124 are 62.90 pct identical to
residues 1 to 123 of 224 from GenPept 118 :
gii 6901601|gb|AAF31104.1| (AF069529) Gp14 [Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="putative structure; Structural component (Phage
or Prophage Related)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAG55501.1"
//d_xref="GI:12514212"
/ta_sref="GI:12514212"
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VVSRAPVRRGKLRRNVVVLSRRSRDGGMESGVHIRGVNPDTGNSDNTMKADNPRNAFY
                                                                                                                                                                                                                                                                                                                                   /function="putative factor; Structural component (Phage or
Prophage Related)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKANTQSGDKGAYTCEVTDSAEQPQSITSDACTVTVNGAGG"
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HK97]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Residues 1 to 113 of 114 are 48.24 residues 1 to 114 of 115 from GenPept 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="orf; Other or unknown (Phage or Prophage
Related)"
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752. .1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAG55502.1"
/db_xref="GI:12514213"
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                                              RESULT 9
AE005441/c
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    DEFINITION
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Best Local S
Matches 22
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  AE005441
Escherichia
                                                                                                                                                                                                                                        Similarity 100.0%; 22; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAG55506.1"
/db_xref="G1:12514217"
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SVITQFSQALAQGVLRGEEFNSVNESGDRIVRALAAGMGVARKDLKAMADDGQLTADK
VVPALISQLEULRDEYAAMPETVSDGTTKYDENAFMAWVGGANEASGVTKTLSGVLNGV
AQQIDNVATARGGTGCRRGCPVLMQYGLRSDVCHGRTCDGCT"
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2276. .2557
/gene="z1372"
/function="orf; C
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3477. .3812
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2828. .3610
                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:12514218"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="unknown
CP-933M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Residues 14 to 107 of 111 are 35.41 pct identical to residues 300 to 394 of 1089 from GenPept 118 : gi[§30158] gb] pakF31092.11 AF069529_5 (AF069529) tail length tape measure protein [Bacteriophage HK97]"
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CP-933M"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAG55505.1"
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                                                                                                                                                                                                                                                                                                                                4033. .4464
/gene="Z1375"
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Related)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="21374"
/function="orf; Other or unknown (Phage or Prophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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%; Pred. No. 0.4
0; Mismatches
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TITLE
JOURNAL
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SOURCE
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VERSION
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, B., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-OCT-2000) Laboratory of (Wisconsin, 445 Henry Mall, Madison, WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
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Escherichia coli 0157:H7
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                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                 complement(371. .3280)
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                                                                                                                                                                                                                                                                                                                                                 Complement(371. .3280)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="No significant matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(198...374)
/gene="Z3316"
complement(198...374)
/gene="Z3316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="0-island #93; Region of the EDL933 chromosome not homologous to E. coli K-12 MG1655; Cryptic prophage CP-933V; includes one copy of the 21 bp direct repeat that Shiga-like toxin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Related)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="orf; Other or unknown (Phage or Prophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /serotype="0157:H7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Escherichia coli 0157:H7 EDL933"
/strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteobacteria;
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                                                                                                                                                              (Bacteriophage HK97]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics, University of I 53706, USA
gene
                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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complement(3333. .3614)
/gene="Z3319"
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/function="orf; Related)" Other or unknown (Phage or Prophage

/note="Residues 1 to 90 of 93 are 61.11 pct identical to residues 133 to 222 of 224 from GenPept 118 gi|6901601|gb|AAF31104.1| (AF069529) Gp14 [Bacteriophage

/transl_table=11 /codon_start=1

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complement(3638. .4012) /gene="23320"

Related)" /function="orf; Other or unknown (Phage or Prophage

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/transl_table=11

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complement(4018. .4863) /gene="z3322" /translation="MAKDLKTLALARLSGERHXTVKVPEWRNVSVVLREDSAEAWYLW GEVLNGDGEDDDTLSVVAATRRNLEADVTLFCDVLCDTDLQRVFXPDDREQVLAVYGP VHARLLRQALELIADAESARKK"

complement(4018. .4863) /gene="Z3322"

/product="putative major prophage CP-933V" subunit encoded within

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DENINGIGASESISMSGNFYLNQAQNALRDAYDNDTYYAFKVQFPSGKGFKFLAEVRQ
OENINGIGASESISMSGNFYLNQAQNALRDAYDNDTYYAFKVQFPSGKGFKFLAEVRQ
HTWSSGTNGVVAATFSLRLKGKPVSYVVPLAFVKNXXKTLTNNTGALLTMSYSVNGGT PPYKXAWKKDGQPVEGQTTDTFSKANXQSGDKGAYTCXVXDSAEQPQSITSDACTVTV

complement(4793. .5137)

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RESULT 10
AE006459/c
LOCUS
                             SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                              В
                                                                              KEYWORDS
                                                                                                                                                                                      DEFINITION
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Best Local S
Matches 22
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                                                                                                                                                        13624
Escherichia coli O157:H7 EDL9
of 55.
  Escherichia coli 0157:H7 EDL933
Escherichia coli 0157:H7 EDL933
Bacteria; Proteobacteria; gamma
                                                                                                          AE006459 AE005174
AE006459.1 GI:13259579
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    /gene="23325"
    /gene="23325"
    /function="orf; Other or unknown (Phage or Prophage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Residues 6 to 116 of 116 are 45.94 pct identical to residues 4 to 112 of 112 from GenPept 118; gi [5901597]gb] parasilo0.11 (AF069529) putative head-tail adaptor [Bacteriophage HK97]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mietlldfsgledisrdlQllsgaennrvlreatraganvlkee
vvsrapvrrgklrrnvvvlsrrsrdggmesgvhirgvnpdtgnsdntmkadnprnafy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Residues 1 to 148 of 148 are 75.16 pct identical to residues 1 to 149 of 149 from GenPept 118: gi|6901598|gb|AAF31101.1| (AF069529) Gp10 [Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYRATLEFQVTV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5577. .5927)
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/db_xref="GI:12516374"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="maisagrltqmisyLnpvltrnaagemteewvscgkihadirgr
ssrermqsgaemaqaeiriwvrgqsgreitaasrlhvlsgpwrdxxLnvvgxpvpDxt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="23326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MTEADLYPHLAHLAGGQYYPYVVPLLDGRPSVALPWVVFSLISS
VSADVMGGQAESSVSVQIDVYAGTVTQARQIRQDAREAIMLLAPGSVSEMQDYIPENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Related)"
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100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                              5317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 22;
Pred. No.
                                                                                                                                                                                   3624 bp DNA EDL933 genome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5137)
gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 13505;
                                                                                                                                                                                   linear BCT contig 2 of 3, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               within prophage CP-933V"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-FEB-2001) Laboratory of Genetics, Wisconsin - Madison, 445 Henry Mall, Madison, WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of enterohaemorrhagic Escherichia Nature 409 (6819), 529-533 (2001) 21074935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 13624)
Plunkett,G. III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia.
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                                                                                                    /Genee**26035"
/genee**26035"
/function="putative factor; DNA packaging, phage assembly
/function="putative factor; DNA packaging, phage assembly
(Phage or Prophage Related)"
/note="Residues 1 to 92 of 93 are 60.86 pct identical to
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(AF069529) Gp14 [Bacteriophage HK97]"
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IDEIÄHKTPSMSLPEASDNEGRFRAALTEQNRLIDEDASRVKSLQEKIAYQYVLAND
GWTTGDGFMINHLTSVKTVTEGLAQATEQLAVEQSRLAQMQEKAQSIQDVLAGLEDRR
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/note="Residues 1 to 1076 of 1080 are 52.37 pct identical to residues 1 to 1079 of 1089 from Genpept121: gb|AAF31092.1|AF069529_5 (AF069529) tail length tape measure protein [Bacteriophage HK97]"
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YTKTLSGMLNGVAGQIDNVATAVGALVAVGVARYFGNNASGAMSATAGLVTAARNEVA
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                           prophage CP-933P"
                                                                                                                                                                                                                                                                                        complement(3488. .3769)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="26034"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:155864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                   /product="putative tail assembly protein of cryptic
                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /serotype="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coli 0157:H7 EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of cryptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kirkpatrick, H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of I 53706-1577, I
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                                                                                                                                                           gb[AAF31104.1]
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/product="putative structural prophage CP-933P"
                                                                                                                                                                                                                                                                          complement(5305. .5751)
                                                                                                                                                                                                                                                                                                     /gene="Z6039"
                                                                                                                                                                                                                                                                                                                                            /translation="MTEADLYPHLAHLAGGQVYPYVVPLLDGRPSVALPWVVFSLISS
VSAVVMGGQAESSVSVQIDVYAGTVTQARQIRQDAREAIMLLAPGSVSEMQDYIPENR
CYRATLEFQVTV"
                                                                                                               transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                     /product="putative structural component of cryptic prophage Cp-933p" /protein_id="AAK16954.1" /db_xxef="GI:13259584"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4964. 5308)
/gene="26038"
complement(4964. 5308)
/gene="26038"
complement(4664. 5308)
/gene="26038"
/function="putative structure; Structural component (Phage Function="Residues 1 to 113 of 114 are 49.12 pct identical to (AF06929) Gpl1 (Bacteriophage HK97)"
                                                                                                                                                                                                                                                                 /gene="Z6039"
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/db_xref="GI:13259583"
/translation="MTFSFFYKTHTPPRAGFLLSGGRNSALYERSQLTQVMISSAPAT/translation="MTFSFFYKTHTPPRAGFLLSGGRNSALYERSQLTQVMISSAPAT/translation="MTFSFFYKTHTPPRAGFLLSGGRNSALYERSQLTQVMISSAPATLANDKALYLDCTIKVQFTAGQRQDIDVTTLCSTEQENINGLGASSEISNSGNFYLANQAQNALIDAAYDNDALYAFKYLFPSGKGFKFLAEVRQHTWSSGTNGVVAATFSLRIKGKPVPVPLAFVKNLDKTLTVNTGALLTMSVSANGGTPPYKYAWKKDGQPVDGQTTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFSKPGAQSADAGKYTCVVTDSAEKAQSVTSVECTVTVSAAAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative tail component of cryptic prophage
CP-933p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Residues 24 to 257 of 261 are 68.37 pct identical to residues 1 to 234 of 234 from Genpept121: [Bacteriophage HK97]" 4 (AF069529) major tail subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or Prophage Related)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4182. .4967)
/gene="z6037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MHRDSERSRRIRGWVIMKKDLKTLALARLSGFRHKTVKVPEWGN /SVVLREPSAEAWYLWQEVLNGDGEDDDTLSVVAKTERNLEADVTLFCDVLCDTDLQR VFTPDDREQVLAVYGPVHARLLEQALELIADAESARKK"

complement(4182. .4967)

gene="Z6037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="putative structure; Structural component (Phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="putative factor; DNA packaging, phage assembly (Phage or prophage Related)"
/note="Residues 17 to 140 of 140 are 62.90 pct identical to residues 1 to 123 of 224 from Genpept121:
gb|AAF31104.1| (AF069529) Gp14 [Bacteriophage HK97]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Product "putative tail assembly protein of cryptic prophage CP-933p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:13259582"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAK16952.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3793. .4215)
/gene="Z6036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:13259581"
/translation="mrlalrlgrtlselrhslsaseammumefdrisplgdergdirn
AQIVKAVFCAQGMMVALKDAMLCWGEDEDKPEVDFFAALEDALSLAAQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _table=11
                                                                    component of cryptic
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                                                                                                                                                                                                                            KEYWORDS
SOURCE
                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                   RESULT 11
AL139161
LOCUS
                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                DEFINITION
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                                                                                                                                                                                                     ORGANISM
                                                                             JOURNAL
                                                                                                                      AUTHORS
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                         5509 TAATCCGGACACCGGTAACAGC 5488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 TAATCCGGACACCGGTAACAGC 312
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Direct Submission
Submitted (04-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk
                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                     complete sequence.
AL139161
AL139161.8 GI:151
                                                                                                                                                                                                                                            HTG
                                                                                                                                                                                                                                                                                                              Human DNA sequence from
                                                                                                                                                                                                                     human .
                                                                                                                                                                                                                                                                                                                                              AL139161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.0%; F 22; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(6437. .9016)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Z6042"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="Aak16957.1"
/db_xref="G1:13259587"
/tabslation="MTALLTLEBIKAHLRVDHDADDDMLMDKVRQATAVLLAY1QGSR
DKVIREDGELIPGEALTRMKGAAMRLTGMLYRNPDLAEREBLIQGELPESVSVLIYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="unknown protein
CP-933p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Residues 5 to 25 of 108 are 66.66 pct identical to residues 6 to 26 of 104 from Genpept121; pdf laAF27360.1|AF198256_14 (AF198256) unknown [Haemophilus influenzae]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Protein_id="AAK16956.1"
/db_xref="GI:13259586"
/translation="MSCGKIHADIRGRSSRERMQSGAEMAQAEIRIWVRGQSGREITA
ASRLHVLSGWRDRILNVYGLPVPDATGGRLEILCRLGGEK"
complement(6108...6434)
/gene="Z6041"
                                                                                                                                                                                                                                                     GI:15131780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6108. .6434)
/gene="z6041"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="orf; Other or unknown (Phage or Prophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative CP-933P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="putative structure; Structural component (Phage or Prophage Related)"
/note="Residues 6 to 85 of 85 are 53.75 pct identical to residues 35 to 112 of 112 from Genpept121: gb|AAF31100.1|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Residues 6 to 85 of 85 are 53.75 pct identical to residues 35 to 112 of 112 from Genpept121: gb|AAB31100.1| (AFG69529) putative head-tail adaptor (Bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(5748. .6005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MIETLLDESGLEDISRDLOLLSGAENNRVLREATRAGANVLKEE
VVSRAPVRRGKLRRNVVVLSRRSRDGGMESGVHIRGVNPDTGNSDNTMKADNPRNAFY
WRFVEMGTVNMPPHPFVRPAFDVRSEQAAQVAIARMNRAIDEVLRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Z6040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="26040"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAK16955.1"
/db_xref="GI:13259585"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22; DB 1; Pred. No. 0.48; 0; Mismatches
                                                                                                                                                                                                                                                                                            103608 bp DNA linear PRI 04-AUG-2
om clone RP5-940F7 on chromosome 1q42.2-43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .9016)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    head-tail adaptor of cryptic prophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoded by cryptic prophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                   PRI 04-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                           repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Aug 9, 2001 this sequence version replaced gi:14787245. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sections only once, except for a 100 base overlap. The true left end of clone RP4-764D2 is at 101609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence is not the entire insert of clone RP5-940F7 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP5-940F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECTOR: PCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttp://www.sanger.ac.uk/HGP/Chr1
rp5-940F7 is from the library Parties on Structed by the group
refeter de Jong. For further details see
ittp://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                         4812. .4870
/note="MER4D repeat: matches 359.
4870. .5107
                                                                                                                                                                                                                                                                                                                                                                           /note="AluSc repeat: 4574. .4663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              right end of clone RP4-580N22 is at 2000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                           /note="AluSx repeat: matches 6.
                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restriction digest data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001. .2044

/note="Single clone region. Assembly confirmed/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1248. .3222
/note="L1PB2 repeat: matches 3614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1PB2 repeat: matches 5574. .6155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="AluSg/x repeat: matches 145. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MER58B repeat: matches 2. .341 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="AluSp repeat: matches 1. .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone="RP5-940F7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           map="q42.2-43"
  'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .103608
                                                                                                                                                                                                                    e-"MER4D repeat: matches 9.
                                           copies 2 mer ac 84% conserved
                                                                                      repeat:
                                                                                                                                    copies 2 mer ca 97% conserved"
                                                                                                                                                                                                                                                                                                           copies 2 mer ac 100% conserved"
                                                                                         matches 2588.
                                                                                                                                                                                                                                                                                                                                                                                                  matches 5.
                                                                                                                                                                                                                                                                                                                                                      .248 of consensus"
    .303 of consensus"
                                                                                                                                                                           .285 of consensus
                                                                                                                                                                                                                      .234 of consensus"
                                                                                      .2705 of
                                                                                                                                                                                                                                                                                                                                                                                                  .298 of
                                                                                                                                                                                                                                                                  .417 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5574 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                consensus"
                                                                                      consensus'
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/note="61 copies 2 mer ca 80% conserved" 21253. .21557
/note="Aludb repeat: matches 1. 307 ~6 21740. .21793
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13542. .13637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="22 copies 2 mer ca 79% conserved"
17480. .17949
/note="MLT1B repeat; matches 1. .466 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15312. .15622
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/note="MIR repeat: matches 33.
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/note="50 copies 2 mer ca
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                                                                                                           /note="AluSx repeat:
                                                                                                                                                                                           /note="23 copies 2 mer tg 76% conserved"
                                                                                                                                                                                                                                                                                                                                /note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluJo repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L2 repeat: matches 2642.
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/note="AluY repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluJo/FRAM repeat: matches 147.
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/note="L2 repeat: matches 2606. .2733 of consensus"
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                                                                                                                                                                                                                                                                                  note "MLT1B repeat: matches 1. .388 of consensus"
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                                                                                                                                                                                                                                           e="AluSp repeat:
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    ,2 repeat:
28872
                                                                                                                                                      repeat:
                                                                  repeat: matches 5199. .6329 of consensus"
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                         2580. .2706 of consensus"
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                                                                                                                                                      .287 of consensus"
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                                                                                                           .290 of consensus"
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                                                                                                              Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                              Ohnishi,M., Murata.T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagav
                                                                                                                                                                                       Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S., Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida, Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and Shinagawa,H.
                                                                                                                                                                                                                                                                                          Escherichia coli 0157:H7
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                               AP002555
Escherichia coli 0157:H7 DNA, complete
AP002555 BA000007
AP002555.1 GI:13360886
                                                                                                                                                                                                                                                                                                                                                Escherichia coli 0157:H7 (strain:0157:H7, sub_strain:RIMD 0509952)
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38658. .41845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="11PBa repeat: matches -1518. .-1346 of consensus"
36795. .38360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MER46A repeat: matches 196.
36626. .36797
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36585. .36625
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35906. 36181
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35604. .35905
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33996. .34174
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33698. .33995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 1. .301 of consensus"
33563. .33697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER50 repeat: matches 1.
33194. .33485
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100.0%; Pr
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30942. .31167
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29785. .30063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluJo repeat: matches 85.
29508. .29715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .35112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches -184. .1384 of consensus"
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0.53;
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                                                                                                                                                                                                                                                                                                                                                                                                                              section 6/20
                                                                                                                                                                                                                        Kimura,S.,
be,H., Iida,T.,
                                                Shinagawa, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12
DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin I genes of the enterohemorrhagic Escherichia coli Gene 258 (1-2), 127-139 (2000)
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Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli o157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655
Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
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74. .607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:83334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sub_strain="RIMD 0509952"
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/strain="0157:H7"
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'genem'ECS1426'
'genem'Similar to MDOG_ECOLI g1|1787286 percent identity
99 in 511 aa (Conserved in E.coli K-12)"
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complement(2038. .3195)
/gene="ECs1425"
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AWYTPKGEWGKGSVELVE I PTNDETNDN I VAYWTPDQLPEPGKEMNFKYTITFSRDED
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identity 99 in 385 aa (Conserved in E.coli K-12)"
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                                                             Syst. Appl.
20557356
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CDS

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Db 105175 TAATCCGGACACCGGTAACAGC 105196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286485
Escherichia coli O157:H7 DNA,
APO02557 BA000007
                      Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655
                                                                                                                                                                                                                                                                                                                                           Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
                                                                                                                            Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Ha
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K.,
                                                                                                                                                                                                                                                                                    Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                   derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli 0157:H7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental product="acidic protein MsyB" /product="acidic protein MsyB" /protein_id="BaB34852.1" /protein_id="BaB34852.1" /db_xref="g1:13360893" /db_xref="g1:13360893" /translation="MMTMYATLEEAIDAAREEFLADNPGIDAEDANVQQFNAQKYVLQ /translation="MMTMYATLEEAIDAAREEFLADNPGIDAEDANVQQFNAQKYVLQ DGDIMWQVEFFADEGEEGECLPMLSGEAAQSVFDGDYDEIEIRQEWQEENTLHEWDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to MSYB_ECOLI gi|1787289 percent identity
99 in 125 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(8060. .8437)
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/gene="ECs1429"
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/db_xref="GI:13360892"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ECs1428"
7832. .8059
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/gene="ECs1428"
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TPEKLNRDRRLVLLSDPVTMARLHFRVWNSPERYSSWVSYYEGIKLNPLALRKPDAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MRLIVVSIMVTLLSGCGSIISRTIPGQGHGNQYYPGVQWDVRDS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
  Microbiol.
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                                                                                                                                                                                                                                       Syst.
                                                                                                                                                                                                                                     the Sakai outbreak
Syst. 74 (5), 227-239 (1999)
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Pred. No. 0.55;
23 (3), 315-324 (2000)
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                                                                                                                               Shinagawa, H. and
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26 JUN 2000) Ken Kurokawa, Osaka University, Genome Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:ken@gen-info.osaka-u.ac.jp, URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365, Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete nucleotide sequence of the prophage VT1-Sakai carrying the O157:H7 strain derived from the Sakai outbreak (1-2), 127-139 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.,
Yamamoto,K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 286485)
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2024. 4663
Note="similar to YDBH_ECOLI gi|1787646 percent identity
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                                                                                                   'gene="ECs2003"
                                                                                                                                                                                                                                                                                                                                                                                      Complement(827. .1816)

/gene="EC$2002"

/note="similar to LDHA_ECOLI gi|1787645 percent identity

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/db_xref="taxon:83334"
complement(294...716)
/gene="$C$2001"
complement(294...716)
/gene="EC$2001"
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complement(827. .1816)
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99 in 140 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Escherichia coli 0157:H7"
/strain="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
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KSWTVHDDSNTVVPDGVNTSGGITWSYDDDGLHHTKRAGVVVDGTTGNAIEFGNAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="newlear"
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EPSLYDAELDWQENSGOLIVLARONGSPLEDLPWGTTROQLTYSDGRWSRPYAGFPLS
GRLGWKYDNWOAGLENALVSGRLSVLTQGQAGKGNAVLNFGGGKLSDMSQLPLQUTG
GRLGWKYDNWOAGLENALVSGRLSVLTQGQAGKGNAVLNFGGGKLSDMSQLPLQUTG
TQGVYDGRLOAHENELGDEVLHWGGLANDFLPDAGRWOMFWGKGSFTPHNATW
SLDAGQTLETGGSVLPDSTLKFSYDGRDFTYFLFKGDLHASEIGPVRVNGKGSFTPHNATW
SLDAGQTLETGGSVLPPSTLKFSYDGRDFTYFLFKGDLHASEIGPVRVNGKWBGRAL
MPNMOVNGVDFVLPFERADGAGHLCTRGEPVTLHAGLANDFLPSGGAL
MPNMOVNGVDFVLPFERADGAGHLCTRGPVTLRIAEVINUTAKNITADLQGRYBPTE
SGALPLWLNNEKWIVEDGWLANGFDHPALLRLMVLSSSELVSANVBKGFAMSGAF
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TDQGGNTALNGGTVMTVDGDNISLNNDGKTTAIGEGSVVGILTGDNITINNNGETEVD
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5590. .8625
                                                                                                                                                                                                                                                                                                                                                   /Note="unknown, similar to BigA protein [Salmonella typhi] dad|AFI33185-1|AAD29677.1 percent identity 32 in 1006 aa, similar to N-terminal part (1-1128 in 2020 aa) of ydba.2 [Escherichia coli] gi|7465766|pir||C48399 percent identity 49 in 1011 aa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Product="hypothetical protein"
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LQTDAETQALVKDINEARNHSYQQLAKQNNVSTKEIAKLAGQKLVARAKSGQYVQGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5590. .8625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ECs2005"
4850. .5176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="BAB3427.1"
/db_xref="G1:13361470"
/translation="MKUTJAAPASSEMLVGCTPRIEVAAPKEPITINNNVKIEHEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 in 61 aa (Conserved
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4660. .4845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WLEQNAQLPETGCPSGKECEEKQ"
4660.4845
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/gene="ECs2004"
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REFERENCE
AUTHORS
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KEYWORDS
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Best Local
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Escherichia coli O157:H7 DNA,
AP002556 BA000007
APD00555 C
                                                                                                                                                                                                                                                                                                                                           2 (sites)
Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7
Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak
                                                                                                                                                                                                                     Syst. Appl. Microbiol. 23 (3), 315-324 (2000) 20557356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
                                                                                 Shinagawa, H
                                                                                                     Yokoyama, K., Makino, K., Kubota, Y., Watanabe, M., Kimura, S., Yutsudo, C.H., Kurokawa, K., Ishii, K., Hattori, M., Abe, H., Iida, TYamamoto, K., Hayashi, T., Yasunaga, T., Honda, T., Sasakawa, C. and
                                                                                                                                                                                                                                                                                                 Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli 0157:H7
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/gene="ECs2007"
8881. .11304
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OPYFNPSTGVNISGDNNDVTLDGQLTVVADSKTTSRSYADGAQEHIAGIVIAGDD
NTFILNGGVHFVGEKNVMDDGSKPSASRRGIGDTPLINVDGHSPVYLNGESTISGEFP
LGFENLIQLSHGAELEIGADATFDMSDVDSFTYYYRVALSTISIDSGAKATNNGEVEL
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DGATIKQEGDLYVSGGAHGIDVDGNDTFVSNKGNITVIEDNSIGMLLDGDGVSVINMG
DLNVGQAAAGENAIGIQIDGDNATFVNVGDISATNAGTGVSVAGDKANISLAGGLDVG
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AINDQTGVININAENGQAFYNDGTGLIINYGTICTFGVC"
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HSVLNYPAEWNLSDGTSFNNKALGLTGMLASYSSSILNGETGIIDMYGRGSVGMLAID
KSTADNEGQITLDTLWVDENDETSLRNNVANSTAKDFGVGMASGTDAYNGALTKATAT
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/gene="ECs2007"
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/transl_table=11
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100.0%; Pr
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Syst. 74 (5), 227-239 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Information Research Center; 3-1, Yamadaoka, Suita, Osaka 5
Japan (E-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/product="putative TonB dependent outer membrane receptor"
/protein_id="BAB35116.1"
/db_xref="GI:13361158"
/translation="MRLKKHYLCTALSLAFTQOAVAAQESDSLTVWSSPVSSTTTTVL
DOPTMKALDKONVAQALSVVPGVVLQKSGSRNEEQVKVRGFDSRQVPVYFDGVPIYVP
YDGNLDLARILINNLCAVEVSKGYSSLLQGPNQMGGAINITTQKPTKPLEASLGYRQG
WSRSQDNAYDMHASFAASSELGYLQVSGSQLKQDFLGLPHGVNNDIAGKHGKMINSSA
                      complement(2426. .3280)
/gene="ECs1694"
                                                                           /gene="ECs1694"
                                                                                                                                                                                                                                        DDKRGIVKLGFTPRENDEYTLTYIKQDGEKDNPPYSGNSGQXSRYWQWPEYDKESFYY
GGTTGLUTDRTLKSRLYRDTENTLMYNSLADLKNKKGSYSHYADYSUGAGLQLAAD
VRENDLLTFRVNWKDDVHREKGAPHAAYDRYEDTWSLASEYQWAAADNUVVAGISY
DWRDSYEAKKHEKDGSITHYDDNNQSAFNWQVMGKYHFVNEDTLALSYYDRKRFPTLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor, similar to Tonb dependent outer membrane receptor PrrA [Escherichia coli CFT073] gi|3661477|gb|AAC61709.1| percent identity 97 in 656 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(430. .2400)
/gene="ECs1693"
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/gene="ECs1693"
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/protein_id="BAB35115.1"
/db_xref="G1:13361157"
/thanslation="MGIIAWIIFGLIAGIIAKLIMPGRDGGGFFLTCILGIVGAVVGG
WLATMFGIGGSISGFNLHSFLVAVVGAILVLGVFRLLRRE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to YMGE_ECOLI gi|1787445 percent identity
97 in 84 aa (Conserved in E.coli K-12)"
                                                                                                                                                                  QTMTAWMTLKPWEPLSVTLSEEARSSSYSNSDGSQKAAGFAVTHIRADYTLGHGFSVN
                                                                                                                                                                                      ERYTTSKPAYNQIAIVNPQLKPERARGVDLTWNGAFTHDWGFEVSVYYNRVSDAILSH
NIDADTIQNQNSGTVDYSGLDAGIKGKISNILDVGLSYALIHADAKRKDIGKITDLPT
                                                                                                                                   ASVNNLFDTQYAYSEGFVEEGRNFWAGVEYTF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
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126. .380
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/note="molybdenum transport protein,similar to molybdenum
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AP002556

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/note="probable ABC transporter protein (permease), similar to ABC transporter permeases e.g. [Haemophilus influenzae] gi|2501391|sp|Q57130|YE71_HAEIN percent identity 40 in 323
                                                                                                                                                                                     /evidence-not_experimental
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/product="putative ferric enterobactin transport
ATP-binding protein"
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TCGLPTEQLTTNKLAALXTVSADQIHHHLSAISH"
TCGLPTEQLTTNKLAALXTVSADQIHHHLSAISH"
                                                                                                                                     /gene="ECs1698" .5834)
                                                                                                                                                                              /gene="ECs1698"
                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"probable ferric enterobactin transport, similar ferric enterobactin transport ATP-binding protein [Escherichia coli CFT073] 91|3661480|gb|AAC61712.1|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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DSYLOQLIAKIDLOGAQTLFDMGCGPGTVSLALADKLTTIYGVDYSQGMLNVAARRAA
VSTSFVSPAIQRAWEEDWSDLPRCDIAVASRSTLVADMRQAMSKLNNQARLRVYTTHL
complement(4099...4857)
/gene="ECS1697"...4857)
                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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/gene="ECs1697"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unknown.similar to hypothetical proteins e.g. Orf2 (Escherichia coli CFT073) gil3661479|gb|AAC61711.1| /codon_start=1 214 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Product="hypothetical protein"
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INNKMLVPSPLPAATGRSSGGIAYRRHCDDFPFSGTNRCVTSGRYPGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3445. .4089)
/gene="ECs1696"
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complement(3219..3500)

/gene="ECs1695"
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CVSGVSVACKMLTTLGLTIDDAVSDGSQANAGQRLIRAQGNAAALHQGWKAIQNVLEW
SCGVSDYLDQMLALLRERYPDGNIACTKKALPGTRLLASQAILAAGGLIHRAGCAETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unknown"
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/protein_id="BAB35117,1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLEANHRHFLHDNODWSGAINQLRRHAPEKKIVVEADTPKEAIAALRAQPDVLQLDKF
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identity 91 in 284 aam
/codon_start=1
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SOURCE
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Comparision of phylogenetic hypotheses among different dwarf dandelions (Krigia): additional information from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGHRGBEHA

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AGOSeris heterophylla partial 18S ribosomal RNA (18S rRNA)

ribosmal RNA (25S rRNA) genes; complete 5.8s ribosomal RNA

rRNA) gene; complete internal transcribed spacers 1 and 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18S ribosomal RNA, 25S rib
Agoseris heterophylla DNA.
Agoseris heterophylla
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    /gene="25S rRNA"
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                                                   /product="25s ribosomal RNA
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                                                                                    /gene="25S rRNA"
                                                                                                                                                                                         /gene="5.8S rRNA"
/product="5.8S ribosomal
279. .442
                                                                                                                                                                                                                                                            'product="internal
                                                                                                                                                                                                                                                                                             /gene="18S rRNA"
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                                                                                                                                                                                                                                                                                                                                                                                              /organism="Agoseris heterophylla"
/db_xref="taxon:19017"
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/gene="ECS1699"

/note="probable ABC transporter, weakly similar to iron

(iii) ABC transporter, ATP-binding protein [Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mrivngcillaaisitfaavsgayhldmoollalilroenvpy
DEQIVFWOIRVERILAALLIGAALAGAGTTYOGMLRNELVSPOILGVSAGAGIGACTA
ILMGLSIVYIOLYAFCGGLMVVAGVWLITRRVTRHDFILTLVLVGIALFLOGAGISL
IKTLADPYOLDSITFWLLGGLSTVTLEDLCYAAFIILIGSLFLFFLRWRMNLLTLSD
DEARSIGLNVTRLRFVLIVCATLITASTYAIAGIIGWYGLVVPHIABLLTGHNHQOLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(5834. .6856)
/gene="ECs1699"
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/product="putative ABC transporter permease protein"
/protein_id="BAB35121.1"
/db_xref="GI:13361163"
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PLN 26-JUL-1993 3S rRNA) and 25S pmal RNA (5.8S

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1: sp_archea:*
2: sp_bacteria
3: sp_fungl:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
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12: sp_vtrus:*
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sp_virus:*
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054381 rickettsia
Q9f9f2 rickettsia
Q9f9f2 rickettsia
052252 rickettsia
052252 rickettsia
Q9k2n6 male-killin
Q31065 rickettsia
Q9k4w8 male-killin
Q53154 rickettsia
Q9f9q1 rickettsia
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86.5	87.5	88	89.5	90	91	93	93.5	94	95	95.5	97	97	98	99	99.5	99.5		100.5		104	105	106.5	108.5	108.5	109	109	111.5	0
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ОЭНИРО	Q9VS43	046171	Q9PGD9	Q9HU07	Q983Y0	Q98P93	Q9AL49	Q9SUX1	P76572	Q92NT4	Q9KSR1	Q9XAX8	Q9CN83	Q9A9X2	Q91762	Q92LP2	Q9A8M8	069776	Q9XCA4	Q52854	Q9RB08	Q9RA95	Q92ST9	Q9F6B1	Q9PGX0	in	Q914S1	Q92R89
g	drosophi	046171 nephila cla		Q9hu07 pseudomonas		ω	ຜ	Q9sux1 arabidopsis		Q92nt4 rhizobium m	_	ש	Q9cn83 pasteurella		Q91762 pseudomonas		Q9a8m8 caulobacter	-		Q52854 rhizobium l	pectobact	Q9ra95 serratia sp	Q92st9 rhizobium m	Q9f6b1 edwardsiell	Q9pgx0 xylella fas		Q9i4s1 pseudomonas	Q92r89 rhizobium m

ALIGNMENTS

Q9F9K8; 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 17 KDA ANTIGEN. OSPA. Piscirickettsia salmonis. Bacteria; Proteobacteria; gamma subdivision; Piscirickettsia group Piscirickettsia. NCBL_TaxID=1238; [1] SEQUENCE FROM N.A. STRAIN=LF-89; KUZYK M.A., Burian J., Thornton J.C., Kay W.W.; "Identification of a genus-common Rickettsial surface antigen in t salmonid pathogen Piscirickettsia salmonis."; SUBMITTED SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64; SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64; SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64; Duery Match SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64; Query Match 162 RGCLOGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 164 164									-																	
Irel. 16, Created) Irel. 16, Last sequence update) Irel. 16, Last sequence update) Imonis. Iteria; gamma subdivision; Piscirickettsia group Iteria; gamma subdivision; Piscirickettsia group Iteria; gamma subdivision; Piscirickettsia group I., Thornton J.C., Kay W.W.; I., Thornton J.C., Kay W.W.; I., Thornton J.C., Kay W.W.; I., Thornton J.C., Kay W.W.; I., Thornton J.C., Kay W.W.; I., Thornton J.C., Kay W.W.; I., Thornton J.C., Kay W.W.; I., Thornton J.C., Kay W.W.; I., Thornton J.C., Kay W.W.; I., I., I., I., I., I., I., I., I., I.,	Db	Qy	DЪ	Qy	Db	Qy .	Ma Ma	Ď	SQ	RL	RT	RT	R 7	ָ ק	0 X) X	ô	8	SO	ON O	DE	DJ !	3 5	3 2	3 5	1 (
0;	RQQYCREFQQKAMIAGQKQEIYGTACRQPDGRWQVISTEK	ROOYCREFOOKAMIAGOKQEIYGTACPOPDGRWQVISTEK			RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL	RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL	98.8%; Pred. No. 1.5e-65; vative 1; Mismatches 1; Indels 0; Gaps	98.0%; Score 815; DB 2;	162 AA; 17661 MW;	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.	salmonid pathogen Piscirickettsia salmonis.";	"Identification of a genus-common Rickettsial surface antigen in the	KIZVK M.A. CU. Thornton J.C. Kav W.W.:	CHRATE FACE	CEDITENCE EDOM N >	NCBI_TaxID=1238;	Piscirickettsia.	Bacteria; Proteobacteria; gamma subdivision; Piscirickettsia group;	Piscirickettsia salmonis.	OSPA.	GEN.	(TrEMBLrel. 16,	(TrEMBLiel 16.	2001 (Frener to) 16	OFFICE PRELIMINARY; PRT; 162 AA.	

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RESULT
QPF9F2
ID P09
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054381
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O1-MAR-2001 (TrEMBLrel 16, C)
O1-MAR-2001 (TrEMBLrel 16, L)
O1-DEC-2001 (TrEMBLrel 19, L)
T KDA GENUS-COMMON ANTIGEN
                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-21217364; PubMed-11321078;

Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,

Zavala Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsia felis (Rickettsia azadi).
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=42862;
                                                                                                                                                                                                                                                                                                                                                                         Rickettsia felis: molecular characterization of a
                                       8 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-98007556; PubMed=9425244;

Davis M.J., Ying Z., Brunner B.R., Pantoja A., Ferwerda F.H.;

"Rickettsial relative associated with papaya bunchy top disease.";

EMBL; U76907; AAC02809.1; 1.98).
SKIMITALAASMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                61;
                                                                                                                                                            Similarity 37.9
61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQRALEAAPSGSSVQWRNPDNGNYGTVTPSKAY----KNNTGQYCREYTQTVVVGGKQQ 131
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148 AA;
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37.98;
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                                                                                                                                        Score 283; DB 2;
Pred. No. 6.9e-18;
30; Mismatches 54
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Pred. No. 9.2e-20;
30; Mismatches 43;
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                                                                                                                                     Indels
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Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Bertrand D., Hurst G.D.D., Majerus M.E.N.;
"On the evolution of male-killing: Monophyletic origin and horizontal generic ladybirds, Adalia bipunctata L. and A. decempunctata L. Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ269518; CAB96383.1; -.
EMBL; AJ269517; CAB96382.1; -.
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Best Local S
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052252
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                                                                                                                                 O9K2NG;
O1-CCT-2000 (TrEMBLITE1 15, Created)
O1-CCT-2000 (TrEMBLITE1 15, Last sequence update)
O1-CCT-2000 (TrEMBLITE1 15, Last sequence update)
17KDA ANTIGEN (17 KDA ANTIGEN) (FRAGMENT),
male-killing Rickettsia from Adalia bipunctata
Ricketta; Proteobacteria; alpha subdivision; Rickettsiales;
NCBI_TaxID=38028;
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                                                                                                                                                                                                                                                                                           121 GKQQKAYGNACRQPD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Billings A.N., Teltow G.J., Walker D.H.;

Molecular characterization of a novel spotted fever group species from Ixodes scapularis in Texas.",

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

NON_TER 1 AAB95267.1;
                                                                                                                                                                                                                                                                                                                        137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
Rickettsiaceae; Rickettsi
                                                                                                                                                                                                                                                                                                                                                                                                             22
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                                                                                                                                                                                                                                                                                                                       AELTSQRALEAAPSGSSTEWRNPDNGNYGYVTPNKTY-----RNSTGQYCREYTQTVVIG
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53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAVLGGOIGAGMDEQDRRLAELTSQRALEATPSGTSVEWRNPDNGNHGYVTPNKTY----
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Pred. No. 9e-
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Last sequence update)
Last annotation updat
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Best Local S
Matches 52
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Q9K4W8;
Q9K4W8;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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O31065; 99W02;
O1-JAN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-OCT-2001 (TrEMBLrel. 18, Last annotation update)
TRDA ANTIGEN (17 KDA PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stenos J., Roux V., Walker D., Raoult D.;
"Rickettsia honei sp. nov., the aetiological
spotted fever in Australia.";
Int. J. Syst. Bacteriol. 48:1399-1404(1998).
EMBL; AF027124; AAB81846.1;
EMBL; AF060706; AAD20231.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Billings A.N., Yu X.-J., Submitted (SEP-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsia honei.
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=37816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                     TSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY---
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39.4%; Pred. NO. 3.3e-15;
39.4%; Mismatches 45;
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                                                                                                                                                                                                                                                                                                                                                                             score 251.5;
Pred. No. 3.8e

24; Mismatches
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93084757; PubMed=1452660;
Baird R.W., Lloyd M., Stenos J.,
"Characterization and comparison
group rickettsiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsia sp.
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                                       J. Clin. Microbiol. 30:2896-2902(1992). EMBL; M99391; AAA73386.1; -. NON_TER 154 154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-NOV-1996 (TrEMBLrel. 08, Last annotation
(CLONE PRB FISF 1), 5' END CDS (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coccinellidae).";
Appl. Environ. Microbiol. 67:270-277(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 KDA ANTIGEN (FRAGMENT).
male-Killing Rickettsia from Adalia decempunctata.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsiaee; Rickettsia.
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rickettsiaceae;
NCBI_TaxID=789;
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KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR
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                                                      GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGSYGYVTPNKTYRNST
                                                                                                                          SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
                                                                                                                                                          SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLEGKGSGRVSMAIG-GAVL
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                                                                                       GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSQRALEAAPSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ
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52; Conserv
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                      154 AA;
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                                                                                                                                                                                                                                                                                                                                                                                             PubMed=1452660;
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                                                                                                                                                                                                                                                                      15849 MW;
                                                                                                                                                                                                                29.3%;
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                                                                                                                                                                                               Score 244; DB 2;
Pred. No. 2.1e-14;
1; Mismatches 54
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                                                                                                                                                                                                                                                                      F5C35855EDB439D2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                          Ross B.C., Stewart R.S., Dwy of Australian human spotted
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                    153
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GQD-----CRVYTQTVVIGGKQQKAYGNACRQPDGQ 154

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PRELIMINARY;

PRT;

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Matches 49
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                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CALIFORNIA 2;
ROUX V., ROUIT D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210693; AAG48554.1; -.
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9F0Q1 PRELIMINARY; PRT; 131 AA.
Q9F0Q1; Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TREMBLRel. 16, Last annotation update)
ARICKETTSIA SP. California 2.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsiaee; Rickettsiaee; Rickettsiaee;
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Best Local Similarity 35.9
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Raoult D.;
"A new SFG rickettsia isolated from fleas.";
"Leas.";
"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CALIFORNIA 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQP 150
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                                                                 al Similarity
49; Conserv
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"Novel peptide diagnostic reagent and kit for detection rickettsiosis.";
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-EMBLREL. 16, Last annotation update)
01-EMBLREL. 16, Last annotation update)
Rickettsia helvetica.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae, Rickettsiaee; Rickettsia.
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01-MAR-2001
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131 AA;
                                                                 Conservative
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A; 13374 MW;
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15621 MW; B77407B9C71E4B39 CRC64;
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35.9%;
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                                              Score 236.5; DB
Pred. No. 8e-14;
4; Mismatches
                                                                                                                                           23C8819B29FFF860 CRC64;
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Pred. No. 5
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                                                                                             DB 2;
                                        44;
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5.7e-14;
les 54;
                                                                                   Length 131;
                                  Indels
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01-0CT-2000 (TrEMBLrel. 15, Last seq)
01-DEC-2001 (TrEMBLrel. 19, Last annotate ANTIGEN (FRAGMENT).
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Best Local S
STRAIN-DAE100R;
MEDLINE=21091941; PubMed=11157215;
Simser J.A., Palmer A.T., Munderloh U.G.,
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                                           SEQUENCE FROM N.A.
                                                              Rickettsia peacockii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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MEDLINE-94117373; PubMed=8288533;

Werren J.H., Hurst G.D., Zhang W., Breeuwer J.A., Stouthamer R.,

Majerus M.E.;

"Rickettsial relative associated with male killing in the ladybird
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    beetle (Adalia bipunctata).",
J. Bacteriol. 176:388-394(1994).
EMBL, U04162; AAA19235.1;
                                                                                                                                                                                                                                                                                 80 KLNOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickettsia sp.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                          PRELIMINARY;
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131 AA;
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.; 13344 MW;
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                                                                                                              15, Created)
15, Last sequence update)
19, Last annotation update)
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Pred. No. 8e-14;
24; Mismatches 44;
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Q9AGC7;
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Q1-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
17 KDA ANTIGEN (FRAGMENT).
Rickettsia typhi.
Bacteria; Proteobacteria; al
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O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-JAN-1998 (TrEMBLrel. 19, Last annotation update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
17 KDA ANTIGEN (FRAGMENT).
Rickettsia sp. 'La Copita'.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
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MEDLINE-98367252; PubMed-9701930;
Billings A.N., Yu X.J., Teel P.D., Walker
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Detection of a spotted fever group rickettsia (Acari: Ixodidae) in South Texas.";
J. Med. Entomol. 35:474-478(1998).
EMBL; AF033499; AAB86943.1;
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EMBL; AF260571; AAF69012.1; -.
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49; Conservative
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131 AA;
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       alpha subdivision;
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                                                                      Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 216.5; DB 2;
Pred. No. 3.7e-12;
""smatches 34;
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Pred. No. 9.8e-14;
14; Mismatches 44
                                                                                                                                                                 PRT;
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01-OCT-2001
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"Complete genome structure of the complete genome 
                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome structure of Mesorhizobium loti.";
DNA Res 7:331-338(2000).
EMBL; AP003012; BAB54098.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-MAFF303099;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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Paspaliaris V., Liedtke B., Vitetta L., Whiting J.L.;

"Rickettsia typhus and Rickettsia felis rickettsioses in Australia.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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NCBI_TaxID=785;
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                     2002,
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Last annotation updat
                                                                                                                                                                                                                                                                      Score 137; DB 16;
Pred. No. 0.00011;
6; Mismatches 50;
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Sugimoto M.
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P05372 rickettsia
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Best Local Similarity
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61;

Conservative

34.6%; Score 288; DB 1; L 37.9%; Pred. No. 3.1e-18; 37.9%; Mismatches 52;

DB 1; Length 159;

Indels

16;

Gaps

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roduced through a collaboration ics and the EMBL outstation re are no restrictions on its as its content is in no way Usage by and for commercial http://www.isb-sib.ch/announce/	J.O., R.M., Naeslund A.K., and the origin of er membrane by a lipid	Rickettsiales;	P19482 bos taurus P46724 mycobacteri P1599 rattus norv P25705 homo sapien P06813 oryctolagus P19483 bos taurus Q03265 mus musculu P46199 homo sapien P04985 bos taurus Q04270 drosophila P07389 bluetongue

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Or Senu ...

EMBL; D16515; BAA03965.1;

PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

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BY SIMILARITY
CHAIN 20 159
17 KDA SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PROBABLE).

16554 MW; CDDCE7CEBDCD6B41 CRC64;

1-ongth 159;
                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Specific amplification of Rickettsia japonica DNA from clinical specimens by PCR.;
J. Clin. Microbiol. 33:487-489(1995).
-!-SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE....
STRAIN=YH;
MEDLINE=95229950; PubMed=7714214;
MEDLINE=95229950; PubMed=7714214;
V. Katayama T., Yoshida Y., Kaiho I.;
Of Rickettsia japonica DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                      KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                                                                              GAVLGGOIGAGHDEODRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS
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                        EMBL; M28479; AAA26379.1; --
EMBL; M28480; AAA26376.1; --
EMBL; M28480; AAA26381.1; --
EMBL; M16486; AAA26381.1; --
EMBL; M16486; AAA26381.1; --
EMBL; M16486; AAA26381.1; --
EMBL; M18486; AA3881.1; --
PIR; A35971; A35971.
PIR; A33971; B33971.
PIR; B33971; B33971.
PIR; B33971; B33971.
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SPECIES-R.rickettsii;
MEDLINE-89008059; PubMed-3139629;
Anderson B.E., Baumstark B.R., Bellini W.J.;
"Expression of the gene encoding the 17-kilodalton antigen Rickettsia rickettsii: transcription and posttransiational
                                                                                                                                                                                                                                                                                                                                                                                            modification.";
J. Bacteriol. 170:4493-4500(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P05372;
01-NOV-1988 (Rel. 09, Created)
01-AUG-1990 (Rel. 15, Last sequence
01-MAR-2002 (Rel. 41, Last annotat:
17 kDa surface antigen precursor.
OMP OR RC1287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87222152; PubMed=3108232;
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MEDLINE-21442074, PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fo
Ramson D., Roux V., Cossart P., Weissenbach
Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson
   Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=R.conorii, and R.rickettsii, MEDLINE=89359171; PubMed=2768201; Anderson B.E., Tzianabos T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparative sequence analysis of a gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 169:2385-2390(1987).
                                                                                                                                                                                                                                                                                                                                                           anchor (Probable).
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Rickettsiaceae; Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsia conorii, and Rickettsia rickettsii.
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                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Attached to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B.E., Regnery R.L.,
Bellini W.J.;
                                                                                                                                                            NOT_ANNOTATED_CDS
                                                                          PROKAR_LIPOPROTEIN;
ipoprotein; Antigen;
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783;
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17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
N -> D (IN REF. 3).
G -> E (IN REF. 3).
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Signal;
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IRESULT 2

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DT Q1-NOV-1997 (
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SEQUENCE FROM N.A.

Rickettsia japonica.

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STANDARD;

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RESULT 3
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SEQUENCE FROM N.A.
MEDLINE-89359171; Pubmed-2768201;
Anderson B.E., Tzianabos T.;
Anderson B.E., Tzianabos T.;
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17KD_RICTY P22882;
                                                                                                                                                                                    PROSTITE; PSO0013; PROKAR LIPOPROTEIN; 1.
                                                                                                                                                                                                         EMBL; M28481; AAA26377.1; -. PIR; C33971; C33971.
                                                                                                                                                                                                                                                                                                                                                                                                        Rickettsiaceae;
NCBI_TaxID=785;
                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
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01-OCT-1996
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QEIYGTACPQPDGRWQVIS
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                            TSQRALESAPSGSNIEWRNPDNGNHGYYTPNKTY---
                                                                   NKQGTGTLLGGAGGALLGSQFGHGKGQL-VGVGVGALLGAVLGGQIGASLDEQDRKLLEL
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                                                KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
                                                                                                                  Similarity
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159 AA;
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39.6%; Pred. No. 3.1e-17;
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7; Mismatches
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Submitted (OCT-1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
STRAIN-MACULATUM
                 SEQUENCE FROM N.A
                                                   NCBI_TaxID=35792;
                                                                        Rickettsiaceae;
                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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mbrane; Lipoprotein; Antigen; Signal.
1 19 BY SIMILARTY.
20 >154 17 KDA SURPACE ANTIGEN
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eae; Rickettsia.
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e EMBL/GenBank/DDBJ databases
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon'profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                    EMBL; U11020; AAB07706.1;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiaae; Rickettsia
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01-OCT-1996 (Rel. 34 Last sequence update)
01-OCT-1996 (Rel. 34 Last annotation update)
17 kDa surface antigen precursor (Fragment).
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P50931;
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EMBL; U17008; AAA82040.1; -.

PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

Outer membrane; Lipoprotein; Antigen; Signal.

SIGNAL 19 BY SIMILARITY.

20 >154 17 KDA SURFACE ANTIGEN.

N-ACYL DIGLYCERIDE (PROBABLE).
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PSO0013; PROKAR_LIPOPROTEIN; 1.

mbrane; Lipoprotein; Antigen; Signal.

1 19 BY SIMILARITY.

20 >154 17 KDA SURFACE ANTIGEN.

20 >20 N-ACYL DIGLYCERIDE (PROBABLE).
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57; Conserv
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Pred. No. 9.
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120 -RNSTGOYCREYTOTVVIGGROOKAYGNACLOPDGO 154
                                       118 KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 153
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal.
SIGNAL 1 19 BY SIMILARITY.
CHAIN 20 >154 17 KDA SURFACE ANTIGEN.
LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are not restrictions on its mon-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a
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154 AA;
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15895 MW;
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RESULT 10
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Best Local :
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01-APR-1993 (Re)
01-APR-1993 (Re)
01-OCT-1996 (Re)
17 kDa surface a
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P50927;
SEQUENCE FROM N.A.
MEDLINE=92108069; PubMed=1729713;
                                                     Bacteria; Proteobacteria; Rickettsiaceae; Rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Stothard D.R., Ralph
Submitted (JAN-1995)
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
                                                                             Rickettsia
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                                        NCBI_TaxID=788;
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                                                                                                                                                                                                                                                                                                                                                               SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch).
                                                                                                               (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 34, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                           154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
20
154
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                       antigen
                                                                                                                                                                    STANDARD;
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                                                     Rickettsieae;
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20
                                                                                                                                                                                                                                                                                                                                                                                                                                           15879
                                                                                                                                                                                                                                                                                                                                                                                                     30.6%;
36.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor (Fragment).
                                                                                                       (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                           MW.
                                                     alpha subdivision;
sae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.1e
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Score 255; Db 1,
No. 2.1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
17 KDA SURFACE ANTIGEN
N-ACYL DIGLYCERIDE (PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen;
                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           E4FBE4C29D943581 CRC64;
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                                                                                                                 update)
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                                                                 Rickettsiales
                                                                                                                                                                                                                                                                                                                                                                                                               Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 11
PCP_YEREN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCP_YEREN P31484;
                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 51872 / WA-C / SEROTYPE
MEDLINE=92121089; PubMed=1732192;
                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
15-DEC-1998 (Rel. 37, Last ann
Outer membrane lipoprotein pcp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 typhus-like rickettsia found in cat fleas.";
Proc. Natl. Acad. Sci. U.S.A. 89:43-46(1992).
-i- SUBCELLULAR LOCATION: Attached to the outer membrane by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Azad A.F., Sacci J.B. Jr., Schmidtmann E.T., Carl M.;
EMBL; X60448; CAA42977.1;
                                                                                                                                                           +
                                                                                                                                                                                      -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                uptake
                                                                                                                                                                                                                                              Baeumler A.J., Hantke K.; "A lipoprotein of Yersinia enterocolitica"
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=630;
                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                              Yersinia enterocolitica.
                                                                                                                                                                                                                                                                                                                                                                                               PCP OR PCPY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer membrane; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000437; Prok_lipoprot. PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M82879; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genetic characterization and transovarial
                                                                                                                                                                                                     take in Escherichia coli.";
Bacteriol. 174:1029-1035(1992)
- FUNCTION: FACILITATES FERRIOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                             H. INFLUENZAE
                                                                                                                                                         SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLYB
                                                                                                                                                                           anchor
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                                                                                                                                             PCP.
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8372 MW;
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                                                                                                                                                                                      FERRIOXAMINE UPTAKE. Attached to the oute
                                                                                                                                                                                                                                                                                                                                                                gamma subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                           pcp
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                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
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Pred. No. 3.9e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AD289A48EAB19E0E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                         otation update) precursor.
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                                                                                                                                                                                                                                                                                          0:8;
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                                                                                                                                                                                       the outer membrane
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SESULT 12
SLYB_SALTY
AC Q53549;
DT Q1-MAR.
DT Q1-NOV-DT 
SEQUENCE FROM N.A.

SPECIES=S.typhi; STRAIN-CT18;
MEDLINE=21534947; pubMed=11677608;
MEDLINE=21534947; pubMed=11677608;
Parkhill J. Dougan G. James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T. Connerton Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
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Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                           Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                               McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=S.typhimurium;
MEDLINE=96133688; Pubw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
outer membrane lipoprotein slyB precursor
SLYB OR STM1445 OR STY1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLYB_SALTY
Q53549;
Q1-NOV-1997
Q1-NOV-1997
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium, and Salmonella typhi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 VQKQGPTRFSVGQ--RVMLASSGSTVTVSP
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CHAIN
LIPID
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HSSP; P00778; 1P04
PROSITE; PS00013; PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 GAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gen. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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SITE; PS00013; PROKAR_LIPOPROTEIN; 1.

er membrane; Lipoprotein; Signal.

NAL 1 POTENTIAL.

IN 18 15 OUTER MEMBRAN

ID 18 18 N-ACYL DIGLYC

UENCE 155 AA; 15362 MW; 8AD6BE2132E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAVLGGFLGNTVGGGTGRSLATAAGAVAGGMAGQGVQGAMNRTDGVQLEVRKDDGTTILV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVAĪAAVTLTGCĀNNNTLSGDVĒŠASQAKQVQTVTYGTLLSVRPVTIQGGDDNNVMGAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulatory protein from Salmonella typhimurium, induces
ic and pore-forming protein in Escherichia coli.";
. Genet. 249:474-486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8544813;
C., Bauer S., Bubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%;
24.7%;
                                                                                                                                                                                                                                                                                                                                             of Salmonella
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Pred. No. 0.00.
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OUTER MEMBRANE LIPOPROTEIN PCP
N-ACYL DIGLYCERIDE (POTENTIAL)
BAD6BE2132E849FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subdivision;
                                                                                                                                                                                                                                                                                                                        enterica serovar Typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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(P SEQUENCE FROM N.A.

RX MEDLINE-96133688; PubMed-8544813;

RA Ludwig A., Tengel C., Bauer S., Bubert A., Benz K.,

RA Goebel W.;

RT "SlyA, a regulatory protein from Salmonella typhimurium, induces a hamolytic and pore-forming protein in Escherichia coli.";

RT haemolytic and pore-forming protein in Escherichia coli.";

Mollenkopf H.-J.,

Escherichia coli, and Escherichia coli 0157:H7 Bacteria; Proteobacteria, Escherichia NCBI_TaxID=562, 83334;

gamma

subdivision;

Enterobacteriaceae;

SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Per
Riley M., Collado-Vides J., Glasner J.D., RodeGregor J., Davis N.W., Kirkpatrick H.A., Goeden

Goeden M.A.,

Perna N.T., Burland V., ode C.K., Mayhew G.F.,

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or send an email to license@isb-sib.ch).
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SIMILARITY: TO E.COLI SLYB, H.INFLUENZAE PCP AND
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Matches 3
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MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy Hayashi T., Makino K., Ohnishi M., Kurokawa K., Tanaka M., Tobe Ilda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasuna, Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasuna, Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                  EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                     This SWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kikpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lin A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Itch T. Kasai H. Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mo Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yanamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28 0-40.1 min region on the linkage m DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                      use by non-profit institutions as round in this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                      Match
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A -> 543EBBA4069A5FA3 CRC64;
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                                                     Outer membrane;
SIGNAL 1
CHAIN 19
LIPID 19
  CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95350630; PubMed-7542800:
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Sprigss T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-88115138; PubMed-2828309;

MEDLINE-88115138; PubMed-2828309;

Deich R.A., Metcalf B.J., Finn C.W., Farley J.B., Green B.A.;

"Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton protein from Haemophilus influence.";

J. Bacteriol. 170:489-498(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCP_HAE
P10325;
                                                                                                                                                                                                                                                                                        use by non-profit institutions us tony modified and this statement is not removed entities requires a license agreement (Secons send an email to license@isb-sib.ch).
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PCP OR LPP OR HI1579.
Haemophilus influenzae.
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influenzae Rd.";
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Y.ENTEROCOLITICA PCP.
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U32832; AAC23228.1;
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                                                                                                                                                        PS00013; PROKAR_LIPOPROTEIN;
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lipoprotein PCP precursor (15 kDa lipoprotein) (PAL
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1 P37796; P75951;

1 01-OCT-1994 (Rel. 30, Created)

1 01-W-1997 (Rel. 35, Last sequence update)

T 01-MAR 2002 (Rel. 41, Last annotation update)

E Hypothetical protein ycfJ.

YCFJ OR Billo.
        EMBL; AE000211; AAC74194.1; -
EMBL; D90746; BAA35925.1; -
EMBL; V00306; -; NOT_ANNOTATED
                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             IDENTIFICATION.

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Borodovsky M., Rudd K.E., Koonin E.V.;

"Intrinsic and extrinsic approaches for detecting genes bacterial genome.";

Nucleic Acids Res. 22:4756-4767(1994).

Nucleic Acids Res. 22:4756-4767(1994).
                                                                                                                                                                                                                                                                                                              Nucleic acids Res. 22:4756-4767(1994).
-!- SIMILARITY: TO RICKETTSIA 17 kDa SURFACE ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97061202; PubMed-8905232;
OShima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kinura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
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"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=81236546; PubMed=6265208;
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STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 5 25
SEQUENCE 179 AA; 18920 MW; BASEBODRAGAAGGG CECCA.
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                                                                           TACPQPDGRWQVISTEK
                                                                                          ---------TYTTTQQRCKTVYDKSEKMLGYDVTYK----IGDQQGKIRMDRDPG 162
                                                                                                                  AGOVTEWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY-----G 144
                                                                                                                                                                                                            36;
                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                           179 AA;
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                         18920 MW;
                                                                                                                                                                                              12.0%; Score 100; DB 1; Length 179; 26.3%; Pred. No. 0.061; Indels
                                                   178
                                                                            161
                                                                                                                                                                                                                                                      BA5EB0DB56D45609
                                                                                                                                                                                                                                                      CRC64;
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                                                                                                                                                                                              Gaps
                                                                                                                                             120
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4;

10:56:30

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                               Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
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    Pred. No.
score grea
and is der
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length: 2000000000
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832
1 MRGCLQGSSLIIIS
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Match
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Gapop 10.0 , Gapext 0.5
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  122.0001114556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                    Length
   DB
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B33971
A33971
G97860
C33971
A25972
            D97478
A10693
C64921
F90922
B85771
S58234
AG0443
AG0443
AG0443
C64855
D85674
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AI3418
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D33971
Pickettsial common antigen precursor - Rickettsia prowazekii
N:Alternate names: 17kD surface antigen; outer membrane protein (omp); RP833
C;Species: Rickettsia prowazekii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 03-Nov-2000.
C;Accession: D33971; B71645
R;Anderson, B.E.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971; MUID:89359171
A;Accession: D33971
A;Accession: D33971
A;Residues: 1-159 <AND>
A;Cross-references: GB:M28482; NID:g152461
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45	44	43	42	41	40	39	ა 8	37	3 6	35	34	33	32	31	30
90	90	90.5	92	92	92.5	92.5	94	94	94	95	95	95	97	97	99
10.8	10.8	10.9	11.1	11.1	11.1	11.1	11.3	11.3	11.3	11.4	11.4	11.4	11.7	11.7	11.9
526	137	691	100	100	220	220	808	278	278	172	172	172	223	179	332
	N	N	N	N	N	N	N	2	N	Ŋ	N	Ŋ	N	N	2
KRBOVI	в82998	F91251	AE2897	G97672	A12910	G97685	T05442	н98195	AB3091	D85894	н65026	G91049	C82230	AC0198	D87353
keratin, 54K type	hypothetical prote	probable tape meas	conserved hypothet	hypothetical prote	porin [imported] -	probable outer mem	glycine-rich prote	hypothetical prote	hypothetical prote	probable outer mem	hypothetical prote	probable outer mem	probable lipoprote	probable exported	hypothetical prote

ALIGNMENTS

	A; Note: the sequence in GenBank entry RIRANT17KC, release 109.0, (PID:q152462) omits
	R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
	A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochond
	A; Reference number: A71630; MUID: 99039499
	A; Accession: B71645
1	A;Status: nucleic acid sequence not shown; translation not shown
common	A; Molecule type: DNA
common	A; Residues: 1-159 < AN2>
common	A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15258.1; PID:g386
antige	A; Experimental source: strain Madrid E
common	C; Genetics:
precur	A; Gene: omp; RP833
pothet	C; Superfamily: rickettsial common antigen
antige	C; Keywords: surface antigen
ne lip	
pothet	Query Match 34.6%; Score 288; DB 2; Length 159;
reted	Best Local Similarity 37.9%; Pred. No. 1.7e-18;
prote	Matches 61; Conservative 32; Mismatches 52; Indels 16; Gaps 6;
pothet	
[impo	QY 8 SSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 61
oprote	
[impo	Db 5 SKIMIIALAASMLQACNGQSGMNKQGTGTLLGGAGGALLGSQFGQGKGQL-VGVGVGALL 63
lip	
ne lip	Qy 62 GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
er mem	
er mem	Db 64 GAVLGGQIGASMDEQDRRLLELTSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY 119
- RIL	
ne pro	
acting	Db 120 -RNSAGOYCREYTOTVIIGGCOOKTYGAACROPDGOWOVVI 159
prote - Esc	
prote	RESULT 2 B33971
prote	Rickettsial common antigen precursor - Rickettsia conorii

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17K surface antigen precursor [imported] - Rickettsia conorii (Strain Malish C.) Species: Rickettsia conorii (Strain Malish C.) Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C;Accession: G97860 R. Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; San Frience 293, 2093-2098, 2001
                                                                                                        RESULT 4
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A33971
Rickettsial common antigen precursor - Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_char
C;Accession: A33971
R;Anderson, B.E.; Tzianabos, T.
R;Anderson, B.E.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989
                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M28480; NID:g152457; PIDN:AAA26376.1; PID:g152458
C;Superfamily: rickettsial common antigen
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-159 <AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Comparative sequence analysis of a A;Reference number: A33971; MUID:89359171
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C:Date: 16-Mar-19
C:Accession: B339
R:Anderson, B.E.;
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A; Residues: 1-159 <AND>
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J. Bacteriol. 171, 5199-5201, 1989
A; Title: Comparative sequence analysis of A; Reference number: A33971; MUID: 89359171
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;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 20-Aug-1999
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                                                                                                                                                                                                                            GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                                                                                                                                                           SKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL 63
                                                                                                                                                                                                                                                                                        SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 61
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                                                                                                                                                                                                                                                                                                                                               34.3%;
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37.9%; Pr
tive 31;
                                                                                                                                                                                                                                                                                                                                   31;
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Pred. No. 3.1e-18;
1; Mismatches 53;
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Pred. No. 3.1e
31; Mismatches
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.1e-18;
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   Barbe, V.; Samson,
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C;Accession: A25972
R;Anderson, B.E.; Regnery, R.L.; Cal
J. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 1:
A;Reference number: A25972; MUID:87;
A;Accession: A25972
                                                                         RESULT 6
A25972
17K antigen precursor - Rickettsia rickettsii
C:Species: Rickettsia rickettsii
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M28481; NID:g152459; PIDN:AAA26377.1; C;Superfamily: rickettsial common antigen
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A; Residues: 1-159 < AND>
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A;Title: Comparative sequence analysis of
A;Reference number: A33971, MUID:89359171
A;Accession: C33971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Accession: C33971
R;Anderson, B.E.; Tzianabos,
J. Bacteriol. 171, 5199-5201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsial common antigen precursor -
c;Species: Rickettsia typhi
C;Date: 16-Mar-1990 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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C;Superfamily: rickettsial common antigen
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A; Residues: 1-159 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN
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                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 39.6
55; Conservative
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              A25972; MUID:87222152
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                                                    Carlone, G.M.; Tzianabos, T.;
                                                                                                                                                                                                                                                                                                                                                                                                        27;
          17-kilodalton-antigen gene from Rickettsia ricketts
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 276.5; DB 2
Pred. No. 1.8e-17;
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Pred. No. 3.1e-18;
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                                                 McDade, J.E.;
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; : Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, E. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella A;Reference number: AD3252; PMID:11756688
A;Accession: A13418
                                                                                                                                                                                                                      C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002
C;Accession: AI3418
                                                                                                                                                                                                                                                                             RESULT 8
AI3418
17K surface antigen precursor [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: C; Genetics: A; Gene: PA3819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-182 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337 A;Accession: D83169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83169
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J.Dry, S.; Olson, M.V.; LOTY, S.; Olson, M.V.; Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
D83169
A; Molecule type: DNA, A; Residues: 1-131 <KUR>
A; Residues: 1-131 <KUR>
A; Cross-references: GB: AE008917; PIDN: AAL52516.1; A; Experimental source: strain 16M
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C; Species: Pseudomonas aeruginosa
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                                                                              A; Status: preliminary
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QIAGTAIGAVVGGLLGNQIGGGTGKKIATVAGAVGGGYAGNKVQEGMQERDTYTTETRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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32; Conserv
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ilarity 34.8%;
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Pred. No. 0.00037;
3; Mismatches 28;
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Pred. No. 2e-17;
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                     PID:g17983328;
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                     GSPDB:GN00190
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outer membrane lipoprotein precursor - Yersinia en C;Species: Yersinia enterocolitica C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 C;Accession: S23787 R;Baeumler, A.J.; Hantke, K. J. Bacteriol. 174, 1029-1035, 1992 J. Bacteriol. 174, 1029-1035, 1992 A;Reference number: S23786; MUID:92121089 A;Accession: S23787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <BABS
A:Cross-references: EMBL:X60448; NID:g48577; PIDN:CAA42977.1;
C:Superfamily: PAL cross-reacting lipoprotein
C;Accession: B83514
R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.;
                                                                                               conserved hypothetical protein PA1053 [imported] - C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision #sequence_revision
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                    82 -- NQSLEKVKAGQVTRWRNPDTGNSYSVEP 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 QVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGTACPQPD
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nes 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLITISVFLVGCAQN-----FSRQE-----
                                                                                                                                                                                                                                                                                                                                                    VQKQGPTRFSVGQ -- RVMLASSGSTVTVSP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Conserv
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31.7%;
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Pred. No. 0.0068;
9; Mismatches 4
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                                                                                                      15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                                                                          Pseudomonas aeruginosa
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A;Cross-references: GB:AE004537; GB:AE004091; A;Experimental source: strain PAO1

NID: g9946960;

PIDN: AAG04442.1;

GSPDB

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-154 <570>

A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337 A;Accession: B83514

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Nature 406, 959-964, 2000

Coulter, S.N.; Folger, P.

; Warrener, K.R.; Kas,

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Hickey, Larbig,

X.J.;

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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.;
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A,Title: Complete Genome Sequence of Caulobacter crescentus.

A Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                           C; Date: 20-ApC; Accession:
                                                                                                                                                                                                                                                   hypothetical protein CC3073 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: G87629
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.;
A;Title: Complete genome sequence of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a multiple of a mu
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AL513382; PIDN:CAD08336.1; PID:g16502381; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-179 <PAR>
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Best Local
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A;Gene: PA1053
C;Superfamily: PAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 IPL-DGNGQLVLNNK 178
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37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.1%; Score 109; DB 2; 27.4%; Pred. No. 0.016;
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                                                                                                                                                       Nelson, K.E.; Eisen, J.; Heidelberg, J.
in, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
Shapiro, L.; Venter, J.C.; Fraser, C.M.
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.0.0083;
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R.M.; Dowd,
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lipA protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens (c;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AD2696 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Cher erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li; Karp, P.; Romero, P.; Zhang, S.
                                                                                                                                                                                                                                                             RESULT 14
AD2696
                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
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DЬ

Matches

105 GTAIGALIGGLVÖNOFGHGNGRKALTAAGAVAGGFIGNEV 144

D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo D.; Kutyavin, T.; Levy, R.; Li, M.; MCCL

9,

12;

0,

Gaps

0,

Length 257; Indels

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A;Cross-references: GB:AE003872; GB:AE003849; NID:g9104975; PIDN:AAF82991.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrero, J.D.; Jungueira, M.L.; Kenper, E.L.; Kitajima, J.P.; Franca, S.C.; Franco, M.C.; Fr
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
A;Authors: Martins, E.M.F.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
A;Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A;Reference number: A59328
                                                                                                      A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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R;anolymous, The Xylella fastidiosa
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein XF0178 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <5TO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: G87629
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Best Local Similarity
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Gene: CC3073
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                                             Local
                                                                                                  XF0178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 VVGCKASGKKQEVGAVVGALLGAAAGSNLAKNDQGTGTAIGAVVGAGAGSLIGCKMQKSD 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 LVGCAQNESRQEVGAATGAVVGGVAGQLEGK---GSGRVSMAIGGAVLGGLIGSKIGQSM 73
          Similarity 47.5
19; Conservative
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                             13.18;
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33.7%;
Score 109; DB 2;
Pred. No. 0.024;
9; Mismatches 1
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Pred. No. 0.021;
14; Mismatches 33; Indels
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                                   DB 2;
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C:Genetics:
A:Gene: slyB
C:Superfamily: PAL cross-reacting lipoprotein
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0289
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A;Molecule type: DNA
A;Residues: 1-155 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC91178.1; PID:g15980369; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AF0289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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A; Accession: AD2696
A; Status: preliminary
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
Search completed: October 27, 2002, 10:58:40 Job time : 11.5665 secs
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A;Gene: lipA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: circular chromosome
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A; Residues: 1-142 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.9%; Score 107.5; DB Best Local Similarity 27.2%; Pred. No. 0.017; Matches 41; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 QNCRQYSHTLTVDGRDTRVRGAACRNDDGSW 138
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                                                                                                                                                                                                      67 GAVLGGFLGNAVGGGTGRSLATAAGAVAGGIAGQGVQGALNRTDGVQLEIRKDDGQTILV 126
                                                                                                                                                                                                                                   34 GAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL---
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                                                                                                                                                  82 -- NQSLEKVKAGQVTRWRNPDTGNSYSVEP 109
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                                                                                                                                                                                                                                                                                                                                    9 SLIIISVFLVGCAQN-----FSRQE-----
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                                                                                                                                                                                                                                                                                                       7 AVAIAVVTLTGCANNNTLSGDVFTASQAKQVQTVSYGTLISVRPVTIQGGDDNNVVGAIG 66
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                                                                                                VOKOGPTOFSVGORVMLAN--SGSTITVSP 154
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%; Score 107.5; DB 2; 24.0%; Pred. No. 0.019;
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Perfect score:
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s derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Gapop 10.0 , Gapext 0.5
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Database

Query Match 9.4%; Score 78.5; DB.4; Length Best Local Similarity 35.3%; Pred. No. 1.7; Matches 24; Conservative 4; Mismatches 17; Indel:	US-08-556-978B-19 US-08-556-978B-19 Sequence 19, Application US/08556978B Patent No. 6568169 GENERAL INFORMATION: NOVEL RECOMBINANTLY PRODUCED TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED TITLE OF INVENTION: SPIDER SILK ANALOGS INVENER OF SEQUENCES: 107 CORRESPONDENCE ADDRESS: ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET COUNTRY: ULIMINTON STATE: DELAWARE COUNTRY: UNITED STATES OF AMERICA LIP: 19898 COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS 95 SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 CURRENT APPLICATION NUMBER: US/08/556,978B FILING DATE: JUNE 15, 1993 APPLICATION NUMBER: 08/077,600 FILING DATE: JUNE 15, 1993 ATTORNEY/AGENT INFORMATION: AAPPLICATION NUMBER: 33.692 REFERENCE/DOCKET NUMBER: 33.692 REFERENCE/DOCKET NUMBER: 33.692 REFERENCE/DOCKET NUMBER: 33.692 REFERENCE/DOCKET NUMBER: 30.692 REFERENCE/DOCKET NUMBER: CR-9389-A TELEPHONE: 302-892-8112 INFORMATION = 302-773-0164 INFORMATION = 3	ALIGNMENTS	28 71 8.5 970 1 US-08-752-929-7 29 71 8.5 970 4 US-09-090-793-5 30 71 8.5 2703 1 US-08-185-432-9 31 70.5 8.5 248 4 US-09-033-523-1 32 70.5 8.5 731 2 US-08-913-364-0 33 70.5 8.5 792 2 US-08-678-039A-40 470 8.4 606 4 US-09-247-806-6 35 69.5 8.4 470 1 US-08-40-203A-3 36 69.5 8.4 547 1 US-08-452-567-3 38 69.5 8.4 547 2 US-08-452-567-3 39 69.5 8.4 547 2 US-08-452-427-3 39 69.5 8.4 547 2 US-08-452-760-12 41 69.5 8.4 1021 1 US-08-407-519-12 42 69.5 8.4 1021 1 US-08-40-549-12 43 69.5 8.4 1021 1 US-08-40-549-12 44 69.5 8.4 1021 4 US-08-913-832A-2 45 69 8.3 101 4 US-08-556-978B-20
ength 651; Indels 23;			Sequence Sequence
Gaps	,		7, Appli 19, Appli 11, Appli 1, Appli 1, Appli 1, Appli 40, Appli 3, Appli 3, Appli 3, Appli 3, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli

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Sequence 2, Application US/08425069

Patent No. 5728810

GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Lewis, Randolph V.
APPLICANT: Himman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
STATE: Viginia
COUNTRY: Viginia
COUNTRY: U.S.A.
TIP: 22046
                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,069
FILING DATE: 19-APR-1995
CLASSIFICATION: 435
ATMICIANTONIM TURCHUMTANI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 651
TYPE: PRT
ORGANISM: Nephila clavipes
US-09-247-806-1
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                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/247,806
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PHILLIPPE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Pierre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING A
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6338-0335-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 LGGQGAGQ 558
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35.3%;
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Pred. No. 1
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                                             US-08-317-844B-2
                                                                                             TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: amino acid
              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
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Patent No.
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                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/POCKET NUMBER: 14.
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK

TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESS:
                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                         TELEPHONE: (/Us) 21-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5989894th Washington Street STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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LENGTH: 718 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
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o. 5989894
                                                                                          amino acids
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     9.48;
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35.3%;
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Score 78.5;
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Pred. No. 1
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US-09-034-177-3
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US-09-034-177-3
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                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 747 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Guegler, Karl J. APPLICANT: Corley, Neil C. TITLE OF INVENTION: HUMAN F
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CORRESPONDENCE ADDRESS:
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551 LGGQGAGQ 558
                                                         491 QGAGAAAAAVGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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                           64 LIGSKIGQ 71
                                                                                27 QEVGAATGAVVG----GVAGQ-----
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35.3%;
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                                                                                                                           Score 78.5;
Pred. No. 2;
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                                                                                                                                      Length 747;
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; LENGTH: 255
; TYPE: PRT
; ORGANISM: E. (
US-09-553-498-8
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US-09-553-498-8
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US-09-067-351-2
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Best Local Similarity
Matches 37; Conserv
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CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: EP99107412.1
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 8
LENGTH: 255
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TITLE OF INVENTION: Process for the production of naturally folded and secreted
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION NUMBER: US/09/067,351
                  TELECOMMUNICATION INFORMATION:
                                                      ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                      STREET: 31..
STREET: 31..
STREET: PALO ALTO
CITY: PALO ALTO
CALIFORNIA
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Corley, Neil C. APPLICANT: Baughn, Mariah TITLE OF INVENTION: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tang, Y.
APPLICANT: Hillman,
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 SVEPVRTYORYNKOERROOYCREFOOKAMI--AGOKQEIYGTACPOPDGRWQVISTE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 MSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARFSGSGSGTSY 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 LQMTSLRSEDTAMYYCARDYGAY-WGQGTTVTVSSGGGGSGGGGGGGGGDIELTQSPAI 141
                                          REFERENCE/DOCKET NUMBER:
                                                                                                                  CLASSIFICATION:
                                                                                                                                      FILING DATE:
TELEPHONE:
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                                                                                                                                                                                                                                                                                           94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09067351
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Schwarz, Elisabeth
                                                                                                                                                                                                                                                                                                                                                                  3174 PORTER DRIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                        INCYTE PHARMACEUTICALS, INC
  (650) 855-0555
                                                                                                                                    Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN KERATINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jennifer L.
                                                    39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 77.5; DB 4; Pred. No. 0.62;
                                        PF-0511 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

<u>ب</u>

amino acids

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US-09-360-490-2
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                                                                  TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2,
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-067-351-2
         IMMEDIATE SOURCE
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                      STREET: 31,
STREET: 9ALO ALTO
CITY: PALO ALTO
CWATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                               TYPE: amino acids
STRANDEDNESS: single
LIBRARY:
                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 EQQNK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: KERANI
CLONE: 2029060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 QRYNK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 PSFPVCPPGGIQEVTVNQSLLTPLHLQIDPTIQRVRAEEREQIKTLNNKFTSFIDKVRFL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 SK------IGOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 GASFGSRSLYNLGGAKRVSLNGCGSSCRSGFGGRASNGFGVNSG---FGYGGGVGGGFSG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 22.4 les 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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NO. 6221843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  94304
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                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang, Y. :
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Baughn, Mariah
                                                                                                            (650)
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                                                                                                           855-0555
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22.4%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jennifer L.
                                                                                                                                                                                               09/067,351
                                                                                                                                                                                                                                               US/09/360,490
                                                                                                                                     39,132
ER: PF
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QΥ
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                                                                                              Query Match
Best Local Similarity
Tatches 32; Conserve
                                                                                                                                                                    TOPOLOGY: 1.

MOLECULE TYPE:
US-08-374-077C-2
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FILING DATE: 19-TAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCGOWAN, Malcolm M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 0226
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE:
US-09-360-490-2
                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Applipatent No. 602791
                                      2389 IGSSNÖSIFÖGSÄGGLGGÄÖSGGVG-GLGGSSSIRNAFGGSGSÖPSSLSPOHOPYSGTLN 2447
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2516 amino acids
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                         29 VGAATGAVVGGVAGQLFGKGSGRVSMAIGG--AVLGGLIGSKIGQS----MDQQDKIKLN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                     TELEPHONE: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible operATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 699 Princ
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 EQQNK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22314-3187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 QRYNK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 PSFPVCPPGGIQEVTVNQSLLTPLHLQIDPTIQRVRAEEREQIKTLNNKFTSFIDKVRFL 170
-----QSLEKYKAGQYTRWRNPDTGNSYSVEPYRTYQRYNKQERRQQYCREFQQKAMIA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 GASFGSRSLYNLGGAKRYSLNGCGSSCRSGFGGRASNGFGVNSG---FGYGGGVGGGFSG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SK------IGOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEBVRTY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                          Conservative
                                                                                                                                                                                            linear
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Ren, Dejian
Zheng, Wei
Dubald, Manuel Marcel Paul
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                                                                                                                                                                                protein
                                                                                                    9.2%; Score 76.5; E
24.8%; Pred. No. 17;
tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes Encoding an Invertebrate Alpha1 Calcium Channel Subunit 57
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                                                                                                                                                                                                                                                                                                                                                                                         US/08/374,077C
                                                                                                                                                                                                                                                   2:
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                                                                                                                              DB 3;
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                                                                                                    66;
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                                                                                                                            Length 2516;
                                                                                            Indels 13; Gaps
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RESULT 11
US-07-803-633A-13
: Sequence 13, Application US/07803633A
: Patent No. 5369025
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Best Local
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                                                                                                                                                                                                                                                                                            Matches
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCGGWan, Malcolm M.
REGISTRATION NUMBER: 39,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             2389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                               2508
                                                                                                                                                               2448
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dubald, Manuel TITLE OF INVENTION: Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                               137
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                                                                                                                                                                                             83
                                                                                                                                                                                                                                                          29 VGAATGAVVGGVAGQLFGKGSGRVSMAIGG--AVLGGLIGSKIGQS----MDQQDKIKLN 82
                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                            IGSSNGSIFGGSAGGLGGAGSGGVG-GLGGSSSIRNAFGGSGSGPSSLSPQHQPYSGTLN 2447
                                                                                               GQGNQTYSS 2516
                                                                                                                              GOKOEIYGT
                                                                                                                                                              SPPIPDNRLRRVATVTTINNNNKSQVSQNNSSSLNVRANANSQMNMSPTGQPVQQQSPLR 2507
                                                                                                                                                                                            -----QSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIA 136
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                                                                                                                                                                                                                                                                                          l Similarity
32; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall, Linga .
Ren, Dejian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                              145
                                                                                                                                                                                                                                                                                                                                                                         protein
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                                                                                                                                                                                                                                                                                                       9.2%; Score 76.5;
24.8%; Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/374,888
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                                                                                                                                                                                                                                                                                            18; Mismatches
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Encoding an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWECKER & MATHIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         022650-263
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                                                                                                                                                                                                                                                                                                                          DB
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US-08-220-151-6
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                                                                                                                                                                           Sequence 6, Application US/08220151 Patent No. 5529780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                           GENERAL INFORMATION:
APPLICANT: Paoletti,
APPLICANT: Limbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 865 amino acids
TYPE: AMINO ACID
TROPACTORY. 12022
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SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/803,633A
FILING DATE: 19911210
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CORRESPONDENCE ADDRESS:
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                                                                CORRESPONDENCE ADDRESS
                                                                               NUMBER OF SEQUENCES:
                                                                                              TITLE OF INVENTION:
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TELEFAX: 248345
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                                                                                                                                                                                                                                                                                                        119 QERROQYCRE-FQQKAMIAGQKQ 140
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                                                                                                                                                                                                                                                                                                                                          747 AAFL--AYRYVNKLKSNPMKALYPMTTEVLKA-QATRELHGEESDD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                             16 FLVGCAQNFSRQ-EVGAATGAVVGGVAGQLFGKGSGRVS-------MAIGGAVLGGLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH STREET: 301 No. 5369025th Washington Street CITY: Falls Church
                  ADDRESSEE: Curum, Amprest: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 241-13
TELEFAX: (703) 241-2848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Murphy Jr., Gerald REGISTRATION NUMBER: 28,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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37; Conserv
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New York
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                                                                                                                                             Paoletti, Enzo
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25.98;
                                                                               NUCLEOTIDE AND AMINO ACID SEQUENCES OF CANINE HERPESVIRUS gB, gC AND gD AND USES THEREFOR 91
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RESULT 13
US-08-413-118-6
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FRAGMENT TYPE:
US-08-220-151-6
                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08413118 Patent No. 5688920 GENERAL INFORMATION:
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIO Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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      PRIOR
                                                                                                                                                                                                    APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: CHOICEOTI
TITLE OF INVENTION: CANINE HI
NUMBER OF SEQUENCES: 128
                                                                                                                                                                                                                                                                                                        APPLICANT: PAOLETTI, ENZO
APPLICANT: LIMBACH, KEITH
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TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 6:
                CLASSIFICATION:
                                 FILING DATE:
                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     873 QQEHKARKKNSGPALLASRVGAMATRRRHYQRLESED 909
                                                                                                                                                         COUNTRY: UZIP: 10036
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LENGTH: 913 amino acid
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NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 GQVTRWRNPDTGNSYSVEPV-----RTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,151
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTROBUEV A-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 VFLVGCAQNF-SRQEVGAATGAVVGGVAGQLFGKGSGRVS------MAIGGAVLGGLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: amino acid
STRANDEDNESS: single
APPLICATION DATA:
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                                                                                                                                                                                    NEW YORK
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                                                                                                                                                              UNITED STATES OF AMERICA
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N-terminal
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                                      US/08/413,118
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; Pred. No. 7.4;
18; Mismatches
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RESULT 14
US-08-473-446-6
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; FRAGMENT TYPE: N-terminal
US-08-413-118-6
   INFORMATION FOR SEQ
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ZIP: 10036

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: IBM PC COMPATIBLE

TOMPUTER: PC-DOS/MS-DOS

TOP-BASE #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08473446
Patent No. 6017542
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Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                          NAME: FROMMER, WILLIAM S.
REGISTATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45,4
TELECOMMUNICATION INFORMATION.
TELEPHONE: (212) 840-3333
                                                                                                                                  CLASSIE LULL PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
08/413,118
                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,446
                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD,
STREET: 530 FIFTH AVENUE, 25TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PAOLETTI, ENZO
APPLICANT: LIMBACH, KEITH J.
                                                                                                 NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                STREET: 530 FI
CITY: NEW YORK
STATE: NEW YOR
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                              NEW YORK
                   (212)
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840-0712
ID NO: (
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RESULT 15
US-09-232-468A-2
US-09-232-468A
Sequence 2, Application US/09232468A
Patent No. 6207165
GENERAL INFORMATION:
APPLICANT: AUDONNET et al.
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
FILE REFERENCE: 454313-2230
CURRENT APPLICATION NUMBER: US/09/232,468A
CURRENT FILING DATE: 1999-01-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 913
TYPE: PRT
ORGANISM: Pseudorables virus
US-09-232-468A-2
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; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-473-446-6
Search completed: October 27, 2002, 11:00:28 Job time : 9.34197 secs
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.0%; Score 74.5; DB 4; Length 913; Best Local Similarity 23.6%; Pred. No. 7.4; Matches 37; Conservative 18; Mismatches 51; Indels 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               873 QQEHKARKKNSGPALLASRVGAMATRRRHYQRLESED 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          813 AAFLAYRHISRLRRNPMKALYPVTTKTLKEDGVDEGDVDEAKLDQARDMIRYMSIVSALE 872
                                                                                                873 QQEHKARKKNSGPALLASRVGAMATRRRHYQRLESED 909
                                                                                                                                                                                           813 AAFLAYRHISRLRRNPMKALYPVTTKTLKEDGVDEGDVDEAKLDQARDMIRYMSIVSALE 872
                                                                                                                                                                                                                                                                                    753 VLLRGIANFFQGLGDVGAAVGKVVLGATGAVISAVGGMVSFLSNPFGALAIGLLVLAGLV 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      753 VLLRGIANFFQGLGDVGAAVGKVVLGATGAVISAVGGMVSFLSNPFGALAIGLLVLAGLV 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 GOVTRWRNPDTGNSYSVEPV-----RTYORYNKOE 120
                                                                                                                                                                                                                                     66 GSKI-----A 90
                                                                                                                                                                                                                                                                                                                15 VFLVGCAQNF-SRQEVGAATGAVVGGVAGQLFGKGSGRVS-------MAIGGAVLGGLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 GSKI-----A 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 VFLVGCAQNF-SRQEVGAATGAVVGGVAGQLFGKGSGRVS-------MAIGGAVLGGLI 65
                                                                                                                                          91 GQVTRWRNPDTGNSYSVEPV-----RTYQRYNKQE 120
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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length: 2000000000
                                                                                                                                                                                                                                  Query
Match
                                                                                                                                                                                                                                                                                                                               is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    October 27, 2002, 10:55:57; Search time 21.6891 Seconds (without alignments) 824.509 Million cell updates/sec
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100.0
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13.3
12.3
12.3
12.3
112.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A_Geneseq_032802:*

1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1985.DAT:*

8: /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1986.DAT:*

9: /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1988.DAT:*

9: /SIDS1/gcgdata/geneseg/geneseqp-embl/AA1988.DAT:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                      //SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT: *
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                                                                                                                                                                                                                                      Length
  161
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AAB81128
AAG78025
AAB81126
AAB81130
AAB20105
AAB20105
AAY34362
AAR03434362
AAR034362611
                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                             Optimised OspA pro
C17E2 OspA constru
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OspA antigen amino
OspA B-cell epitop
Moraxella catarrha
Porphorymonas ging Porphorymonas ging Porphorymonas ging PBOMP-2 gene prod.
Novel human diagno Spider recombinant
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9.2					9.3						9.3			٠	٠		9.3			9.4	9.4	9.4	9.6	9.7	٠	9.7	9.7		٠		10.1	10.4	10.5
2516	2599	551	285	285	285	223	514	354	302	285	285	285	285	255	255	255	255	102	718	718	718	651	618	542	542	542	666	2017	423	116	1251	2309	147
17	21	21	22	21	21	21	22	22	22	22	22	21	20	22	22	22	21	22	21	19	12	20	21	22	22	22	22	22	22	19	22	22	
AAW01875	AAY75098	AAY52398	328	AAY73440	AAY87280	AAB57121	S.	AAU19445	AAM40157	AAM39011	AAU29025	AAB44244	AAY41688	AAY72020	AAB70769	AAB74199	AAB11398	AAM41943	AAY59070	AAW53346	AAR1,4308	AAY40097	AAB56803	ABB70501	ABB65791	ABB65790	2	ABG06301	AAB30695	AAY11028	ABB61254	623	ABB69847
Neuronal invertebr	Neisseria meningit	Human keratin KERT	Human protein HP10	ä.	Human signal pepti	Human prostate can	Pseudomonas aerugi	Human diagnostic a	Human polypeptide	Human polypeptide	こ	Human PRO284 (UNQ2	Human PRO284 prote	E. carotovora PelB	Expression plasmid	PelB-scFvOxazolon	E. coli expression	m	N. clavipes spider	Nephila clavipes s	pes d	Spider silk protei	C.			melano	=	Novel human diagno	A fusion of anti-C	ORF 01c	la	Drosophila melanog	Drosophila melanog

ALIGNMENTS

RESULT 1 AAB81127

vaccine; SRS.

Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease;

Optimised OspA protein 17E2 amino acid sequence.

11-JUL-2001 (first entry)

AAB81127;

AAB81127 standard; Protein; 161

Å

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Key
Region
Kay WW,
         (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                17-MAR-2001.
                                                          CA2281913-A1
                                                                                       Synthetic
                                                                                            Piscirickettsia salmonis.
                             17-SEP-1999;
                                       17-SEP-1999;
Burian J,
                              99CA-2281913
                                       99CA-2281913
                                                                   Location/Qualifiers
109..128
/label= B_cell_epitope
Kuzyk MA;
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RESULT 2
AAB81128
ID AAB8
XX AAB81128
AC AAB8
XX Poik
C17E
XX Poik
KW Poik
KW Vaccc
KW SRS;
OS Pisc
OS Synt
XX PN Regi
FT Regi
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Best Local !
                  17-SEP-1999;
                                                                             CA2281913-A1
                                                                                                                                                                                       Key
Region
                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                         Region
                                                                                                                                                                                                                                                                       Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease;
                                                                                                                                                                                                                                               Piscirickettsia
                                                                                                                                                                                                                                                                                                                          C17E2 OspA construct with N-terminal fusion partner
                                                                                                                                                                                                                                                                                                                                                                11-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB81128 standard; Protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of Pisalmonis specific antigen termed OspA, or an immunogenic fragment of particularly poikilothermic fish, against the bacterial pathogen pathogen method is also useful for protecting animals, rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents optimised P. salmonis OspA protein 17E2 (AAP66247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGGLIGSKIGOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161;
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DB; AAF86247.
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ilarity 100.0%;
Conservative (
                                                                        /label= C17E2_OspA
/note= "Product of OspA gene optimised for expression
Escherichia coli"
                                                                                                                                                   /label= Undefined_N-terminal_fusion_partner
96...256
                                                                                                                                                                                                                                              salmonis
                                                                                                                                                                                              Location/Qualifiers
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Pred. No. 3e-81;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 3
AAG78025
ID AAG7
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Best Local :
11-MAR-2000; 2000GB-0005838.
01-JUL-2000; 2000GB-0016080.
                                                                    12-MAR-2001; 2001WO-GB01055
                                                                                                                                      20-SEP-2001
                                                                                                                                                                                                                                                                                                    Piscirickettsia salmonis; septicaemia; SRS; surface
                                                                                                                                                                                       WO200168865-A2
                                                                                                                                                                                                                                   Piscirickettsia
                                                                                                                                                                                                                                                                                       septicaemia;
ATCC VR-1361
                                                                                                                                                                                                                                                                                                                                                                      Piscirickettsia salmonis polypeptide P10.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG78025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG78025 standard; Protein; T62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. Salmonis specific antigen termed OspA, or an immunogenic amount of a OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a P. salmonid construct optimised for expression in Escherichia coli, fused to an undefined N-terminal fusion partner. The fusion protein is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 MRCCLOGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGGLIGSKIGOSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161;
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                                                                                                                                                                                                                                   salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99CA-2281913
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                                                                                                                                                                                                                                                                                                    piscirickettsiosis; salmonid
antigen; vaccine; antibacter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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Pred. No. 5.4e-81;
Mismatches 0;
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                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                    antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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ial; fish;
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Best Local S
(KAYW/)
(BURI/)
(KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to nucleic acid sequences and the encoded protein of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity to protect fish against P. salmonis which causes piscirickettsiosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      surface antigen present on Pisciricketts protect fish against piscirickettsiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids encoding surface antigen present on
                                                                                                                                                                           CA2281913-A1
                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                     Piscirickettsia
                                                                                                                                                                                                                                                                                                                                         vaccine;
                                                                                                                                                                                                                                                                                                                                                          Poikilothermic
                                                                                                                                                                                                                                                                                                                                                                                           OspA antigen
                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB81126 standard;
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29-JUL-2000;
                                                                       17-SEP-1999;
                                                                                                          17-SEP-1999;
                                                                                                                                           17-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Fig 5;
) KAY W W.
) BURIAN J.
) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQUA HEALTH
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                                                                                                                                                                                                                                                                                                                                       OspA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                           amino acid sequence
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2000GB-0018599
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                        fish;
                                                                       99CA-2281913
                                                                                                                                                                                                                                                                                                                                         salmonid
                                                                                                          99CA-2281913
                                                                                                                                                                                                                                                                                     salmonis
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                                                                                                                                                                                                                                Location/Qualifiers
110..129
                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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nid rickettsial septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.0%;
                                                                                                                                                                                                                B_cell_epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162
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Pred. No. 2e-79;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                         pathogen;
al disease;
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RESULT 5
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Best Local :
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                                                                                                                                                                                                                           Poikilothermic praccine; Ospa; sess; antibody.
                       (KAYW/)
(BURI/)
(KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of ospA in the form of a vaccine. The method is used for protecting animal particularly poikilothermic fish, against the bacterial pathogen p. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRR) and other rickettsial diseases. The preses sequence represents P. salmonis ospA protein. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                          17-MAR-2001.
                                                                                                                                                                                                Piscirickettsia
                                                                                                                                                                                                                                                                                     OspA B-cell
                                                                                                                                                                                                                                                                                                                 11-JUL-2001
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                                                                                 17-SEP-1999;
                                                                                                              17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVAMAIGGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-316844/34
                                        BURIAN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF86246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                          KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burian
Burian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 AA;
                                                                                                                                                                                                                                                                                   epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                         fish; Pis
salmonid
                                                                                   99CA-2281913
                                                                                                              99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŗ
                                                                                                                                                                                                                                                                                                                                                                        Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuzyk
Kuzyk
                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.0%;
                                                                                                                                                                                                                                                       Piscirickettsia
                                                                                                                                                                                                                                           rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 815; DB 22; Pred. No. 2e-79; 1; Mismatches
                                                                                                                                                                                                                                                                                     #2
                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                         a salmonis; r
septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amount of a fragment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present
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0

2001-316844/34.

This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a particularly poikilothermic fish, against the bacterial pathogen of a particularly poikilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial septicaemia (SRS) and other rickettsial diseases. The presents an immunogenic epitope of the P. salmonis ospanic poitope of the P. salmonis ospanic protecting against salmonid protein. The peptide is used to raise rabbit anti-Ospa antibodies.

present

5.

Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -

Page 17; 35pp; English.

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The present sequence is that of BASB113 protein from Moraxella cattarrhalis strain Mc3931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adults. The invention provides BASB113 polypeptides, and polynucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB113 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB113 polypeptide, an immunogenic
                                                                                                         Claim 1; Page 67; 86pp; English.
                                                                                                                 New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                          Thonnard
                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                       25-JUN-1999;
                                                                                                                                                                                                                                                                                             23-JUN-2000;
                                                                                                                                                                                                                                                                                                                      04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                            WO200100836-A1
                                                                                                                                                                                                                                                                                                                                                                     BASB311; infection; otitis media; pneumonia; therapy; diagnosis; antibacterial; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                              Moraxella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB20105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB20105 standard; Protein; 224 AA.
                                                                                                                                                                                     2001-112458/12.
)B; AAF30043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVRTYQRYNKQERRQQYCRE
                                                                                                                                                                                                                                                                                                                                                               catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                  Catarrhalis BASB113 protein
                                                                                                                                                                                                                                                                                        2000WO-EP05851.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                  99GB-0015044.
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AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas ginglvalis (PG) polypeptide sequences given in AAX AAX34583. AAX31802 to AAX91989 represent PCR primers used in the

in AAY34318 in the

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Claim 1;

Page

469; 588pp;

English.

Antigenic Porphorymonas gingivalis peptides gingivitis

for preventing

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RESULT 7
AAY34487
                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1998;
05-MAY-1998;
22-MAY-1998;
                                                                          N-PSDB;
                                                                                                                                                                                        04-AUG-1998;
10-DEC-1997;
31-DEC-1997;
30-JAN-1998;
10-MAR-1998;
                                                                                                             Agius
                                                                                                                           (CSLC-) CSL LTD
                                                                                                                                             29-ЈИГ-1998;
                                                                                                                                                                                09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local ;
                                                                                                                                                                                                                                           10-DEC-1998;
                                                                                                                                                                                                                                                            17-JUN-1999
                                                                                                                                                                                                                                                                             W09929870-A1
                                                                                                                                                                                                                                                                                             Porphorymonas
                                                                                                                                                                                                                                                                                                                                 Porphorymonas gingivalis protein PG3.
                                                                                                                                                                                                                                                                                                                                                         25-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                            AAY34487;
                                                                                                                                                                                                                                                                                                                                                                                     AAY34487 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment of a BASB113 polypeptide, or a polypeptide having at least 85% amino acid sequence identity to BASB113, or comprising a diagnosing a Moraxella infection involves identifying a BASB113 polypeptide or antibody. A claimed therapettic composition useful antibody directed against a BASB113 in treating humans with M. catarrhalis infection comprises at least polypeptides also have utility in raising specific antibodies, and in screening for antibacterial drugs.
                                                                      1999-385613/32.
DB; AAX91705.
                                                                                                    S CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         59 -----AVLGGLIGSKIGOSMDOODKIKLNOSLEKVKAGOVTRWRNPDTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                        EKTGRDAILGAAVGAAAGAYNERQAK----OIEQQMQGTGVTVTHDTDTGN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVVLLASSMALAGCANTGT----TGNGTGFGGANVNKAVIGAVAGAL---GGTAISKATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSSLIIISVELVGCAQNESRQEVGAATG-----AVVGGVAGQLEGKGSGRVSMAIGG
                                                                                               Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                            monas gingivalis; PG; periodontal disease;
antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                 98AU-0001546.
98AU-0002264.
98AU-0002911.
98AU-0003128.
98AU-0003338.
98AU-0003654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 AA;
                                                                                                                                                                                                                                                                                          gingivalis
                                                                                                                                             98AU-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                     97AU-0000839
97AU-0001182
                                                                                                                                                                                                                                       98WO-AU01023
                                                                                                                                          -0004917
                                                                                              Hocking DI
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%;
                                                                                                      DM,
                                                                                                                                                                                                                                                                                                                                                                                      223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 111;
Pred. No. 0.
                                                                                                  Margetts MB,
                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
                                                                                               Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                                           gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
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Вb Š

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109 PVRTYQRYNKQERRQQYCRE 128

Conservative

0;

100.0%; 13.5%;

Score 112; Pred. No. Mismatches

; DB 22; . 3.3e-05; ches 0;

Indels Length 20;

0, Gaps

0;

Query Match Best Local Similarity

Matches

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RESULT 8
AAY34362
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Best Local S
Matches 25
                                                                                                                                                                                                                                                          30-JAN-1998;
10-MAR-1998;
09-APR-1998;
23-APR-1998;
                                                                                                                                                                                                                           05-MAY-1998;
22-MAY-1998;
29-JUL-1998;
AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX94318 to AAX91802 to AAX91899 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can
                                                                                                                                                                      Agius
Ross I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
                                                                               Claim 1; Page 325-326;
                                                                                                     gingivitis
                                                                                                              Antigenic Porphorymonas gingivalis
                                                                                                                                     N-PSDB;
                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                       10-DEC-1997;
31-DEC-1997;
                                                                                                                                                                                                                                                                                                                             04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                    Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY34362 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                W09929870-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porphorymonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY34362;
                                                                                                                                                                                                       (CSLC-) CSL
                                                                                                                                                                                                                                                                                                                                                    10-DEC-1998;
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                                                                                                                                                                      S CT,
BC,
                                                                                                                                    1999-385613/32.
DB; AAX91580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSLITISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSM-AIGGAVLGGLIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASVLAVALVFAGCGLN--NMAKGGLIGAGVGGAIGAGVGNVAGNTAVGAIVGTAVGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         monas gingivalis;
antigenic.
                                                                                                                                                                     Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
                                                                                                                                                                                                       LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                    gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gingivalis protein PG3
                                                                                                                                                                                                                           97AU-0000839.
97AU-0001182.
98AU-0001264.
98AU-0002911.
98AU-0003128.
98AU-0003128.
98AU-0003338.
98AU-00034917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%;
                                                                                                                                                                      Hocking Dr
Webb EA;
                                                                             588pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 102.5; DB 20 Pred. No. 0.0079; 3; Mismatches 31;
                                                                                                                                                                                DΜ,
                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     periodontal disease;
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                                                                                                                                                                               Margetts
                                                                                                               peptides
                                                                                                                                                                                 MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                               for
                                                                                                               preventing
                                                                                                                                                                                 Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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20

29

VGAATGAVVGGVAGQLEGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL

Query Match Best Local

Similarity

12.1%;

Score 101; DB Pred. No. 0.00 9; Mismatches

DB 11; .0071; es 23;

Indels

Gaps

0;

0;

Length 154;

Conservative

Matches

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RESULT 9
AAR05799
  В
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Best Local
                                       The PBOMP proteins were isolated from a PBOMP-enriched insoluble cell wall fraction from physically disrupted cells of H. influenzae and then solubilising the PBOMP from the cell wall fraction by heating in the presence of a detergent or digesting the cell wall fraction with lysozyme, opt. in the presence of a detergent. The genes encoding the PBOMP proteins were isolated by screening a DNA library with an oligonucleotide probe based on the amino acid sequence of the PBOMP protein, or using antibodies to PBOMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
                                                                                                                                                                                                                                                                                                                                   Outer membrane protein epitopes of Haemophilus the prodn. of antibodies, in vaccines and for productions of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the production of the producti
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anilionis A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-1988;
21-AUG-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR05799
                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-1989;
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  154
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                                                                                                                                                                                                                                                                Fig 15; 164pp;
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89US-0396572.
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34.7%;
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                                                                                                                                                                                                                                                                English.
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polynucleotides are also used in diagnostics as expressed sequence tags (CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or impartitating a polypeptide in tissue, as molecular weight markers and as consisted and polynucleotide sequences are useful in medical continuity of sites expressing (II). (I) and (II) are useful in medical continuity of sites expressing (II). (I) and (II) are useful in medical continuity of the polypeptide and polynucleotide sequences have applications in the produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent normal mutations continuity and sequence data for this patent did not appear in the printed context of the sequence data for this patent did not appear in the printed context of the sequence of the invention.
                                                                                                                               Query Match
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                       12 IISVELVGCAQNESR-----QEVGAATGAVVGGVAGQLEGKG--SGRVSMAIGGAVLGGL 64
                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID No 46265; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                      IISILPAKVAVDNSONKRNAQAFGALIGAVAGGVIGHNVGSGSNSGTTAGAVGGGAVGAA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #15897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 VGTLGGGALGGIAGSTIGGGRGQAIAAVVGAIGGAIAGSKIEEKMSQVNGAEL
                                                                                                               Similarity
                                                                                                                                                            309
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                                                                                                           11.48;
33.08;
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Pred. No. 0.07
12; Mismatches
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                                                                                     DB 22; ;
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nes 39;
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RESULT 11
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Recovering structural polypeptides in a biological sample, useful purifying and spinning spider silks and other structural proteins, comprises treating the sample containing the polypeptides with an
                                                                                        WPI; 2001-483136/52.
                                                                                                                                                                   (BUTL/)
                                                                                                                                                                                 (ARCI/)
                                                                                                                                                                                                                  20-JAN-2000; 2000US-0490291.
                                                                                                                                                                                                                                            01-NOV-2000; 2000WO-US30086
                                                                                                                                                                                             (MELL/)
                                                                                                                                                                                                                                                                                                         WO200153333-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nephila clavipes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spider; orb-weaver; silk protein; pETNcDS; structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spider recombinant silk protein pETNcDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2001 (first entry)
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                                                                                                                                               BUTLER M M.
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                                                                                                                                                                        ARCIDIACONO S.
                                                                                                                                                                                             MELLO C M.
                                                                                                                   Arcidiacono s,
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                                                                                                                   Butler
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Claim 2; Page 41-42; 49pp; English.

acid for

The present sequence is that of the orb-weaver spider (Nephila Clavipes) recombinant silk protein pETNoDS. The invention Structural proteins. Organic acids are used to lyse recombinant CC cells or other biological samples (such as non-recombinant) proteins. Organic acids are used to lyse recombinant CC derived cells), and enrich the purity and yields of structural proteins intact. In the case of silk proteins, the structural proteins intact. In the case of silk proteins, the chromatography and processed into an aqueous-based mixture for CC into metography and processed into an aqueous-based mixture for CC into vector pET24 for recombinant expression in Escherichia coli, CC containing denaturant (3 M guanidine-HCl) and by affinity content organic or not in such protein was obtained using formic acid methods of the invention can be used in the construction of many combinant protection, parachutes and parachute cords. The new CC method has the following advantages over prior art: it involves contents, requires less time and smaller volumes of reagents,

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RESULT 12
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Matches 36
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Best Local S
Matches 23
                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental blology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                      The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 36333;
                                                                                                                                                                                                                                                                            New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila;
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                                                                                        Sequence
                                                                                                                                                       insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                    (PEKE
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                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
QEVGAATGAVVGGVAGQ--LFGKGSGRVSMAIGGAVLGGLIGSKIGQ
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                                                                                                                                                                                                                                                                                                                                               JC,
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                                                       Similarity
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                                            18;
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                                          Score 87.5; D
Pred. No. 0.19
18; Mismatches
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Pred. No.
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                                             39;
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RESULT 13
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                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIGITA), expressed DNA sequences (ABLIGITA) and the encoded proteins (ABBIGITA).
                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published pct sequences
                                                2124
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 25488; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
N-PSDB; ABL10335.
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11-JUL-2000;
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2179 GSVGQS----GGGGQGRYPTPIQRPNNYPQHP----QQQQQQQQQQQQQQQQREQAAAAAVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY.
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                        79 IKLNQSLEKVKAGQVTRWRNP-DTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAG
                                                                        22 QNFSRQEVGAATGA---VVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDK 78
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                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanogaster
                                                                                                                                                2309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developmental biology;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams
                                                                                                Conservative
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2000US-0614150
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                                                                                                            10.4%;
27.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                   PWD,
                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                             18;
                                                                                                            Score 86.5;
Pred. No. 8
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IJ
                                                                                                                        DВ
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                                                                                                55;
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                                                                                                 Indels
                                                                                                                       Length 2309;
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                                                                                                                                                                                                                                                                                              reagent
                                                                                                                                                                                                                                                                      invention alling and
                                                                                               Gaps
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Db Qy

2231 QRAQ

2234

138 QKQE 141

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Best Local
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ABB61254
           1023 QKKPRYFVAMFDYDP
                                                             119
                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                        972
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                             915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capable of detecting 1000 or more genes from Drosophila. The inventuation in developmental biology and in elucidating cell signalling insecticides, therapeutics and pharmaceutical drugs. The inventuations of the development of discloses genomic DNA sequences (ABLI18176-ABL180511), expressed DNA ABRITTTT-ABRTTTT-ABRTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRTTT-ABRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences (ABL01840 (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 10554; 21pp + Sequence Listing; English.
                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                    1 MRGCLOGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 10554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB61254 standard; Protein; 1251
                                     QERROQYCREFOQKAMIAGQKQEIYGTACPQPDG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB61254;
                                                                    PGQMMGPRGPLNQQQQQQQQQQQQQQQQQQQQQQQQQQQQQPG----QQAQPG-----QPGQPGQMPGA 1022
                                                                                                               LGGLIGSK--IGOSMDOODKIKLNOSLEKVKAGOVTEWRNPDTGNSYSVEPVRTYORYNK 118
                                                                                                                                                            МОСОМОСОМОСОМЕСТ---QMPGQMPGQMPGQMAGQMAGQMPGQMPGQMPGQMPGQMSGQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-656860/75.
DB; ABL05357.
                                                                                                                                                                                                                                                                       Similarity 22.7
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                 1251 AA;
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2000US-0614150.
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                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                             Score 84; DB;
Pred. No. 7.1;
28; Mismatches
-STMSPNPDG 1046
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7.1;
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                                                                                                                                                                                                                                                             67;
                                                                                                                                                                                                                                                                                                 Length 1251;
                                                                                                                                                                                                                                                        Indels
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Matches 31
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AAY11028
                                                                                                                                                                                              are disclosed, together with the nucleic acids encoding them. In all, cytoplasmic proteins, secreted proteins or other cellular proteins, vaccines containing the nucleic acids or proteins are claimed, as are probes containing the nucleic acids or proteins are claimed, as are sequences. The vaccines are useful for treating or reducing the risk of detecting the process of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                        Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all,
                                                                                                                                                                                                                                                                                                                                                Claims 37, 41; Page 190-191; 339pp; English.
                                                   83
                                                                                                                                                                                                                                                                                                                                                                       New isolated Helicobacter pylori nucleic acids - use products for the diagnosis, prevention and treatment H. pylori and other Helicobacter species
                                                         61 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-1997;
05-DEC-1996;
25-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-333051/29.
N-PSDB; AAX30557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alm RA,
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secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H. pylori ORF 01cp20708_10628177_c2_50 secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY11028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY11028 standard; Protein; 116 AA.
                                                                                                      MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                        -GGYIGSEVGDRV--EDYIRGVDREPQNKEPQTPR-
                                                                                MSGLRTFSCVVVLCGAMVNVAVAGPKIEARGELGKFVGGAVGNFVGDKMGGF---VGGAI 67
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Castriotta
                                                                                                                                                                                         116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe; diagnostic; ORF; cell envelope protein;
protein; cytoplasmic protein; cellular protein
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0823745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0891928
96US-0759625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US22104
            27,
                                                                                                                                                   10.0%; 26.7%;
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                                                                                                                                          16;
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                                                                                                                                   Score 83; DB 19;
Pred. No. 0.42;
6; Mismatches 51
        10:57:56
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kabok Z,
                                                                                                                                     51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith
                                                                                                                                                         Length 116;
                                                                                                                                  Indels
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 27, 2002, 11:00:01; Search time 18.0743 Seconds (without alignments) 1540.986 Million cell updates/sec

MRGCLQGSSLIIISVFLVGC.....IYGTACPQPDGRWQVISTEK 161

US-09-677-374-4 832 1 MRGCLQGSSLIIIS

Title: Perfect score:

Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 562222 seqs, 172994929 residues

562222

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_archea:*
sp_bacteria:*

sp_organelle:*
sp_phage:* sp_mammal: * sp_mhc:*

sp_plant:*
sp_rodent:*
sp_virus:*

sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	_	Result
127.5	137	139	216.5	235.5	236.5	236.5	239	244	251.5	251.5	252.5	258.5	283	303.5	815	Score
15.3	16.5	16.7	26.0	28.3	28.4	28.4	28.7	29.3	30.2	30.2	30.3	31.1	34.0	36.5	98.0	Query Match
182	199	77	105	131	131	131	151	154	144	137	144	137	159	148	162	Length
16	16	N	N	N	N	N	N	N	N	N	N	N	N	2	2	DB
Q9HXI3	Q985G4	Q9AGC7	031208	Q9L522	Q52637	Q9F0Q1	Q9F9Q9	Q53154	Q9K4W8	031065	Q9K2N6	052252	Q9F9F2	054381	Q9F9K8	ID
Q9hxi3 pseudomonas	Q985g4 rhizobium l	Q9agc7 rickettsia	O31208 rickettsia	Q91522 rickettsia	Q52637 rickettsia		Q9f9q9 rickettsia		Q9k4w8 male-killin	O31065 rickettsia	Q9k2n6 male-killin	O52252 rickettsia		O54381 rickettsia	Q9f9k8 pisciricket	Description

ć	5	44	43	42	41	40	39	38	37	36	35	34	<u>ω</u>	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
	2 78	87.5	88	89.5	90	91	93	93.5	94	95	95.5	97	97	98	99	99.5	99.5	100.5	100.5	102.5	104	105	106.5	108.5	108.5	109	109	111.5	120.5
	10 4	10.5	10.6	10.8	10.8	10.9	11.2	11.2	11.3	11.4	11.5	11.7	11.7	11.8	11.9	12.0	12.0	12.1	12.1	12.3	12.5	12.6		13.0	13.0	13.1	13.1	13.4	14.5
3	90	147	544	242	137	105	105	838	809	172	79	223	220	154	332	304	83	257	153	223	139	155	155	221	155	257	232	154	136
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	DOMMBO	09VS43	046171	Q9PGD9	Q9HU07	Q983Y0	Q98P93	Q9AL49	Q9SUX1	P76572	Q92NT4	Q9KSR1	Q9XAX8	Q9CN83	Q9A9X2	Q91762	Q92LP2	Q9A8M8	069776	Q9XCA4	Q52854	Q9RB08	Q9RA95	Q92ST9	Q9F6B1	Q9PGX0	Q9A3X8	Q914S1	Q92R89
Kollado Pocacononas	Oghwan naeudomonae	drosoph	_			Q983y0 rhizobium l	Q98p93 rhizobium l		Q9sux1 arabidopsis	P76572 escherichia	Q92nt4 rhizobium m	Q9ksrl vibrio chol	~	Q9cn83 pasteurella		Q9i762 pseudomonas		Q9a8m8 caulobacter	-				Q9ra95 serratia sp	Q92st9 rhizobium m	Q9f6b1 edwardsiell	Q9pgx0 xylella fas		Q9i4s1 pseudomonas	Q92r89 rhizobium m

ALIGNMENTS

Фр	Qy Db	Qy	Query Best Matc	SQ	DR.	RT	RT	RA	RC	RP	RN	o _x	8	8	SO	GN	DE	DT	DT	DT	AC	ΙĐ	RESULT Q9F9K8
122 RQQYCREFQQKAMIAGQKOEIYGTACPQPDGRWQVISTEK 161 	62 GGLIGSKIGOSMDOODKIKLNOSLEKVKAGOVTRWRNPDTGNSYSVEPVRTYORYNKOER 121 	2 RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 61	Query Match 98.0%; Score 815; DB 2; Length 162; Best Local Similarity 98.8%; Pred. No. 1.5e-65; Matches 158; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64;	Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL: AF184152; AAG17000.1;	salmonid pathogen Piscirickettsia salmonis.";	"Identification of a genus-common Rickettsial surface antigen in the	Kuzyk M.A., Burian J., Thornton J.C., Kay W.W.;	STRAIN=LF-89;	SEQUENCE FROM N.A.		NCBI TaxID=1238:	Piscirickettsia.	Bacteria; Proteobacteria; gamma subdivision; Piscirickettsia group;	Piscirickettsia salmonis.	OSPA.	17 KDA ANTIGEN.	EMBLrel. 16, Last	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	(TrEMBLrel.	Q9F9K8;	Q9F9K8 PRELIMINARY; PRT; 162 AA.	Л 1 (8

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RESULT
Q9PPF2
ID Q9P
AC Q9
DT Q1
DT Q1
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Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AA628455.1; -
SEQUENCE 159 AA; 16497 MW; 34C5B020AF470A1F (
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MEDLINB=21217364; PubMed=11321078;
BOUYEr D.H., Stenos J., Crocquet-Valdes P., Moror
Zavala-Velazquez J.E., Foil L.D., Stothard D.R.,
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Q9F9F2;
01-MAR-2001 (TrEMBLrel 16, Created)
01-MAR-2001 (TrEMBLrel 16, Last seq
01-DEC-2001 (TrEMBLrel 19, Last ann
17 KDA GENUS COMMON ANTIGEN
                                                                                                                                                                                                                                                    "Rickettsia felis: molecular characterization of
                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia felis (Rickettsia azadi).
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                     8 SSLIIISV---FLVGC--AQNESRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
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Bacteria; Proteobacteria; alpha subdivision;
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17 KDA COMMOI
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SKIMITALAASMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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                                                                                    Score 283; DB 2; I
Pred. No. 6.9e-18;
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Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,

Schulenburg H.J.G.V.D., Majerus M.E.N.;

Bertrand D., Hurst G.D.D., Majerus M.E.N.;

Ton the evolution of male-killing: Monophyletic origin and horizontal generic ladybirds, Adalia bipunctata L. and A. decempunctata L.

[Coleoptera: Coccinellidae]."
                                                                                                                                               Q9K2N;
Q9K2N;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)
Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)
Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)
MARIGEN (17 KDA ANTIGEN) (FRAGMENT)
MAIL RICKETTSIA From Adalia bipunctata.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiaae; Rickettsia.
NON_TER
       Q9K2N6
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"Molecular characterization of a novel spotted fever group rickettsial species from Ixodes scapularis in Texas.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF031534; AAB95267.1; -.
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Rickettsiaceae; Rickettsieae;
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eae; Rickettsia.
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Pred. No. 9e-16;
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RESULT
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Best Local S
Matches 52
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Best Local
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Q9K4W8;
Q9K4W8;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AFO
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Rickettsia honei sp. nov., the aetiological spotted fever in Australia."; Int. J. Syst. Bacteriol. 48:1399-1404(1998). EMBL; AF027124; AAB81846.1; -. EMBL; AF060706; AAD20231.1; -. EMBL; AF060704; AAD202330.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99045882; PubMed=9828442; Stenos J., Roux V., Walker D., Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsia honei
                                                                                                                                                        124
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                                                                                                                                                      QKAYGNACRQPD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEIYGTACPQPD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I
                                                                                                                                                                                        QEIYGTACPQPD 151
                                                                                                                                                                                                                         TSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ
                                                                                                                                                                                                                                                       KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK
                                                                                                                                                                                                                                                                                           NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OKAYGNACROPD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSQRALEAAPSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL
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39.4%; Pred. No. 3.36
ive 24; Mismatches
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19,
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he EMBL/GenBank/DDBJ
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Created)
Last sequence up
Last annotation
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Pred. No. 3.8e
24; Mismatches
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the aetiological agent
                                                                     PRT;
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hes 45;
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MEDLINE=3084757; PubMed=1452600,
Baird R.W., Lloyd M., Stenos J., Ross B.C., Ste
Baird R.W., Lloyd M., Stenos J., Ross B.C., Ste
Baird R.W., Lloyd M., Stenos J., Ross B.C., Ste
Baird R.W., Lloyd M., Stenos J., Ross B.C., Ste
Baird R.W., Lloyd M., Stenos J., Ross B.C., Ste
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Baird R.W., Lloyd M., Stenos J., Ross B.C., Ste
Baird R.W., Lloyd M., Stenos J., Ross B.C., Ste
Baird R.W., Lloyd M., Stenos J., Ross B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C., Stenos B.C
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01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-NOY-1998 (TrEMBLrel. 08, Last annotation updat
(CLONE PRB FISF 1), 5' END CDS (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20575219; PubMed=11133455;
Schulenburg H.J.G. V.D., Habig M., Sloggett J.J., Webberley M.K.,
Bertrand D., Huzst G.D.D., Majerus M.E.N.;
"Incidence of male-killing Rickettsia spp. (alpha-Proteobacteria)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 KDA ANTIGEN (FRAGMENT).
male-killing Rickettsia from Adalia decempunctata
Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsiaee; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsiaceae;
NCBI_TaxID=789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q53154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Ten-Spot Ladybird Beetle Adalia decempunctata Coccinellidae).";
Appl. Environ. Microbiol. 67:270-277(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia sp.
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                 118
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                                                                                                                    G
                                                                                                                                                      8
KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR
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                                                 GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGSYGYVTPNKTYRNST
                                                                                                                                                  SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEIYGTACPQPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL
                                                                                   GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                    SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSQRALEAAPSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ
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                                                                                                                                                                                        55; Conserv
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52; Conserv
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha subdivision;
eae; Rickettsia.
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                                                                                                                                                                                        31;
                                                                                                                                                                                    Score 244; DB 2;
Pred. No. 2.1e-14;
1; Mismatches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9F001 PRELIMINARY; PRT; 131 AA.

109F001; (TrembLrel. 16, Created)
101-MAR-2001 (TrembLrel. 16, Last sequence update)
17 KDA PROTEIN (FRAGMENT).
Rickettsia sp. California 2.
Bacteria, Proteobacteria; alpha subdivision; Rickettsiales;
       -y,
                                                                                                                                                                                                                                                                                Raoult D.;
"A new SPG rickettsia isolated from fleas.";
"A new SPG rickettsia isolated from fleas.";
"Chaitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CALIFORNIA 2;
                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
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SEQUENCE
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Q9F9Q9;
01-MAR-2001
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WALLSSON K., Pahlson C.;
"Novel peptide diagnostic reagent and rickettsiosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nilsson K.,
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                                               49;
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                                                                                                                                 131
131
                                        Conservative
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(TrembLrel 16, Last ann
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                                                                                                           131
13374 MW;
                            28.4%; Score 236.5;
38.3%; Pred. No. 8e-
Live 24; Mismatche
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35.9%;
                            Pred. No. 8e-
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Pred. No. 5.7e-14;
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                                               8e-14;
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                                                           DB 2; Length 131;
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131 AA;
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O91522 PRELIMINAKK;
O91522;
O1-OCT-2000 (TrEMBLrel 15, Created)
O1-OCT-2000 (TrEMBLrel 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel 19, Last annotation update)
17 KDA SURFACE ANTIGEN (FRACMENT).
             MEDLINE=21091941; PubMed=11157215; Simser J.A., Palmer A.T., Munderlo
                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID-47589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beetle (Adalia bipunctata).",
J. Bacteriol. 176:388-394(1994).
EMBL: U04162; AAA19235.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-94117373; PubMed-8288533; Werren J.H., Hurst G.D., Zhang W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Rickettsial relative associated with male
                                                                                                                                                                                                                                                                                                                                                             69 TSORALBAADSGSNVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTOTVVIGGKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                            10 NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                            69 TSQRALEATPSGTSVEWRNPDNGNHGYVTPNKTY----RNSTGQYCREYTQTVVIGGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL
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 Palmer A.T., Munderloh
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Pred. No. 8e-
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Kurtti
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Matches 46
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Best Local :
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                                   Q9AGC7
Q9AGC7;
Q9AGC7;
O1-JUN-2001 (TrEMBLrel. 17, C)
O1-JUN-2001 (TrEMBLrel. 17, L)
O1-JUN-2001 (TrEMBLrel. 17, L)
17 KDA ANTIGEN (FRAGMENT).
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Rickettsia sp. 'La Copita',
Bacteria; Proteobacteria; alpha subdivision;
Bacteria; Rickettsiaee; Rickettsia.
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Appl. Er
EMBL; AF
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EMBL; AF033499; AAB86943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsiaceae; Rickettsieae; NCBI_TaxID=69475;
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01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-LA COPITA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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  Bacteria; Proteobacteria;
                         Rickettsia typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                        42 GQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWR
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                                                                                                                                                                                                                                                                                                                                                                  GQLVGVGV-----
                                                                                                                                                                                                                                                                                                                 NPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIYGTACPQPD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OKAYGNAC
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AF260571; AAF69012.1; -.
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105 AA;
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 19, Last annotation updat
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; 13413 MW;
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  alpha subdivision;
                                                                                                                                                                                                                                                                         -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPD
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                                                               Created)
Last sequence up
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Pred. No. 3.7e-12;
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Pred. No. 9.8e-14;
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  Rickettsiales;
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Paspallaris V., Liedtke B., Vitetta L., Whiting J.L.;

"Rickettsia typhus and Rickettsia felis rickettsioses in
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF336794; AAK21272.1; -.

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Complete
SEQUENCE
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                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-MARF303099;
MEDLINE-Z1082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., A.
                                                                                                                                                                                                              "Complete genome structure of the nitrogen-fixing Mesorhizobium loti."; DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                        Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=381;
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NCBI_TaxID=785;
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completed: October ne : 18.0743 secs
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P30430 ascherichia
P10837 sacharomyc
O66867 aquifex acov
Q92158 rattus norv
P344601 mus musculu
P34309 caenorhabdi
P13135 bos taurus
P13645 homo sapien
P30656 escherichia
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77.5 9.3 359 1 ATPA_BOVIN 77.5 9.3 467 1 HEMI_MYCLE 77.5 9.3 543 1 ATPA_RAT 77.5 9.3 553 1 ATPA_HUMAN 77.9 9.3 256 1 CANS_RABIT 76.5 9.2 553 1 ATPA_MOUSE 76.5 9.2 553 1 ATPA_MOUSE 76.5 9.2 553 1 ATPA_MOUSE 76.5 9.2 553 1 KICJ_MOUSE 76.5 9.2 727 1 FEXH_HUMAN 76.5 9.2 747 1 ELS_BOVIN 76.5 9.2 2516 1 CCAD_DROME 76 9.1 526 1 VP5_BTV10
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ALIGNMENTS

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Query Match 34.6%; Score 288; DB 1; Length 159; Best Local Similarity 37.9%; Pred. No. 3.1e-18; Matches 61; Conservative 32; Mismatches 52; Indels 1	EMBL: M28482; AAA26378.1; ALT_S EMBL; AJ235273; CAA15258.1; - PIR; D33971. D33971. PROSITE: PS00013; PROKAR_LIPOPR Outer membrane; Lipoprotein; An SIGNAL 1 19 CHAIN 20 159 LIPID 20 20 17 LIPID 20 20 N- SEQUENCE 159 AA; 16672 MW;	This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are use by non-profit institutions as long as its modified and this statement is not removed. Usage entitles requires a license agreement (See http://or send an email to license@isb-sib.ch).	SEQUENCE FROM N.A. STRAIN-MADRID E; MEDLINE-99039499; PubMed-9823893; Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alamark U.C.M., Podowski R.M., Naeslund Eriksson AS., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin mitochondria." Nature 396:133-140(1998) SUBCELLULAR LOCATION: Attached to the outer membrane by anchor (Probable).		SUL KD_
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Furuya Y., Katayama T., Yoshida Y., Kaiho I.;
"Specific amplification of Rickettsia Japonica DNA from clinical specimens by PCR.";
J. Clin. Microbiol. 33:487-489(1995).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsia japonica.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiaae; Rickettsia.
NCBI_TaxID-35790;
                                                                                                                                    KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 158
                                                                                                       -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
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Lipoprotein; Antigen; Signal.

1 19 19 87 SIMLARITY
20 159 17 KDA SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PROBABLE).
21 159 AA; 16554 MW; CDDCE7CEBDCD6B41 CRC64;
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                  CONFLICT
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                                                                            SIGNAL
                                                                                                                                 EMBL: AE008675; AAL03825.1; --
EMBL: M16486; AAA26381.1; --
EMBL: J03371; --
PIR: A25972; A25972.
PIR: A31836; A31836
PIR: A33971; A33971.
PIR: A33971; A33971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson B.E., Regne
Fu Z.Y., Bellini W..
"Sequence analysis crickettsii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    modification.",
J. Bacteriol. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89008059; PubMed=3139629;
Anderson B.E., Baumstark B.R., Bellini W.J.;
"Expression of the gene encoding the 17-kilodalton antigen
Rickettsia rickettsii: transcription and posttranslational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=R.rickettsii;
MEDLINE=89008059; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-30 FROM N.A.
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SPECIES-R.Tickettsii;
MEDLINE-87222152; Pubmed-3108232;
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MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiff:
Samson D., Roux V., Cossart P., We
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Science 293:2093-2098(2001)
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Raoult D.;
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.6; A.
.71; A339/.
.3971; B33971.
.8; PS00013; PROKAR_Li.
.membrane; Lipoprotein; A.
.1 19
.70 159
.70 20 20
.746 146
.153
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"Comparative sequence analysis of a gene.";
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Rickettsiaceae; Rickettsieae;
NCBI_TaxID=781, 783;
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01-NOV-1988 (Rel. 09, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
17 kDa Surface antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 kDa surface antigen precursor OMP OR RC1287.
                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                 anchor (Probable).
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                                                                                                                                                                                                                                 M28480;
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Bellini W.J.;
e analysis of the 17-kilodalton-antigen
                                                                                                                                                                                                                              AAA26376.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169:2385-2390(1987).
                                                                               PROKAR_LIPOPROTEIN; 1.
ipoprotein; Antigen; Si
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Cossart P., Welssenbach J., Claverie J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.rickettsii;
                                                                                                                                                                                                                                                                                                                                                                                                             Attached
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17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE):
N -> D (IN REF. 3).
G -> E (IN REF. 3).
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eae; Rickettsia.
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                                                                       Signal; Complete proteome
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Outer membrane; Lipoprotein; Antigen;
SIGNAL 1 1
CHAIN 20 159 17 KDA SU
LIPID 20 20 N-ACYL DI
SEQUENCE 159 AA; 16549 MW; 08973E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-AUG-1991 (Rel. 19,
01-OCT-1996 (Rel. 34,
17 kDa surface antiger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-89359171; PubMed-2768201;
Anderson B.E., Tzlanabos T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsiaceae;
NCBI_TaxID=785;
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Rickettsiaceae; Rickettsieae;
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                                                                                                                               SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
QEIYGTACPQPDGRWQVIS
                                                        TSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY - -
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                                                                                           KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK 139
                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                       33.2%; Score 276.5; DB 1; 39.6%; Pred No. 3.1e-17; Mismatches 46;
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eae; Rickettsia.
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                                                                                                                                                                                                                                                                                 17 KDA SURFACE ANTIGEN N-ACYL DIGLYCERIDE (PRO); 08973E2648FD8CD8 CRC6
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P50928;
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01-OCT-1996 (Rel.
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Submitted (OCT-1991)
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 STRAIN=MACULATUM
                                       NCBI_TaxID=35792;
[1]
                                                                          Bacteria; Proteobacteria; alpl
Rickettsiaceae; Rickettsieae;
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01-OCT-1996
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                     SEQUENCE FROM N.A.
                                                                                                             Rickettsia
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mitted (OCT-1991) to the EMBL/GenBank/DDBJ databases
SUBCELLULAR LOCATION: Attached to the outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anchor (Probable).
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1 19 BY SIMILARITY.
20 >154 17 KDA SURPACE ANTIGEN.
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P50931;
P50931;
Ol-OCT-1996 (Rel. 34, Created)
Ol-OCT-1996 (Rel. 34, Last sequence update)
Ol-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
                                                                        Outer membrane;
                                                                                                       EMBL; U11020; AAB07706.1;
                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.; Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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ipoprotein; Antigen; Signal.
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20 N-ACYL DIGLYCERIDE (PROBABLE).
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Query Match
Best Local
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                   Outer membrane;
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01-OCT-1996
17 kDa surfa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsia montana.
Bacteria; Proteobacteria; alpi
Rickettsiaceae; Rickettsieae;
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SEQUENCE
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-RNSTGQYCREYTQTVVIGGKQQKAYGNACLQPDGQ
                             KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 153
                                                                                       GGLIGSKIGOSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN
                                                         GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
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57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    surface antigen precursor (Fragment)
                                                                                                                                                                                                                                                                                        PS00013; PROKAR_LIPOPROTEIN; 1.
mbrane; Lipoprotein; Antigen; Signal.
1 19 BY SIMILARITY.
20 >154 17 KDA SURFACE ANTIGEN
20 20 N-ACYL DIGLYCERIDE (PRO
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154
154 AA;
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(Rel. 34, Last sequence up
(Rel. 34, Last annotation
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154 AA;
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; 15895 MW;
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                                                                                                                                                                                                               Score 256; DB 1;
Pred. No. 1.7e-15;
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RESULT 10
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Best Local
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01-APR-1993;
01-APR-1993;
01-OCT-1996;
17 kDa surfac
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Stothard D.R., Ral
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
17 kDa surface antigen precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
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  SEQUENCE FROM N.A. MEDLINE-92108069;
                                                                                                    Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
                                                                                                                                                  Rickettsia
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Ull013; AAB07704.1; -.
UTE; PS00013; PROKAR_LIPOPROTEIN; 1.
ITE; PS00013; PROKAR_LIPOPROTEIN; 1.
I BY SIMILARITY.
INL 1 19
N-ACYL DIGLYCERIDE (PRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anchor (Probable).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAVLGGQVGAGMDEQDRRIAELTSQKALETAPNGSNVEWRNPDNGNYGYVTPNKTY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
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                                                                                                                                                                                                      surface
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57; Conserv
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(Rel. 25, Last sequence update)
(Rel. 34, Last annotation update)
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                                                                                                                                                                                                        antigen
                                                                                                                                                                                                                                                                                                                               STANDARD;
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       PubMed=1729713
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                                                                                                                                                                                                      (Fragment).
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                                                                                                    alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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Pred. No. 2.1e-15;
                                                                                                                                                                                                                                                                                                                               PRT;
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RESULT 11 PCP_YEREN
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01-JUL-1993
15-DEC-1998
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                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                               "A lipoprotein of versinia enterocolitica faci
uptake in Escherichia coli.";
J. Bacteriol. 174:1029-1035(1992).
-!- FUNCTION: FACILITATES FERRIOXAMINE UPTAKE.
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 51872 / WA-C / SEROTYPE 0:8;
MEDLINE=92121089; PubMed=1732192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    typhus-like rickettsia found in cat fleas."; Proc. Natl. Acad. Sci. U.S.A. 89:43-46(1992).
                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane
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                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
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PROSITE; PS00013; PROKAR_LIPOPROTEIN;
Outer membrane; Lipoprotein; Antigen.
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                                                                                                                                                                                                                                                                                                                                               Yersinia
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X60448; CAA42977.1;
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31; Conservative
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Pred. No. 3.9e-07;
5; Mismatches 27
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
101-MAR-2002 (Rel. 41, Last annotation update)
101-MAR-2002 (Rel. 41, Last annotation update)
101-MAR-2002 (Rel. 41, Last sequence update)
101-MAR-2002 (Rel. 47, Last annotation update)
101-MAR-2002 (Rel. 47, Last annotation update)
101-MAR-2002 (Rel. 35, Created)
101-MAR-2002 (Rel. 35, Created)
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101-MAR-2002 (Rel. 35, Created)
101-MAR-2002 (Rel. 35, Last sequence update)
101-MAR-2002 (Rel. 41, Last sequence update)
101-MAR-2002 (Rel. 41, Last sequence update)
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SEQUENCE FROM N.A.

SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
Parkhill J. Dougan G. James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Baker S., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barreil B.G.;
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Best Local
                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                    McClelland M., Sanderson K.E., Spieth J., Clifton S.W. Courtney L., Porwollik S., Ali J., Dante M., Du F., Ho Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Ryan E., Sun H., Florea L., Miller W., Stoneking T., N Waterston R., Wilson R.K.;
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MEDLINE=96133688; PubM
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HSSP;
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18 18
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TE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulatory protein from Salmonella ic and pore-forming protein in Esche . Genet. 249:474-486(1995).
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37; Conserv
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Tengel C., Bauer S., B
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Pred. No. 0.
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N-ACYL DIGLYCERIDE (POTENTIAL).
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Escherichia coli.
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STRAIN*K12 / MG1655;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Escherichia.
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EMBL; AE008762; AAL20367.1; -.
EMBL; AL627271; CAD01922.1; -.
Stycene; SG10573; SlyB.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Signal; Complete proteome.
Outer membrane; Lipoprotein; Signal; Complete proteome.
STGNAL
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Nature 413:848-852(2001).
-!- SUBCELLULAR LOCATION: Attached to the outer
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ic and pore-forming protein in Escherichia coli.";
. Genet. 249:474-486(1995).
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C., Bauer S., B
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasuna, Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
                                                                                                                   CONFLICT
                                                                                                                                                                                           ECOGENE; EG13409; slyB.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Itch T. Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mor Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage m DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          This
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Hayashi T
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[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Boutin A., Shav Y., Miller L., Posfai G., Hackett J., Klink S., Boutin A., Shav Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
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İtoh T.,
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Alba H., Baba T., Fujita K., Hayashi K.,
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                                                                         Local
 10
                               12
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                                                                                                                                                                                                                                                                                                                                                                                                                                     anchor (Potential).
SIMILARITY: TO S.TYPHIMURIUM SLYB, H.INFLUENZAE
Y.ENTEROCOLITICA PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION:
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 MVGLSLVGCVNNDTLSGDVYTASEAKQVQNVSYGTIVNVRPVQIQGGDDSNVIGAIGGAV
                             IISVFLVGCAQN-----FSRQE---
                                                                                                                                                                                                                                       AE000259; AAC74713.1; -. D90807; BAA15402.1; -. AE005387; AAG56630.1; -. AP002558; BAB35773.1; -.
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                                                         33; Conservative
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277:1453-1474(1997).
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1 17
8 155
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8 98
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PubMed=11206551;
                                                                         12.6%;
                                                                                                                      MW;
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                                                                                                                  n; Signal; Complete proteome.

POTENTIAL:

OUTER MEMBRANE LIPOPROTEIN S

N-ACYL DIGLYCERIDE.

A -> T (IN REF. 2).

4W; 543EB8A4069A5FA3 CRC64;
                                                           21;
                                                                         Score 104.5;
Pred. No. 0.
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                                                           Indels
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Tobe T.,
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RESULT 14
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane lipoprotein PCP precursor (15 KDa PCP OR LPP OR HI1579.
Haemophilus infi
                             Outer membrane;
SIGNAL 1
CHAIN 19
LIPID 19
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                          This SWI
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Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Heblom E., Cotton M.D.,

Weidman J.F., Phillips C.A., Spriggs T., Heblom E., Cotton M.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Fine L.D., Fritchman J.L., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-88115138; PubMed=2828309;

MEDLINE-88115138; PubMed=2828309;

Deich R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;

"Cloning of genes encoding a 15,000-dalton peptidoglycan-associated outer membrane lipoprotein and an antigenically related 15,000-dalton protein from Heemophilus influenzae.";

J. Bacteriol. 170:489-498(1988).
                                                                                                                                    EMBL;
                                                                                                                                                    EMBL;
                                                                                                                                                                             use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (see http://www.lsb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 Science
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Haemophilus.
                                                                                                                      PIR; B28543;
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Science 269:496-512(1995).
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                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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              N-ACYL DIGLYCERIDE CSLVAEFVF -> VAGRRY
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Query Match

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Similarity

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RESULT 15
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                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@eisb-sib.ch).
                                                                                                                                                                                         MEDLINE=95075659; PubMed=7984428;
Borodovsky M., Rudd K.E., Koonin E.V.;
"Intrinsic and extrinsic approaches for detecting genes bacterial genome.";
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=7061202; PubMed=8905232;
Oshina T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
DNA Res. 3:137-155(1996).
                                                                                                                                                                                   Nucleic Acids Res.
                                                                                                                                                                                                                                                                   MEDLINE=81236546; PubMed=6265208; Young J.G., Rogers B.L., Campbell H.D., Jaworowski A., Shaw D.C.; "Nucleotide sequence coding for the respiratory NADH dehydrogenase of Escherichia coli. UUG initiation codon."; Escherichia coli. UUG initiation codon.";
                                                                                                                                                        Nucleic Acids Res. 22:4756-4767(1994).
-!- SIMILARITY: TO RICKETTSIA 17 kDa SURFACE ANTIGEN.
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STRAIN=K12 / MG1655;

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

Riley M., Collado-vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

Mau B., Shao Y.;
                                                                                                                                                                                                                                                        DENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YCFJ_ECOLI STANDARD; PRT; 179 AA. P37796; P75951; 30, Created) 01-0CT-1994 (Rel. 30, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) YCFJ OR B1110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12.", Science 277:1453-1474(1997).
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V00306;
                         AE000211; AAC74194.1; -.
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                   BAA35925.1;
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NOT_ANNOTATED_CDS
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39.6%;
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Pred. No. 0.043;
9; Mismatches 2
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Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 5 25 POTENTIAL.
SEQUENCE 179 AA; 18920 MW; BA5EBODB56D45609 CRC64;
                                                  163 TQIPL-DSNGQLILNNK 178
                                                                           145 TACPQPDGRWQVISTEK 161
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                                                                                                                   AGQVTEWRNPDTGNSYSVEDVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY-----G
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Pred. No. 0.061;
7; Mismatches 48; Indels
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Compugen Ltd 5.1.3

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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pir2:*
pir3:*
pir4:*
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C64855
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AG0443
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                         RESULT
B33971
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C;Superfamily: rickettsial of
C;Keywords: surface antigen
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A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499
A;Accession: B71645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Rickettsia prowazekii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 03-Nov-2000
C;Accession: D33971; B71645
R;Anderson, B.E.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a genus-common rickettsial antigen gene.
A;Reference number: A33971; MUID:89359171
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A; Residues: 1-159 <AN2>
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A;Note: the sequence in GenBank entry RIRANT17KC,
R;Andersson, S.G.E.; Zommrodipour, A.; Andersson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-159 < AND>
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  Rickettsial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown; translation not shown
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Matches
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                                                                                                                                                    64 GAVLGGQIGASMDEQDRRLLELTSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY----
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                                                                                                                                                                                                                                                                                                                           5 SKIMITALAASMLQACNGQSGMNKQGTGTLLGGAGGALLGSQFGQGKGQL-VGVGVGALL
                                                                                                                                                                                                                                                        GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 117
                                                                                                                             -RNSAGQYCREYTQTVIIGGKQQKTYGNACRQPDGQWQVVN 159
common antigen precursor - Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                                                                                                            61,
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 37.151; Conservative
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Pred. No. 1.7e-18;
2; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 159;
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RESULT 4

G97860

17K surface antigen precursor [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #Sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C;Accession: G97860
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rickettsia conorii
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1
C;Accession: B33971 #sequence_revision 16-Mar-1
R;Anderson, B.E.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a ger
A;Reference number: A33971; MUID:89359171
A;Status: prellminary
A:Molecule turn. num
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A; Residues: 1-159 <AND>
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J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a
A;Reference number: A33971; MUID:89359171
A;Accession: A33971
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A; Residues: 1-159 <AND>
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37.9%; Pro
ative 31;
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Pred. No. 3.1e-18
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3.1e-18;
nes 53;
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RESULT 6
A25972
17K antigen precursor - Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change / Carlone: A25972
C-Arcession: A25972
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R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.; McDage, J.E.; ru, 4.1. J. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia ricketts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M28481; NID:g152459; PIDN:AAA26377.1; C;Superfamily: rickettsial common antigen
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A;Molecule type: DNA
A;Residues: 1-159 <AND>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Comparative sequence analysis of a genus-common A;Reference number: A33971; MUID:89359171
A;Accession: C33971
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Best Local Similarity 39.6
55; Conservative
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C;Superfamily: rickettsial common antigen
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A; Residues: 1-159 < KUR>
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A;Accession: G97860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                    141 QTTYGNACRQPDGQWQVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 SRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVLGGLIGSKIGQSMDQQDK----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QEIYGTACPQPDGRWQVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLNOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERROQYCREFOQKAMIAGQK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKQGTGTLLGGAGGALLGSQFGHGKGQL-VGVGVGALLGAVLGGQIGASLDEQDRKLLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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39.6%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 276.5; DB ;
Pred. No. 1.8e-17;
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Pred. No. 3.
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.1e-18;
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A; Experimental:
C; Genetics:
A; Gene: PA3819
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AI3418
17K surface antigen precursor [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AI3418
C;Accession: AI3418
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.;
Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
                                                                           A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten. A;Reference number: AD3252; PMID:11756688
A;Accession: AI3418
A;Status: preliminary
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           A; Molecule type: DNA
A; Residues: 1-131 <KUR>
A; Cross-references: GB: AE008917; PIDN: AAL52516.1;
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A; Residues: 1-182 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406, 959-964, 2000
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A; Residues: 1-159 < AND>
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Best Local S
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strain
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37.3%; Pred. No. 2e-17;
Live 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 127.5; DB 2
Pred. No. 0.00037;
3; Mismatches 28
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                   PID:g17983328;
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                   GSPDB:GN00190
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A.; Larbig,
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K.; Lim,
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LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sec
A;Reference number: A82950;
A;Accession: B83514
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                                                                                                                       C;Accession: B83514
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas,
A; Molecule type: DNA
A; Residues: 1-154 <STO>
                                                                                                                                                                                       conserved hypothetical protein PA1053 [imported] - Pseudomonas aeruginosa (
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A; Residues: 1-155 <BAE>
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J. Bacteriol. 174, 1029-1035, 1992
A;Title: A lipoprotein of Yersinia
A;Reference number: S23786; MUID:92
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                                A; Status: preliminary
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Best Local S
Matches 37
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                                                                                                                                                                                                                                                                                                                   VQKQGPTRFSVGQ--RVMLASSGSTVTVSP
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39; Conserv
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                                                                 sequence of Pseudomonas
50; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.5%;
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31.7%;
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MUID:92121089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 112.5; DB Pred. No. 0.0068;
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                                                                                     aeruginosa
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                                                                                   opportunistic
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Larbig,
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A;Cross-references: A;Experimental source

strain

PAO1

GB:AE004537; GB:AE004091; NID:g9946960;

PIDN: AAG04442.1;

GSPDB:

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hypothetical protein CC3073 [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: 687629 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rut
A; Title: Complete genome sequence of
A; Reference number: AB0502; PMID:11(
A; Accession: AE0644
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G87629
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A;Gene: STY1252
C;Superfamily: PAL cross-reacting lipoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross references: GB:AL513382; PIDN:CAD08336.1; PID:g16502381; GSPDB:GN00176
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A; Molecule type: DNA
A; Residues: 1-179 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable secreted protein STY1252 [imported] - Salmonella enterica subsp. enterica serovar Typhi C; Species: Salmonella enterica subsp. enterica serovar Typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 14-Dec-2001 C; Accession: AE0644 R; Barkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.: Moule, S.: O'Gaora, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: PA1053
C;Superfamily: 1
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                                                                                                                                                                                                                                                                                                                                                                                                         GSVLGAVAGGVIGHQFGGGRGKDVATVVGALGGGYAGNQIQGSMQESD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:; Quail, M.; Rutherford, K.; genome sequence of a multiple r: AB0502; PMID:11677608
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                                                                                                                                                                                                                                                                                                                              -TYTTTQQRCKTVYDKSEKMLGYDVTYKIGDQQGKIRMDKDP--GTQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.1%; Score 109; DB 2; 27.4%; Pred. No. 0.016;
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Pred. No. 0.0083;
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ple drug resistant
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, J.; Karp, P.; Romero, P.; Zhang, S.
                                                               lipA protein [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #
                                                                                                                                                                     RESULT 14
AD2696
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-reference: GB:AED03872; GB:AED03849; NID:g9104975; PIDN:AAF82991.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
chado, M.A.; Madeira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
A;Authors: Marcins, E.M.F.; Matsukuma, Ar.; Menck, C.F.M.; Marques, M.V.; Martins
A;Authors: da Silva, A.G.R.; da Silva, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                                                                                                                                                      DЪ
                                                                                                                                                                                                                                                                                          QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 47.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 406, 151-157, 2000
A,Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717
A; Note: for a complete list of authors see reference number A59328 bel
A; Accession: B82837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-257 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; anonymous, \ \mbox{The xylella fastidiosa Consortium of the Nature 406, 151-157, 2000}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein xF0178 [imported] - xylella fastidiosa (strain C;Species: Xylella fastidiosa
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A; Residues: 1-232 <ST
A; Cross-references: C
C; Genetics:
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A;Status: preliminary
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                                                                                                                                                                                                                                                                    30 GAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AAQEVGGIYKSGGFRYAQTVQAAPLVKIEKKMVTR 175
                                                                                                                                                                                                                                                                                                                                                                                                                       XF0178
                                                                                                                                                                                                                             GTAIGALIGGLVGNQFGHGNGRKALTAAGAVAGGFIGNEV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 DQQDKIKLNQS-----LEKVKAGQVTR 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 LVGCAQNFSRQEVGAATGAVVGGVAGQLFGK---GSGRVSMAIGGAVLGGLIGSKIGQSM 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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ences: GB:AE005673; NID:g13424723; PIDN:AAK25035.1; GSPDB:GN00148
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47.5%;
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33.7%;
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Pred. No. 0.024;
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; Pred. No. 0.021;
14; Mismatches 33;
                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                   11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     see reference number A59328 below
         D.; Chen, L.; Wood, G.E.; Chen, D.; Kutyavin, T.; Levy, R.; Li, N
                                                                                                                                                                                                                                                                                                                                                       DB 2;
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                                                                                                                       (strain C58,
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probable lipoprotein slyB [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AF0289
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AD2696
A:Status: preliminary
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C;Superfamily: PAL cross-reacting lipoprotein
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A;Molecule type: DNA
A;Residues: 1-155 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AF0289
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL590842; PIDN:CAC91178.1; PID:g15980369; GSPDB:GN00175
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A; Residues: 1-142 <KUR>
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                                                                                               127
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                                                                                                                                                                                                                                          34 GAVVGGVAGOLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL--
                                                                                                                                                                                                                                                                                                                                                                                       Match 12.9%; Score 107.5; DB Local Similarity 24.0%; Pred. No. 0.019; es 36; Conservative 19; Mismatches
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                                                                                                                                                                                                                                                                                                                                         9 SLIIISVFLVGCAQN-----FSRQE-----------VGAAT 33
                                                                                          VOKOGPTOFSVGORVMLAN--SGSTITVSP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGQSMDQQDKIKL----NQSLEKVKAGQVTRWRNPDT-GNSYSVEPVRTYQRYNKQERRQ 123
                                                                                                                                                                                          GAVLGGFLGNAVGGGTGRSLATAAGAVAGGIAGQGVQGALNRTDGVQLEIRKDDGQTILV 126
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                      2002, 11:11:36
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 200000000
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3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/Dackfiles1.pep:*
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         GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
         Gapext 0.5
  US-08-556-978B-19
US-08-42-060-1
US-08-42-060-2
US-08-317-844B-2
US-09-034-177-3
US-09-553-498-8
US-09-0553-498-8
US-09-360-490-2
US-08-317-077C-2
US-08-317-077C-2
US-08-313A-13
US-08-413-118-6
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US-09-057-351-1
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US-09-1928-65
US-08-190-1928-65
US-08-190-1928-65
US-08-190-1928-65
US-09-248-335-40
US-09-248-335-40
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US-08-375-709-7
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                                                    Sequence 2
Sequence 4
Sequence 4
Patent No.
Sequence 1
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                                                                                                                                                                       TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-556-978B-19
                             QY
                                                                        Query Match
Best Local Similarity
Matches 24; Conserv
    27 QEVGAATGAVVG----GVAGQ------
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Result No.

Conservative

9.4%;

Score 78.5; Pred. No. 1. 4; Mismatche Mismatches

DB 4; 17;

Length 651; Indels 23;

Gaps

2

------LFGKGSGRVSMAIGGAVLGG

19:

RESULT 1 US-08-556-978B-19 ISEQUENCE 19, Application US/08556978B PATENT NO. 6268169 PATENT NO. 6268169 PATENT NO. 6268169 PATENT NO. 6268169 PATENT NO. FANNESTOCK, STEPHEN F. APPLICANT: FANNESTOCK, STEPHEN F. APPLICANT: FANNESTOCK, STEPHEN F. APPLICANT: FANNESTOCK, STEPHEN F. APPLICATION: SPIDER SILK ANALOGS NUMBER OF INVENTION: SPIDER SILK ANALOGS NUMBER OF SEQUENCES: 107 CORRESPONDENCE ADDRESS: ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET COUNTRY: WILMLINTON STATE: DELAWARE COMPUTER RADABLE FORM: MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER RADABLE FORM: MICROSOFT WINDOWS 95 SOFTWARE: MICROSOFT WORD FOR WINDOWS 95 CURRENT APPLICATION NUMBER: US/08/556,978B FILING DATE: CLASSIFICATION NUMBER: US/08/556,978B FILING DATE: CLASSIFICATION NUMBER: 08/077,600 FILING DATE: APPLICATION NUMBER: 08/077,600 FILING DATE: APPLICATION NUMBER: 33,692 REFERENCE/DOCKET NUMBER: CR-9389-A TELECOMMUNICATION INFORMATION: TELEPAN: 302-92-8112 TELEPAN: 302-92-8112	28 71 8.5 970 1 US-08-752-929-7 29 71 8.5 970 4 US-09-090-793-5 30 71 8.5 2703 1 US-08-185-432-19 31 70.5 8.5 731 2 US-08-678-039A-40 33 70.5 8.5 792 2 US-08-678-039A-40 34 70 8.4 409 4 US-09-217-349-3 36 69.5 8.4 547 1 US-08-452-567-3 39 69.5 8.4 547 2 US-08-452-567-3 39 69.5 8.4 547 2 US-08-452-567-3 39 69.5 8.4 547 3 US-08-452-73 40 69.5 8.4 1021 1 US-08-407-760-12 41 69.5 8.4 1021 1 US-08-40-519-12 42 69.5 8.4 1021 1 US-08-40-519-12 43 69.5 8.4 1021 1 US-08-40-549-12 44 69 8.3 101 4 US-08-556-978B-20 45 69 8.3 101 4 US-08-556-978B-20
	Sequence 7, Appli Sequence 5, Appli Sequence 19, Appl Sequence 1, Appli Sequence 1, Appli Sequence 40, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 22, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli

US-09-247-806-1

GENERAL INFORMATION:

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491

551 LGGQGAGQ 558

64 LIGSKIGQ

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CURRENT APPLICATION NUMBER: US/09/247,806
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: FR 98/01614
EARLIER FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 14
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 651
TYPE: PRT
ORGANISM: Nephila clavipes
US-09-247-806-1
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lowis, Randolph V. APPLICANT: Xu, Ming APPLICANT: Hinman, Michael B. TITLE OF INVENTION: ISOLATED DN TITLE OF INVENTION: PROTEIN, A NUMBER OF SEQUENCES: 69
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: THE POPPY
COMPUTER: THE POPPY
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09247806 Patent No. 6280747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PHILLIPDE, Michel
APPLICANT: GARSON, Jean-Claude
APPLICANT: ARRAUDEAU, Jean-Plerre
TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING P
TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
TITLE OF INVENTION: ANALOG
FILE REFERENCE: 6388-3355-0
                                                                                                                                                                                                                                                                           NUMBER OF SEVERICE CORRESPONDENCE ADDRESS:
CORRESPONDENCE Birch, Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                    ADUNESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5728810th Washington Street
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 OGAGAAAAAYGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08425069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.48;
35.38;
                                                                                                                                                                                                                                                                                                                                      ISOLATED DNA CODING FOR SPIDER SILK
PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
                                                                                  US/08/425,069
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Pred. No. 1.7;
4; Mismatches
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                                               US-08-317-844B-2
             Query Match
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                                                                                                                                                 TELEFAX: (703) 241-284
TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Lewis, Rai

APPLICANT: N. Ming

APPLICANT: Hinman, M.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2,
Patent No.
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Best Local Similarity
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                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: amino acid
                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 718 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                    TELEPHONE: (703) 241-2848
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 04-OCT-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-106P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 22046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Falls Church
STATE: Virginia
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o. 5989894
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Y: U.S.A.
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Xu, Ming
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                                                                                                                                                                                                      (703) 241-1300
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                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Randolph V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOLATED DNA CODING FOR SPIDER SILK
PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
     9.4%;
                                                                                                                                                                                                                                                                                                                                            US/08/317,844B
                                                                                                                                                                                                                                                                                                                                                                          Release #1.0, Version #1.25
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                                                                                                                                                                                                                                      1447-105P
   Score 78.5;
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Pred. No. 1
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Length 718;
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RESULT 3 US-08-425-069-2

Sequence 2, Apprint No. 5728810

GENERAL INFORMATION:

ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US/01 FILING DATE: 19-APR-1995 OTASSIFICATION: 435

COUNTRY:

E: Virginia TRY: U.S.A. 22046

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Matches Query Match

Local Similarity

24; Conservative

Best Local Similarity

35.38;

Pred. No. 1.9;

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; LIBRARY: GenBank
; CLONE: GI 1174414
US-09-034-177-3
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                                                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN FIBROUS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0486 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                          491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: HEREW
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                           64 LIGSKIGO 71
                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
LGGQGAGQ 558
                                                         QGAGAAAAAAVGAGQEGIRGQGAGQGGYGGLGSQGSGRGGLGGQGAGAAAAAAGGAGQGG 550
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                                                                                                                                                                                                                                                                                 747 amino acids
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                                                                                                                                 Score 78.5;
Pred. No. 2;
                                                                                                                  Mismatches
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                                                                                     DB 3;
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                                                                                                                                              Length 747;
                                                                                                                   Indels
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                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-553-498-8
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                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/067 354

CLASSIEF: Herevit*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application Patent No. 5994081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 8
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APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: Process for the production of naturally folded and secreted
FILE REFERENCE: Case 20379
CURRENT APPLICATION NUMBER: US/09/553,498
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: EP99107412.1
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ambrosius, APPLICANT: Rudolph, 1
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           REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0511 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                   ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                         STREET: 31.
STREET: 9ALO ALTO
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baughn, Mariah TITLE OF INVENTION: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Corley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 SVEPVRTYORYNKOERROOYCREFOOKAMI--AGOKOEIYGTACPOPDGRWQVISTE 160
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                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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(650)
(650) 84
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US-09-067-351-2
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Best Local 9
                                                                         TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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IMMEDIATE SOURCE:
LIBRARY: KERANOJ
CLONE: 2029060
                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/067,351
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hillman, Jennifer L. APPLICANT: Corley, Neil C. APPLICANT: Baughn, Mariah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                           STRANDEDNESS:
                TOPOLOGY:
                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                    NAME: CERRONE, MICHAEL REGISTRATION NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 PUI
CITY: PALO ALTO
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                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                FILING DATE:
                                                            ENGTH:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/360,490
                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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STRANDEDNESS: si
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28; Conservative
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                                                        551 amino acids
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Baughn, Mariah
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                                                                                                                                                  39,132
SER: PF-0511 US
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                                                                                              Query Match
Best Local S
Matches 32
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Best Local Similarity 22.4
Matches 28; Conservative
                                                                                                                                                                                                                          TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                            2389 IGSSNGSIFGGSAGGLGGAGSGGVG-GLGGSSSIRNAFGGSGSGPSSLSPQHQPYSGTLN 2447
                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: McGowan, Malcolm M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Genes Encoding an Invertebrate Alpha1
TITLE OF INVENTION: Calcium Channel Subunit
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                         29 VGAATGAVVGGVAGQLFGKGSGRVSMAIGG--AVLGGLIGSKIGQS----MDQQDKIKLN 82
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                                                                                              Local Similarity
nes 32; Conserv
                                                                                                                                                                                                                                               TELEPHONE: 703-6-1021
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 19-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 QRYNK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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-----QSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIA 136
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                                                                                                                                                                                                  amino acid
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Ren, Dejian
Theng, Wei
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                                                                                                         9.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.3%;
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                                                                                         Score 76.5; DI
Pred. No. 17;
L8; Mismatches
                                                                                                                                                                                                                                                                                                           022650-264
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Pred. No. 2;
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                                                                                                                      Length 2516;
                                                                                          Indels
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RESULT 11
US-07-803-633A-13
; Sequence 13, Application US/07803633A
; Patent No. 5369025
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Best Local S
Matches 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/374,888
FILING DATE: 19-JAN-195
ATTORNEY/AGENT INFORMATION:
NAME: MCGOWAN, MAICOLM M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 022650-263
TELEPHONE: 703-836-6520
TELEPHONE: 703-836-6520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             2448
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dubaid, Manuel Marcel Paul
TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2508
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                                                                                                                                          137 GQKQEIYGT 145
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                                                                                                                                                                                                               83
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                                                                                                                                                                                                                                                                              29 VGAATGAVVGGVAGQLFGKGSGRVSMAIGG--AVLGGLIGSKIGQS----MDQQDKIKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/895,590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                             SPPIPDNRLRRVATVTTTNNNNKSQVSQNNSSSLNVRANANSQMNMSPTGQPVQQQSPLR 2507
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                                                                                                                                                                                                                                                                                                              h 9.2%; Score 76.5; I Similarity 24.8%; Pred. No. 17; 32; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   GY: linear
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Ren, Dejian
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          New York
NY
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Query Match
Best Local Similarity
Vatches 37; Conserv
                                                                                                                                                                                     Sequence 6, Application US/08220151 Patent No. 5529780
                                                                                                                                                                     GENERAL INFORMATION:
                                                                                        APPLICANT: Paoletti,
APPLICANT: Limbach, I
TITLE OF INVENTION: I
TITLE OF INVENTION: (
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/803,63
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TELEPHONE: (703) 241-1300
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MEDIUM TYPE: Floppy disk
                                     ADDRESSEE: Curtis, M
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NAME: Murphy Jr., Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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TELEFAX: 248345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 865 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
ADDRESSEE: Curle,
ADDRESSEE: 530 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22040-0747
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LEE, Lucy F.
TOTOA, No. 5369025oru
                                                                                                                                                 Paoletti,
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, Keith J.
, Keith J.
, NUCLEOTIDE AND AMINO ACID SEQUENCES OF
CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR
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                                     Morris & Safford
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Pred. No. 4.7;
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RESULT 13
US-08-413-118-6
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; FRAGMENT TYPE: N-terminal
US-08-220-151-6
                                                                                                                                                                                                                                                                                                                                                 Patent No. 5688920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: PAOLET
APPLICANT: LIMBAC
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                            APPLICATION NUMBER: FILING DATE: 29-MAI
                                                                                                                                                                                                                                                                                                                                                                                                                                 873 QQEHKARKKNSGPALLASRVGAMATRRHYQRLESED 909
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEPHAY. (712) 640-3333
                 CLASSIFICATION
                                                                                                                                                                                CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                753 VILRGIANFFOGLGDVGAAVGKVVLGATGAVISAVGGMVSFLSNPFGALAIGLLVLAGLV 812
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ATTORNEY/AGENT INFORMATION:
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SOFTWARE: Patenti
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                                                                                                                                                           UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                  LIMBACH,
                                                                                                                                                                                                                                                                                                                  PAOLETTI,
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linear
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IBM PC compatible
                            29-MAR-1995
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23.6%; Pred. No. 7
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NUCLEOTIDE AND AMINO ACID SEQUENCES
CANINE HERPESVIRUS 9B, 9C, AND 9D AN
128
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                                        US/08/413,118
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US-08-473-446-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08473446 Patent No. 6017542
INFORMATION FOR SEQ ID NO:
                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 9.0%;
Best Local Similarity 23.6%;
Matches 37; Conservative 1
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          TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                           ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S
REGISTRATION NUMBER: 25,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 840-071
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LIMBACH, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                STREET: 530 EIFTH AVENUE, 25TH FLOOR CITY: NEW YORK
STATE: NEW YORK
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REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   753 VLLRGIANFFQGLGDVGAAVGKVVLGATGAVISAVGGMVSFLSNPFGALAIGLLVLAGLV 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 913 amino acids
TYPE: amino acid
STRANDEDNESS: single
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NO: 6:
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Pred. No. 7
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Search completed: October 27, 2002, 11:12:13 Job time: 9.34197 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: AUDONNET et al.

TITLE OF INVENTION: POLYNICLEOTIDE VACCINE FORMULA AGAINST PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
FILE REFERENCE: 454313-2230
CURRENT APPLICATION NUMBER: US/09/232,468A
CURRENT FILING DATE: 1999-01-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 913
TYPE: PRT
ORGANISM: Pseudorables virus
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Best Local S
Matches 37
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            Query Match 9.0%; Score 74.5; DB 4; Length 913; Best Local Similarity 23.6%; Pred. No. 7.4; Matches 37; Conservative 18; Mismatches 51; Indels 5
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LENGTH: 913 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                          873 QQEHKARKKNSGPALLASRVGAMATRRRHYQRLESED
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Local Similarity 23.6%; Pred. No. 7.4;
hes 37; Conservative 18; Mismatches 51; Indels 5:
                                                                                                                                                                                                                                                                                                15 VFLVGCAQNF-SRQEVGAATGAVVGGVAGQLFGKGSGRVS------MAIGGAVLGGLI 65
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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Copyright (c) 1993 - 2002 Compugen Ltd
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(without alignments)
835.217 Million cell updates/sec
                   Optimised OspA pro
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Piscirickettsia sa
OspA antigen amino
OspA B-cell epitop
Moraxella catarrha
Porphorymonas ging
Porphorymonas ging
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30			27	26	25	24	23	22	21	20	19	18	17	16	15	14	13 .	12
76.5	77	77	77	77	77	77	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	8	78.5	8	78.5	9		0	80.5	81	82	83	83	84	86.5	7.
9.2		-	9.3		9.3	9.3	9.3	9.3					9.3	9 . 3			9.3	9.3	9.4	9.4	9.4	9.4	9.6	•	9.7	9.7		9.9	0	0		10.4	10.5
2516	2599	551	285	285	285	223	514	354	302	285	285	285	285	255	255	255	255	102	718	718	718	651	618	542	542	542	666	2017	423	116	1251	2309	147
17	21	21	22	21	21	21	22	22	22	22	22	21	20	22	22	22	21	22	21	19	12	20	21	22	22	22	22	22	22	19	22	22	22
AAW01875	AAY75098	AAY52398	AAG93288	AAY73440	AAY87280	AAB57121	AAU36520	AAU19445	AAM40157	AAM39011	AAU29025	AAB44244	AAY41688	AAY72020	AAB70769	AAB74199	AAB11398	AAM41943	AAY59070	AAW53346	AAR14308	AAY40097	AAB56803	ABB70501	ABB65791	ABB65790	ABB58019	ABG06301	AAB30695	AAY11028	ABB61254	w	ABB69847
Neuronal invertebr	Neisseria meningit	Human keratin KERT	Human protein HP10	Human secreted pro	Human signal pepti	Human prostate can	Pseudomonas aerugi	Human diagnostic a	Human polypeptide	Human polypeptide		Human PRO284 (UNQ2	Human PRO284 prote	E. carotovora PelB	Expression plasmid	PelB-scFvOxazolon	E. coli expression	Human polypeptide	N. clavipes spider	Nephila clavipes s	N.clavipes draglin	Spider silk protei	_				Drosophila melanog	Novel human diagno	fusion of ar	$^{\circ}$			Drosophila melanog

ALIGNMENTS

Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease;

Optimised OspA

protein 17E2 amino acid sequence.

11-JUL-2001 (first entry)

AAB81127;

AAB81127 standard; Protein; 161

A

RESULT 1 AAB81127

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Piscirickettsia Synthetic.
                                                                                                    SRS.
Kay WW,
                                               17-MAR-2001.
                                                         CA2281913-A1
                                                                       Key
Region
        (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                             17-SEP-1999;
                                     17-SEP-1999;
Burian J,
                            99CA-2281913
                                      99CA-2281913
                                                                                          salmonis
                                                                       Location/Qualifiers
                                                                  /label= B_cell_epitope
Kuzyk MA;
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RESULT 2
AAB81128
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Best Local S
Matches 161
         17-SEP-1999.;
                                  17-MAR-2001.
                                                          CA2281913-A1
                                                                                                                        Region
                                                                                                                                                                                                                            Polkilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease
                                                                                                                                                                                              Piscirickettsia
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                                                                                                                                              Region
                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia P. salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed Ospa, or an immunogenic fragment of particularly poikilothermic fish, against the bacterial pathogen particularly poikilothermic fish, against the bacterial pathogen rickettsial septicaemia (SRS) and other rickettsial diseases. The present encoding Ospa 17E2 (AAF86247) has been optimised for expression in Ecsherichia coli. An Ospa protein with an N-terminal fusion partner is used in a vaccine to create an anti-Ospa antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                    LGGLIGSKIGOSMDOODKIKLNOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                       OspA
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                                                                                                                                                                                                                                                                   construct with N-terminal
                                                                                                                                                                                                                    fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 AA;
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       99CA-2281913
                                                                                                                                                                                              salmonis
                                                                                                        96..256
/label=
                                                                                                                        /label= Undefined_N-terminal_fusion_partner
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                               * C17E2_OspA
"Product of OspA gene optimised
Escherichia coli"
                                                                                                                                                                                                                                                                                                                                             256
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Pred. No. 3e-81;
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                                                                                                                                                                                                                          septicaemia; rickettsial disease;
                                                                                                                                                                                                                                                               fusion partner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 161;
                                                                                   for expression
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RESULT 3
AAG78025
ID AAG7
XX AAG7
XX AAG7
XX AAG7
XX Pisc
XX Pisc
XX Pisc
XX Sept
KW Sept
KW Sept
KW ATCC
XX Pisc
XX WO20
PX WO20
XX WO20
XX WO20
XX WO21
PF 12-M
PR 11-M
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Best Local
 11-MAR-2000;
01-JUL-2000;
                                        12-MAR-2001;
                                                                   20-SEP-2001
                                                                                              WO200168865-A2
                                                                                                                       Piscirickettsia
                                                                                                                                                  Piscirickettsia salmonis;
septicaemia; SRS; surface
ATCC VR-1361.
                                                                                                                                                                                               Piscirickettsia salmonis polypeptide P10.6.
                                                                                                                                                                                                                                                                                 AAG78025 standard; Protein; 162 AA.
                                                                                                                                                                                                                                   15-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, p. salmonis. The method is also useful for protecting apathogen rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a p. salmonis OspA undefined W-terminal fusion partner. The fusion protein is used in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
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(BURI/) BURIAN J.
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                                                                                                                                                                                                                                                                                                                                                                RRQQYCREFQOKAMIAGGKQEIYGTACPQPDGRWQVISTEK 161
                                                                                                                                                                                                                                                                                                                                                                                                  LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE
                                                                                                                                                                                                                                                                                                                                                                                                                 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           create an anti-OspA antibody response.
                                        2001WO-GB01055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
2000GB-0005838
2000GB-0016080
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative (
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                                                                                                                                                        piscirickettsiosis; salmonid antigen; vaccine; antibacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 832; DB 22;
Pred. No. 5.4e-81;
D; Mismatches 0;
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                                                                                                                                                                   rickettsial;
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Best Loc
Matches
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                                                                                                                                                                                                                                 CA2281913-A1
                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                     Poikilothermic vaccine; OspA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OspA antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acids encoding an amino acid
surface antigen present on Pisciricketts
protect fish against piscirickettsiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simard
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29-JUL-2000;
  (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A
                                                                                              17-SEP-1999;
                                                                                                                                       17-SEP-1999;
                                                                                                                                                                                    17-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                     Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB81126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB81126 standard;
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salmonid
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                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Piscirickettsia salmonis; rickettsial pathogen; nid rickettsial septicaemia; rickettsial disease
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                                                                                                                                                                                                                                                                           B_cell_epitope
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Piscirickettsia salmonis are useful to
rickettsiosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AA.
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Pred. No. 2e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poikilothermic vaccine; OspA; SRS; antibody.
                                                                  (KAYW/)
(BURI/)
(KUZY/)
                          Kay WW
                                                                                                                                                              17-SEP-1999;
                                                                                                                                                                                                       17-SEP-1999;
                                                                                                                                                                                                                                                    17-MAR-2001
                                                                                                                                                                                                                                                                                                 CA2281913-A1
                                                                                                                                                                                                                                                                                                                                              Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OspA B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB81130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
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63

GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER

0

standard;

Peptide;

20 AA

epitope

peptide

#2

fish; Pis salmonid

Piscirickettsia salmonis; rickettsial panid rickettsial septicaemia; rickettsial

(first entry)

KAY W W. BURIAN J. KUZYK M A KAY W

Þ

99CA-2281913 99CA-2281913

Burian

Kuzyk

M

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Query Match
Best Local
                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                             This invention relates to a method for the protection against infection of a polikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animal particularly polikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The presest sequence represents P. salmonis OspA protein. An OspA protein with an N-terminal fusion partner is used in a vaccine to create an anti-OspA antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a septicaemia and other rickettsial diseases comprises administering a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Кау
                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                              Local
                   62
                                                              WW,
GGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-316844/34.
                                                                                                                                                           158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       containing
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF86246
                                                                                                                                                                                                                                                                                              response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burian
                                                                                                                                                                                                                                                      162 AA;
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the OspA protein of Piscirickettsia
                                                                                                                                                                              98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kuzyk
                                                                                                                                                      Score 815; DB 22;
Pred. No. 2e-79;
1; Mismatches 1;
                                                                                                                                                                                                 Length
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          salmonis
                                                                                                                                                           0:
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      animals,
                     121
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2001-316844/34.

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RESULT 6
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The present sequence is that of BASB113 protein from Moraxella catarrhalis strain Mc2931 (ATCC 43617), a causative agent of otitis media in children and pneumonia in adults. The invention provides BASB113 polypeptides, and polypucleotides encoding them, as well as expression vectors, host cells and methods for producing BASB113 polypeptides using recombinant methods. Also claimed is a vaccine composition comprising a BASB113 polypeptide, an immunogenic
                                                                                                                                         Claim 1; Page 67; 86pp;
                                                                                                                                                       New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium, useful for diagnosing and producing vaccines against bacterial infections such as otitis media and pneumonia
                                                                                                                                                                                                                                         WPI; 2001-112458/12.
N-PSDB; AAF30043.
                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                       25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moraxella catarrhalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moraxella catarrhalis BASB113 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB20105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Otitis media;
                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumonia; therapy; diagnosis;
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AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAN AAY34583. AAX91802 to AAX91989 represent PCR primers used in the

AAY34318

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588pp;

English.

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RESULT 7
AAY34487
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                              Claim 1; Page 469;
                                                                                                                                             05-MAY-1998;
22-MAY-1998;
29-JUL-1998;
                                                  gingivitis
                                                    Antigenic Porphorymonas gingivalis
                                                                         WPI; 1999-385613/32
N-PSDB; AAX91705.
                                                                                                                                                                                              04-AUG-1998;
10-DEC-1997;
31-DEC-1997;
30-JAN-1998;
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09-APR-1998;
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                                                                                                                                                                                                                                                                            W09929870-A1
                                                                                                                                                                                                                                                                                            Porphorymonas
                                                                                                                                                                                                                                                                                                                   Porphorymonas gingivalis;
                                                                                                                                                                                                                                                                                                                                      Porphorymonas
                                                                                                                                                                                                                                                                                                                                                         25-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                       AAY34487 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                           AAY34487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment of a BASB113 polypeptide, or a polypeptide having at least 85% amino acid sequence identity to BASB113, or comprising a diagnosing a woraxella infection involves identifying a BASB13 in treating humans with M. catarrhalis infection comprises at least polypeptides also have utility in raising specific antibodies, and in screening for antibacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                               , CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                          EKTGRDAILGAAVGAAAGAYMERQAK----QIEQQMQGTGVTVTHDTDTGN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVVLLASSMALAGCANTGT---TGNGTGFGGANVNKAVIGAVAGAL---GGTAISKATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGN 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSSLIIISVFLVGCAQNFSRQEVGAATG-----AVVGGVAGQLFGKGSGRVSMAIGG
                                                                                                Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Conserv
                                                                                                                                                                                                                                                                                                              antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 AA;
                                                                                                                                           98AU-0001546
98AU-0002264
98AU-0002911
98AU-0003128
98AU-0003338
98AU-0003654
98AU-0004917
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                                                                                                                                                                                                                                                                                                                                  gingivalis protein PG3
                                                                                                                                                                                                     97AU-0001182
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                                                                                                                                                                                                             97AU-0000839
                                                                                                                                                                                                                        98AU-0005028
                                                                                                Hocking DM, Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.3%;
                                                                                                                                                                                                                                                                                                                   PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                        223
                                                                                                                                                                                                                                                                                                           periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 111; DB 22;
Pred. No. 0.00097;
                                                                                                      Margetts
                                                                                                                                                                                                                                                                                                                                                                                       B
                                                    peptides
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                                                                                                     MB,
                                                   for
                                                 preventing
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                                                                                                  Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
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109 PVRTYQRYNKQERRQQYCRE 128

Matches

20; Similarity

Conservative

13.5%; Score 112; DB 22; 100.0%; Pred. No. 3.3e-05; O. Mismatches 0;

Length Indels

20;

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0,: Gaps

0;

Query Match

Local

Sequence

20 AA;

This invention relates to a of a poikilothermic fish by

Example 2; Page 17; 35pp; English.

Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -

of a political particular processes an immunogenic animals, salmonis. The method comprises administering an immunogenic amount of a particularly politic antigen termed OspA, or an immunogenic fragment of particularly politic termed ospA, or an immunogenic fragment of particularly politic termed ospA, or an immunogenic fragment of particularly politic termed ospA, or an immunogenic fragment of particularly politic termed ospA, or an immunogenic fragment of particularly politic termed ospA, or an immunogenic fish, against the bacterial pathogen nickettsial septicaemia (SRS) and other protecting against salmonid sequence represents an immunogenic epitope of the P. salmonis OspA protein. The peptide is used to raise rabbit anti-OspA antibodies.

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RESULT 8
AAY34362
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Best Local S
Matches 25
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10-DEC-1997;
31-DEC-1997;
30-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to AAX94583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can
                                                                               Claim
                                                                                                  Antigenic Porphorymonas gingivalis peptides gingivitis
                                                                                                                                                                     Ross
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09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphorymonas gingivalis; vaccine; antigenic.
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                                                                              1; Page 325-326;
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25; Conservative
                                                                                                                                                                   Barr IG,
Rothel LJ,
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97AU-0001186
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98AU-0003128
98AU-0003318
98AU-0003318
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34.7%;
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Webb EA;
                                                                             588pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 102.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                periodontal
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.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
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                                                                                                                                                                             Patterson
                                                                                                              preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                               gingivitis;
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29 VGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKL

Matches

21;

Conservative

9;

Indels

Gaps

0,

81 0

Local

Similarity

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RESULT 9
AAR05799
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Matches 25
                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                            with lysozyme, opt. in the presence of a detergent. The encoding the PBOMP proteins were isolated by screening with an oligonucleotide probe based on the amino acid s PBOMP protein, or using antibodies to PBOMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The PBOMP proteins were isolated from a PBOMP-enriched insoluble cell wall fraction from physically disrupted cells of H. influenzae and then solubilising the PBOMP from the cell wall fraction by heat
                                                                                                                                                                                                                                                                                                                                               in the presence of a detergent or digesting the cell wall fraction with lysozyme, opt. in the presence of a detergent. The genes encoding the PBOMP proteins were isolated by screening a DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane protein epitopes of Haemophilus the prodn. of antibodies, in vaccines and for produced the produce of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-115815/15.
N-PSDB; AAQ03870.
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21-AUG-1989;
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Biologics Outer Mo
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                 Score 101; DB Pred. No. 0.00 9; Mismatches
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC imaging of sites expressing (II). (I) and (II) are useful in medical CC disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations in CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC whote: The sequences. ABG00010-ABG30377 represent novel human CC wote: The sequence data for this patent did not appear in the printed composition, but was obtained in electronic format directly from WIPO
                                                                                                             Query Match
                                                                                Matches
                                                                                                                                          Sequence
185 IISILPAKVAVDNSQNKRNAQAFGALIGAVAGGVIGHNVGSGSNSGTTAGAVGGGAVGAA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 46265; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
                              12 IISVFLVGCAQNFSR-----QEVGAATGAVVGGVAGQLFGKG--SGRVSMAIGGAVLGGL 64
                                                                                          Local
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                          Similarity
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0.077;
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C proteins by hydrolysing many of the macromolecules while leaving the structural proteins intact. In the case of silk proteins, the C chromatography and processed into an aqueous-based mixture for into vector pET24 for recombinant expression in Escherichia coli, containing denaturant (3 M guanidine-HCl) and by affinity containing denaturant (3 M guanidine-HCl) and by affinity containing denaturant (3 M guanidine-HCl) and by affinity containing denaturant of the invention can be used in the construction of many ballistic protection, parachutes and parachute cords. The new fewer steps, requires less time and smaller volumes of reagents,
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                                                                                                                                                                               The present sequence is that of the orb-weaver spider (Nephila clavipes) recombinant silk protein pETNCDS. The invention provides methods for purifying and spinning spider silks and other structural proteins. Organic acids are used to lyse recombinant cells or other biological samples (such as non-recombinantly derived cells), and enrich the purity and yields of structural
                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                Recovering structural polypeptides in a biological sample, useful for purifying and spinning spider silks and other structural proteins, comprises treating the sample containing the polypeptides with an acid
                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH26304
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Misc-difference 427
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ARCIDIACONO S.
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US SEC OF ARMY.
                                                                                                                                                                                                                                                                                    Page 41-42; 49pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0490291.
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                                                                                                                                                                                                                        The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genes from Dinteractions
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11-JUL-2000;
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is easy
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DB; ABL13950.
VTSGISS--LGLGNRRFSLSRQESSEQQSGIGGAIPGGLVSGQAQQQQQQQVPFPQQPLQ
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2179 GSVGQS----GGGGQGRYPTPIQRPNNYPQHP---
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N-PSDB; ABL10335.
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useful in developmental biology and in elucidating cell signalling
cell-cell interactions in higher eukaryotes for the development of
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pharmaceutical.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
     QKKPRYFVAMFDYDP---
                                              QERROQYCREFQQKAMIAGQKQEIYGTACPQPDG
                                                                                             PGQMMGPRGPLNQQQQQQQQQQQQQMQQGQMMPGQQAGQ----QQAQPG---
                                                                                                                                            LGGLIGSK--IGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNK 118
                                                                                                                                                                                           МОСОМОСОМОСОМЕСТВ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТО В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТЯ В МОСОМЕТСЯ В МОСОМЕТО В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТСЯ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В МОСОМЕТЬ В
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                                                                                                                                                                                                                                                                                                                          Score 84; DB 22;
Pred. No. 7.1;
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                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                          Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 97 ORFS are shown. The proteins are variously cell envelope proteins, cytoplasmic proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Helicobacter pylori nucleic acids - used to develop products for the diagnosis, prevention and treatment of infection H. pylori and other Helicobacter species {\sf H}
                                                                                                                                                                                                                                                                                                                                                   Sequence
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05-DEC-1996;
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                                                     LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRY 116
                                                                                                                                                                         MRGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAV 60
                                                                                                              MSGLRTFSCVVVLCGAMVNVAVAGPKIEARGELGKFVGGAVGNFVGDKMGGF---VGGAI
-GGYIGSEVGDRV--EDYIRGVDREPQNKEPQTPR
                                                                                                                                                                                                                                  31;
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96US-0759625.
97US-0823745.
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Pred. No.
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                                                                                                                                                                                                                                  51;
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AL070512 Drosophil
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AL286627 Tetraodon
BG240789 OV1_38_CO
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BE355894 DG1_11_E1
BF176742 EM1_4_F01
BG052290 RHIZ2_12_BF586874 FM1_31_E0
BG053591 RHIZ2_11_BG0533014 RHIZ2_11_BG0533014 RHIZ2_16_BG73858 EM1_20_CO
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ALIGNMENTS

RESULT 1
AU037653
LOCUS
DEFINITION VERSION KEYWORDS REFERENCE SOURCE ACCESSION JOURNAL TITLE ORGANISM MEDLINE AUTHORS DNA Res. 99156227 Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of AU037653 Dictyostelium discoideum SS (H. Urushihara) Dictyostelium discoideum SS (H. Urushihara) Dictyostelium discoideum CDNA clone SSE138, mRNA sequence.
AU037653 AU037653.1 GI:3984406
EST. Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
1 (bases 1 to 551) development Dictyostelium discoideum. 5 (6), 335-340 (1998)

FEATURES COMMENT Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan Email: d402hu@sakura.cc.tsukuba.ac.jp PROJECT = 'Dictyostelium discoideum cDNA project in Japan'.
Location/Qualifiers

BASE COUNT ORIGIN source D /clone_lib="Dictyostelium discoideum /dev_stage="slug" 63 c 39 g 183 t /organism="Dictyostelium /strain="AX4" /db_xref="taxon:44689" /clone="SSE138" discoideum" SS (H.Urushihara)"

Query Match
Best Local Similarity
Matches 95; Conserv 5.7%; ilarity 52.5%; Conservative O; Mismatches DB 9; , 98 Length 551; Indels 0; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 18 partial 2; on bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 CAAAATCACATATTTTTAAAAAAAGAAATTTTTAAATCAAATTGTACTTCATCAAATCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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uscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-88"
/clone="BACR31D18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0057 row: B column: 14
Seg primer: CGTTGTAAAACGACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 470
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University of Utah Genome Center
University of Utah
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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1 (bases 1 to 470)
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470 bp DNA linear GSS 16-FEB-2002M0057B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic Clone UUGC2M0057B14 F, DNA sequence.
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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                 was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PW042nv: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0057B14"
/clone_lib="Mouse 10kb plasmid UUGClM library"
/sex="Male"
                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/).
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                      Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ dat This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                          Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 976)
Roest-Crollius, H., Jallon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                       Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot
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- Jaillon,O.,
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97 c 132 g 103 t
                                                                                                                                      /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="103P02"
                                                                                         /clone_11b="G"
/note="Genoscope sequence
151 c 137 g 327
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57.6%;
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        Score 42.2; D
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 238)
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OV1_38_C06.g1_A002 Ovary
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                                                                                                                                                                                                                                                                      High quality sequence
                                                                                                                                                                                                                                                                                          Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                          Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An EST database from Sorghum: 
Unpublished (2000)
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706 542 1805
                      63
            /Clone_lib="Ovary 1 (OV1)"
/Clone_lib="Ovary 1 (OV1)"
/note="Organ: Mix of ovaries of varying immature stages from 8-week-old plants; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."

54 c 70 g 51 t
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                     /db_xref="taxon:4558"
                                                                                                                                                                         /organism="Sorghum bicolor"
                                                                                                                                                                                                                                                   stop:
                                                                                                                                                                                                                                                                        start:
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1 (OV1)
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Sorghum bicolor
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Query Match Best Local Similarity

5.5%;

Score Pred.

42; No.

4.8

10;

Length 238;

Matches

345

79

EST

06-MAR-2001

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23 CTAACAAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAACACACATCTG 82
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                         AA 144
                                                                                      ACAGTGATTTAAATTTAAATGACGTAAAAGTTTAGATATTATTACACAAGTGATGGTACAC 142
                                                                                                                        CTAAAAATTCCATTCAGAAAAACTCATTTACAATAATATAGAAAAGAATTAAGCAAGTGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGACGGCCAGATCAACTATGAAGAGTTTGTTAAGGTTATGATGGCCAAGTGAGGAGCGGT
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                                                                                                                                                                                       l Similarity 59.0
                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 273)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ260501 273
CITBI-E1-2509D17.TR CITBI-E1
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                                                                                                                                                                                                                                                   /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
43 c 47 g 70 t
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2509D17"
                                                                                                                                                                                                                                                                                                                                        /clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                        /sex="male"
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BE355894.1
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DG1_11_E11.g1_A002 Dark Grown
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                            sorghum.
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BG356895
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EST.
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Plant Sciences Building, I
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mmpratt@uga.edu
Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG356895
OV2_11_D01.g1_A002 Ovary
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                                                                                                                (DG1) Sorghum bicolor cDNA,
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143

BASE COUNT ORIGIN

FEATURES

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COMMENT

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AUTHORS

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EST 20-JUL-2000

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Matches Query Match

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AUTHORS
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                                                                                Reid,S.P., Cordonnier-Pratt,M.-M.,
An EST database from Sorghum: devei
Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                             sequence.
BF176742
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The University of Georgia
Plant Sciences Building, Rm.
Tel: 706 542 1860
Fax: 706 542 1805
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Contact: Cordonnier-Pratt
The University of Georgia
Plant Sciences Building, Rm.
Plant 8642 1860
Tel: 706 542 1805
                                                                                                                                                                                                                         sorghum bicolor
                                                                                                                                                                                                                                                              EST
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                                                                                                                                                                             BF176742.1
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                                                                  Department of Botany
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/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DG1)"
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/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/note="Organ: 5-day-old dark-grown seedlings; Vector:
/lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 82 c 116 g 119 t
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Pred. No.
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1 (EM1)
                                  2502, Athens,
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                                                                                                                    developing
                                                                                                                                                                                                                                                                                                                             Sorghum bicolor cDNA, mRNA
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                                                                                                                                    Gingle, A.
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                                  GA 30602-7271, USA
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                                                                                                                                    Pratt, L.H
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BASE COUNT
ORIGIN
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AUTHORS
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Best Local Similarity
"~+~hes 72; Conserv!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 CGACGGCCAGATCAACTATGAAGAGTTTGTTAAGGTTATGATGGCCAAGTGAGGAGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 CGGCGAGAAGCTGACCGACGAGGAGGTCGACGACGATGATCCGTGAGGCTGACGTCGATGG 117
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BG052290
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                     The University of Georgia Plant Sciences Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clade; Panicoideae; Andropogoneae;
1 (bases 1 to 446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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Sorghum propinguum
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RHIZ2_12_G04.g1_A003 Rhizome2
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706 542 1805
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/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector:
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/db_xref="taxon:132711"
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/note="Organ: Rhizomes; Vector
                                                                                                                                                                   Location/Qualifiers
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Pred. No. 6.1;
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Vector: pBluescript II from Lambda

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ORIGIN
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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BF586874
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGGCGGCGACCGGTGCGGTTGTGGGCGGTGT 404
                                                                                                                                                                                                                                                                                          High quality sequence start: 8
High quality sequence stop: 495
                                                                                                                                                                                                                                                                                                                           Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                        The University of Georgia
Plant Sciences Building, Rm.
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum propinquum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An EST database from Sorghum: floral-induced meristems Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department
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EST.
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72; Conservative
                                        /organism="Sorghum propinguum"
/db_xref="taxon:132711"
/clone_lib="Floral-Induced Meristem 1 (FM1)"
/clone_lib="Floral-Induced meristems: Vector:
pBluescript II from Lambda Zap II; Site_1: xhoI; Site_2:
ECORI; mature plants were placed in a growth chamber for
induced by short-day conditions); 16 days after being
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
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81 c 124 g 140 t
                                 excision.
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                                                                                                                                                                                                                                                                                                                                       to exclude PolyA, vector and regions threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              2502,
                            154 t
                                                                                                                                                                                                                                                                                                                                                                                                                     Athens, GA 30602-7271,
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ORIGIN
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Best Local
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VERSION
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BG053591
LOCUS
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Best Local Similarity
174 CC
                             465 TC
                                                     114
                                                                                                        345 CCCCAGAACTTCAGCCGCCAGGAAGTTGGGGGGGGCGCCACCGGTGCGGTTGTGGGCGGTGT 404
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                                  CGACGGCCAGATCAACTATGAAGAGTTTGTTAAGGTTATGATGGCCAAGTGAGGAGCGGT 173
                                                     CGGCGAGAAGCTGACCGACGAGGAGGTCGACGAGATGATCCGTGAGGCTGACGTCGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Botany
The University of Georgia
Plant Sciences Building, R
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                              l Similarity
72; Conserv
 175
                           466
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                                                                                                                                                                                                                                                                                                                                                                   High quality sequence start: High quality sequence stop: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An EST database from Sorghum:
Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                             POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                   Email: mmpratt@uga.edu
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum propinguum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A.,
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BG053591
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RHIZ2_11_C03.g1_A003 Rhizome2
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                                                                                                                                                                                                        /Clone_lib="Rhizome2 (RHIZ2)"
/Clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
a 92 c 142 g 164 t
                                                                                                                                                                                                                                                                                                   /organism="Sorghum propinguum"
/db_xref="taxon:132711"
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Pred. No. 6.5;
0; Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                    345 CGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCGGCCACCGGTGCGGCGTGTT 404
                                                                                                                                                                                                                                                   241 CC
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                                                                                                                                                                                                                                                                                                                                                                                 121 CGGCGAGAAGCTGACCGACGAGGAGGTCGACGAGATGATCCGTGAGGCTGACGTCGATGG 180
                                                                                              sequence.
BG713844
BG713844.1
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EM1_20_C08.g2_A002 Embryo 1 (EM1)
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The University of Georgia
Plant Sciences Building, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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BG053014
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l (bases 1 to 531)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                 sorghum.
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uga.edu
Seq primer: PolyTMix
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                                                                                                                                                                                                                                                   242
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706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Sorghum propinquum"
/db_xref="taxon:132711"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
/clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision."
a 101 c 152 g 154 t 2 others
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REFERENCE
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BF587805
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KEYWORDS
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Best Local Sin
Matches 72;
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                                                                                                                                                     AUTHORS
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Reid, S.P., Cordonnier-Pratt, M.-M., Gingle, A. and
An EST database from Sorghum: developing embryos
Unpublished (2000)
                                                                                                                                                        Sorghum propinguum.
Sorghum propinguum
Sorghum propinguum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 561)
                                                                                                                                                                                                                                                                                                              561 bp FM1_40_G05.g1_A003 Floral-Induced propinguum cDNA, mRNA sequence BF587805
                              The University of Georgia Plant Sciences Building,
                                                                Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
                                                                                                                                                     Cordonnier-Pratt, M.-M.,
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BF587805
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High quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mmpratt@uga.edu
Sequences have been trimmed to exclude
below Phred quality 16. The threshold i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The University of Georgia Plant Sciences Building, Rm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cordonnier-Pratt MM
                                                                                                                 An EST database from Sorghum:
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/note="Organ: Embryos germinated for 24 hr; Vector:
/note="Organ: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda Zap II. Clones to be sequenced were
prepared by mass excision."
a 98 c 152 g 169 t
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/db_xref="taxon:4558"
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Pred. No. 6.6;
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Search completed: October 27, 2002, 18:34:59 Job time: 1533.81 secs
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                                                                                                                                                                                                                                                                                               BASE COUNT
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                                                                                                                                                                                                                    Query Match 5.5%; Score 42; DB 10; Length 561; Best Local Similarity 59.0%; Pred. No. 6.8; Matches 72; Conservative 0; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                        322 CC 323
                                                                                                       345 CGCCCAGAACTTCAGCCGCCAGGAAGTTGGGGCGGCCACCGGTGCGGTTGTGGGCGGTGT 404
                                                                                    465 TC 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                           US-08-330-394A-1
US-08-330-394A-3
US-09-006-632-5
US-09-006-632-5
US-09-277-716-21
US-09-198-955A-11
US-08-960-780-31
US-09-073-898-31
US-09-073-898-31
US-08-471-033-6
US-08-471-044-6
US-08-471-044-6
US-08-471-046A-6
US-08-471-046A-6
US-08-471-046A-6
US-08-471-046A-6
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US-08-048-164A-3
US-08-460-462-1
US-08-460-457-1
US-08-460-457-3
US-08-460-458-3
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US-08-460-455-3
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3359.570 Million cell updates/sec
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31. Appl
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US-08-048-164A-1
Query Match
Best Local Similarity
Matches 272; Conserv
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J	Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 22, Appli Sequence 21, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

RESULT 1 US-08-048-164A-1 ; Sequence 1, Application US/08048164A ; Patent No. 5496934 ; GENERAL INFORMATION: TELEFAX: (214) TELEFAX: 66141 PENNIE TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: FRNGTH: 486 base pairs COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFFWARE: PATENTION PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/048,164A APPLICATION NUMBER: US/08/048,164A FILING DATE: 14-APR-1993 FILING DATE: 14-APR-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: MISTOCK, S. Lesile REGISTRATION NUMBER: 18,872 REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 78 TELECOMMUNICATION INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk TITLE OF INVENTION: CELLULOSE BINDING NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: MOLECULE TYPE: DNA APPLICANT: Goldstein, APPLICANT: Doi, Roy H. APPLICANT: Shoseyov, Ode APPLICANT: Shpiegl, Itai TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: unknown COUNTRY: U.S.A. ZIP: 10036 STREET: 1155 Ave CITY: New York STATE: New York ADDRESSEE: PENNIE & L..... STREET: 1155 Avenue of the (212) 790-9090 (212) 869-8864/9741 PENNIE & EDMONDS Oded Marc A. US/08/048,164A 7809-003 Americas Version #1.25 DOMAIN

35.2**%**; 98.9**%**;

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Score 270.2; DB 1 Pred. No. 3.8e-73; 0; Mismatches 3

DB 1;

Length 486; Indels

0;

Gaps

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                                                 Query Match
Best Local Similarity
Matches 272; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/048,164A
FILING DATE: 14-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
DECITEDATION NIMMERD: 18 A77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08048164A Patent No. 5496934
                                                                                                                                                                                              TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                     STRANDEDNESS:
TOPOLOGY: unk
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
          471
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shoseyov, Oded
APPLICANT: Shpiegl, Ital
APPLICANT: Shpiegl, Ital
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: CELLULOSE BINDING DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
TYPE:
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                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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EDNESS: double
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                                                       Conservative
                                                                                                                                  unknown
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                                                                  35.2%;
98.9%;
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                                                 Score 270.2; DB 1;
Pred. No. 3.8e-73;
Niematches 3;
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                                                                                                                                                                                                                                                            7809-003
                                                                                                                                                                                                                                                                                                                                                           Version #1.25
                                                                           Length 486;
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; NAME/KEY:
; LOCATION:
US-08-460-462-1
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,462
FILING DATE: CONCURRENTLY herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-193
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18.872
REFERENCE/DOCKET NUMBER: 7809-006
TELECOMMUNICATION INFORMATION:
"METERPHONE: /212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-460-462-1
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Patent No. 5670623
                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
                                                                                                            FEATURE:
Local 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS OF USE OF CELLULOSE BINDING DOMAIN PROTEINS NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: APPLICANT:
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APPLICANT: Doi,
                                                                                                                                                                                                                       TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                       TOPOLOGY:
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mvPE: nucleic acid
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ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New Yor
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                        Similarity
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         Conservative
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Shpiegl, Itai
Goldstein, Marc A.
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98.9%;
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    Score 270.2; DB 1
Pred. No. 3.8e-73;
0; Mismatches 3
                               DB 1;
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                               Length 486;
    Indels
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US-08-460-462-3/c
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                                                                                                                   ; MOLECULE TYPE: US-08-460-462-3
                                                                                                                                                                                                                               REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7809-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
                                             Query Match
Best Local Similarity
Matches 272; Conserv
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                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/460,462
FILING DATE: CONCULTENTLY herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14 APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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                                                                                                                                                 LENGTH: 486 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A. ZIP: 10036
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GCAAGCCCAACATCAACCTATGATACATATGTTGA 290
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1155 Avenue of the Americas
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Shpiegl, Itai
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                                                  Conservative
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98.9%;
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                                               Score 270.2; DB 1; Pred. No. 3.8e-73; 0; Mismatches 3;
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US-08-460-457-1
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US-08-460-457-1
Query Match
Best Local Similarity
Matches 272; Conserv
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                                                                                                                                                                                                    TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 780
TELECOMMUNICATION INFORMATION:
                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                           MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/460,457 FILING DATE: concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1155 A CITY: New York
                                                                                            NAME/KEY:
                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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Goldstein, Marc A.
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98.9%;
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                Score 270.2; DB 1 Pred. No. 3.8e-73;
                              DB 1;
                              Length 486;
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Conservative

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Best Local Similarity
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APPLICANT: Shoseyov
APPLICANT: Shpieg1,
APPLICANT: Goldstein
APPLICANT: Doi, Roy
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION NUMBER OF COLUMN AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND 
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
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ADDRESSEE: PENNIE & 1
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                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/460,457 FILING DATE: concurrently herewith CLASSIFICATION: 435
STREET: 1155 A
CITY: New York
STATE: New Yor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 GCAAGCCCAACATCAACCTATGATACATATCTGGA 275
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10036
                                                                                                                                                                                                                                                            : 486 base pairs nucleic acid EDNESS: double
                                                                      Conservative
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Shpiegl, Itai
Goldstein, Marc A.
                                                                                                                                                                                                                                           unknown
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                                                                                                 35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18,872
                                                       Score 270.2; DB 1;
Pred. No. 3.8e-73;
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                                                                                                               Length
                                                             Indels
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Best Local :
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, vc
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/460,458
FILING DATE: concurrently herewith
CLASSIFICATION: 435
                                                                                                                                  FEATURE:
                                                                                                                                           TOPOLOGY: us
MOLECULE TYPE:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shoseyov, Oded
TITLE OF INVENTION: KITS AND METHODS OF DETECTION USING CELLULOSE BINDING DOMAI NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GCAAGCCCAACATCAACCTATGATACATATCTGGA 275
                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York COUNTRY: U.S.A. ZIP: 10036
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STREET: 1155 Avenue of the Americas
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                                                                                                                                                                   nucleic acid
DEDNESS: double
                                             Conservative
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                                                                                                                                                        unknown
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                                                      Score 270.2;
Pred. No. 3.
                                         Mismatches
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                                    3.8e-73;
3;
                                                                 DB 1;
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                                                              Length
                                        Indels
                                                              486;
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                                     Gaps
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RESULT 8
US-08-460-458-3/c
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                                                                               Query Match
Best Local Similarity 98.9
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                                                                                                                                                                                                                                      TELEPHONE: (212) 790-5
TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7809
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 01
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
ANAME ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shoseyo TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                         471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                      ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT 120
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                                                                                                                                                                                                                                                                                                                                Misrock, S. Leslie
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KITS AND METHODS
                                                                                                      35.2%;
98.9%;
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                                                                                         Score 270.2; DB 1;
Pred. No. 3.8e-73;
0; Mismatches 3;
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                                                                                                                 Length
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US-08-460-455-1
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                                                                              US-08-460-455-1
                                                                                                                                                                                             TELERA: (414)
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FRIGHT: 486 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08460455 Patent No. 5837814
                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shoseyov, Oded
APPLICANT: Shpiegl, Ital
APPLICANT: Goldstein, Marc
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: CELLULO
                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: US 08/048,164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                              MOLECULE TYPE: FEATURE:
Local 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                    NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/460,455 FILING DATE: concurrently herewith
                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                                                                                                NAME/KEY:
                                                                                                                                                                             STRANDEDNESS:
                                                                                                LOCATION:
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                            Similarity
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                 : (212) 790-9090
(212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0,
            Conservative
                                                                                                                                                                 unknown
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                          35.2%;
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          Score 270.2; DB 2
Pred. No. 3.8e-73;
D; Mismatches 3
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                                           DB 2;
                                          Length
            Indels
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        Gaps
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US-08-460-455-3/c
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                                                                                       Matches
                                                                                                                 Query Match
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Patent No. 5837814
                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9
TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: MISIOCK, S. Leslie
                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CELLULOSE BINDING DOMAIN PROTEINS NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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61 ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT 120
                                                                                      Local Sinhes 272;
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CITY: N
STATE:
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                        241 GCAAGCCCAACATCAACCTATGATACATATCTGGA 275
                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: concu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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Shpiegl, Itai
                                                                                      Conservative
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                                                                                                                                                                       unknown
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                                                                                                35.2%;
98.9%;
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                                                                                  Score 270.2; DB 2;
Pred. No. 3.8e-73;
0; Mismatches 3;
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                                                                                                               ; NAME/KEY:
; LOCATION:
US-08-330-394A-1
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                                                Query Match
Best Local Similarity 98.9
Matches 272; Conservative
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; Patent No. 5856201
                                                                                                                                                                                                                              TELEFAX: (212) 869-886
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,394A
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING DATE: 14-APR-1994
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APPLICANT:
APPLICANT:
                                                                                                                                                        FEATURE:
                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: MISROCK, S. LESLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: Doi, Roy H.
TITLE OF INVENTION: ME
TOPOLOGY:
                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                             TYPE:
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ZIP: 10036
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                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 AVENUE OF THE AMERICAS CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                       486 base pairs
                                                                                                                                                                                                                                                                          (212) 790-9090
(212) 869-8864
                                                                                                                                                                                  unknown
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Goldstein, Marc A.
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CELLULOSE E
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                                                                    Score 270.2; DB 2
Pred. No. 3.8e-73;
                                                         Mismatches
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                                                                                 DB 2;
                                                                              Length 486;
                                                       Indels
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US-08-330-394A-3/c
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                                                            Matches
                                                                                        Query Match
                                                                                                                                                                                                                              TELEX: 66441 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/330,394A
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1155 AVEN
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS OF DETECTION USING THE TITLE OF INVENTION: CELLULOSE BINDING DOMAIN NUMBER OF SEQUENCES: 33
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                                                                                                                                     TOPOLOGY: u
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                                                            Local Sinhes 272;
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                                                                                                                                                                                                                                                                                                         NAME: MISROCK, S. LESLIE REFERENCE/DOCKET NUMBER:
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               GCAAGCCCAACATCAACCTATGATACATATCTGGA 275
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Similarity 98.972; Conservative
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(212) 869-8864
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Goldstein, Marc A.
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                                                                       35.2%;
                                                            Score 270.2; DB 2;
Pred. No. 3.8e-73;
0; Mismatches 3;
                                                                                        DB 2;
                                                                                        Length 486;
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                                                                                                                                                             Best Loc
Matches
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                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shani, Ziv
TITLE OF INVENTION: ARABIDOPSIS THAI
TITLE OF INVENTION: GLUCANASE GENE,
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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 121 TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA 180
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STREET: 1155 Avenue of the Americas
CITY: New York
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TOPOLOGY: lir
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TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Baldwin, Geraldine F REGISTRATION NUMBER: 31,23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                             LENGTH:
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                                                 ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATTGACGTAAAAGTTAGATAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA 232
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                                 ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT 140
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                                                                                                                                                                                                                                                                                      nucleic acid
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98.9%;
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US-09-006-632-5
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SEQUENCE CHARACTERISTICS:
LENGTH: 499 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICANT: Shpigel, Etai
TITLE OF INVENTION: TRAN
TITLE OF INVENTION: MORP
  181 TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA 240
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                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
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                                                                                                                                                          ADDRESSEE:
                                            TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA 180
                                                                                                   ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT 120
                              TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA
                                                                                   ATCAAAATTACTAACACATCTGACAGTGATTTAAAATTTAAATGACGTAAAAGTTAGATAT 140
                                                                                                                                        TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAAGAAACA 240
                                                                                                                                                                                                    272;
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10036-2711
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                               (212) 790-9090
(212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ Version 2.0
                                                                                                                                                                                                    Conservative
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98.9%;
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Pred. No. 3.9e-73;
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Search completed: October 27, 2002, Job time: 61.152 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: DNA encoding a Cellulose Binding Domain (CBD)-Gaussia lucifera US-09-277-716-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/277,716
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER FILING DATE: 1998-06-15
EARLIER FILING DATE: 1998-06-15
EARLIER APPLICATION NUMBER: 60/079,624
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
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US-09-277-716-21
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Best Local Similarity
Matches 272; Conserv
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SEQ ID NO 21
LENGTH: 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION NUMBER: US/09/277,716A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, App.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (1)..(1146)
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                                                                   GCAAGCCCAACATCAACCTATGATACATATGTTGA
                                                                                                                                     TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA
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Pred. No. 6.2e-73;
0; Mismatches 3
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prinand is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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1   /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2:   /SIDSI/gcgdata/geneseg/geneseqn-embl/NA1981.DAT:*
3:   /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
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AAF86246
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AAD11044
AAQ72917
AAV74072
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DNA sequence of E.
Ospa 17kD antigen
Piscirickettsia sa
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C. cellulovorans C
Clostridium cellul
                                                                                                                                                                                                     Description
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                                                                                                     misc_feature
                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                          Synthetic.
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ALIGNMENTS

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Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct; ds.
                                                                                                                                                                                                             DNA sequence of c17e2 ospA construct with N-terminal fusion partner.
                                                                                                                                                       Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                  AAF86248 standard; DNA; 768
                                                                                                                                                                                                                               (first entry)
                                                                        /note=
1..285
                                             /note= "I
286..768
                                                                                                 /*tag= a
                                                                                                                            Location/Qualifiers
                         /note= "Optimised OspA construct c17E2"
                                  /*tag=
                                                                                         /product=
                                                              ′*tag=
                                                                                                                    ..768
                                                    "DNA encoding undefined N-terminal fusion partner"
                                                                             "No stop codon is given"
                                                                                                         D)
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17-MAR-2001

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                    481
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(BURI/)
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                                     CGCCAGGAAGTTGGCGCCGGCCACCGGTGCGGTGTTGTGGGCGGTGTTGCCGGCCAGCTGTTC
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) BURIAN J.
) KUZYK M A.
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Pred. No. 1e-214;
Mismatches 0
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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals
                                                                                       Method for protecting poikilothermic fish against salmonid rickett septicaemia and other rickettsial diseases comprises administering vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                    P-PSDB;
                                                                                                                                                                                                     (KAYW/)
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DB; AAB81127.
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) BURIAN
) KUZYK M
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/product= "OspA"
/note= "Genus specific 17kDa antigen,
/note= not include a stop codon"
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                                                                                                            Poikilothermic vaccine; OspA;
                                                                                                                                             OspA 17kD
                                                                                                                                                                     11-JUL-2001
                                                                                                                                                                                          AAF86246
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                                                                                                             fish; Piscirickettsia salmonis; rickettsial pathogen; salmonid rickettsial septicaemia; rickettsial disease
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/partial
/product= "OspA"
/note= "Genus sp
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                                  /*tag=
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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents DNA encoding the P. salmonis OspA protein. An OspA protein with an N-terminal fusion partner is used in a vaccine to create
                                                                                                                                                                                                                                                                                                                                                              (KAYW/)
(BURI/)
(KUZY/)
                                                                                                                                                                                                    Disclosure; Fig 2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA2281913-A1
 Sequence
                                                                                                                                                                                                                                  vaccine
                                                                                                                                                                                                                                               septicaemia
                                                                                                                                                                                                                                                             Method for
                                                                                                                                                                                                                                                                                                                                    Kay ww,
                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-SEP-1999;
                           anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                       2001-316844/34
                                                                                                                                                                                                                                                                                                                                                              KAY W W.
BURIAN J.
KUZYK M A
                                                                                                                                                                                                                            for protecting poikilothermic fish against salmonid rickettsial emia and other rickettsial diseases comprises administering a containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                          AAB81126
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 BP; 137
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                                                                                                                                                                                                    35pp; English.
                                                                                                                                                                                                                                                                                                                                    Kuzyk
A; 79 C;
                                                                                                                                                                                                                                                                                                                                    MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           include a
144 G; 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stop codon"
T; 0 other;
                                          present
1 OspA
create
                                                                                                                  animals,
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δÃ В δÃ B οy Db Qy В Ş Вb Š DЬ Q DЬ ρ Query Match Best Local Matches 710 590 248 530 470 410 350 AGAACTTCAGCCGCCAGGAAGTTGGCGCGGGCCACCGGTGCGGTTGTGGGGCGGTGTTGCCG 290 GTGGTTGCCTGCAGGCCACCTCTCTGATCATTATCTCTGTTTTTCCTGGTTGGGTTGCGCCC 128 188 89 æ GAGGATGTTTGCAAGGTAGTAGTCTAATTATTATCAGTGTGTTTTTAGTTGGCTGTGCCC TCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAAAAA ACCAGAGTTTGGAAAAGGTAAAAGCAGGGCAAGTGACACGTTGGCGTAATCCAGATACAG ACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGTAATCCGGACACCG GTGGATTAATTGGTTCTAAAATCGGTCAATCGATGGATCAGCAGGATAAAATAAAGCTAA GCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGATAAAATCAAACTGA GCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGG GCCAGCTGTTCGGTAAAAGGCTCTGGTCGTGTGTCGATGGCCATCGGCGGTGCGGTTCTGG AGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTGTTGCTG 364; Similarity Conservative 38.4%; 76.0%; 0; Pred. Score 295; DB 22; Pred. No. 3.1e-76; Mismatches Length Indels 0 Gaps 529 469 127 409 67 349 367 649 307 589 247 187 0;

Вþ

428

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RESULT 4
AAH79040
ID AAH79040
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ID AAH79040
ID AAH79040
ID AAH7
XX AAH7
XX Pisc
XX Pisc
XX Sept
KW ATCC
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XX CDS
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FT 12-b
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PR 20-c
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   Matches
ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acid sequences and the encoded prof a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity protect fish against p. salmonis which causes piscirickettsiosis, known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simard N,
Burzio L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-2000;
01-JUL-2000;
29-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 489 BP;
                                   470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acids encoding an amino acid sequence homologous to surface antigen present on Piscirickettsia salmonis are useful t protect fish against piscirickettsiosis
                                                                              128
                                                                                                                      410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                              350
                                                                                                                                                                                                                                                                     290 GTGGTTGCCTGCAGGCCAGCTCTCTGATCATTATCTCTGTTTTTCCTGGTGGGTTGGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AQUA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piscirickettsia salmonis; piscirickettsiosis; septicaemia; SRS; surface antigen; vaccine; ar ATCC VR-1361; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200168865-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piscirickettsia salmonis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH79040;
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                                                                                       GCCAGCTGTTCGGTAAAGGCTCTGGTCGTCGTCGATGGCCATCGGCGGTGCGGTTCTGG 469
                     GCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGATAAAATCAAACTGA 529
                                                                GCCAGCTGTTTGGTAAAGGTAGTGGTCGAGTTGCAATGGCCATTGGTGGTGCTGTTTTGG
                                                                                                                                                        AGAACTTTAGTCGTCAAGAAGTCGGAGCTGCGACTGGGGGCTGTTGTTGGCGGTGTTGCTG
                                                                                                                                                                               AGAACTTCAGCCGCCAGGAAGTTGGGGGGGGCACCGGTGCGGTTGTGGGGGGGTGTTGCCG 409
                                                                                                                                                                                                                                             GAGGATGTTTGCAAGGTAGTAGTCTAATTATTATCAGTGTGTTTTTAGTTGGCTGTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-639050/73.
B; AAG78025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Fig 4; 25pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; cDNA; 489
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                                                                                                                                                                                                                                                                                                                                                 Conservative
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2000GB-0016080.
2000GB-0016082.
2000GB-0018599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          salmonis polynucleotide P10.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    38.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 79 C; 144 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones
                                                                                                                                                                                                                                                                                                                                          Score 295; DB Pred. No. 3.1e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                              0;
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3.1e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Τ;
                                                                                                                                                                                                                                                                                                                                          115;
                                                                                                                                                                                                                                                                                                                                                                                                                                    0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s; salmonid rickettsial; antibacterial; fish;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Valenzuela
                                                                                                                                                                                                                                                                                                                                                                                  Length 489;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٦,
                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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, also
                                                                  187
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RESULT 5
AAD11043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вþ
                                                       Example 1.2; Fig le-1g; 121pp; English.
                                                                                          Preparation of a desired structura
                                                                                                                                                     Levy
                                                                                                                                                                          (CBDT-)
                                                                                                                                                                                                       08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                             Polysaccharide modification; polysaccharide binding domain; PBD; paperty; fiber; textile; biological crosslinker; mechanical property; clostridium cellulovorans cellulose binding domain; wet strength; durability; elasticity; CBDclos; cellulose binding protein A; CBP A;
                                                                                                                                                                                                                                    02-NOV-2000;
                                                                                                                                                                                                                                                                              WO200134091-A2.
                                                                                                                                                                                                                                                                                                                                                                       Clostridium
                                                                                                                                                                                                                                                                                                                                                                                           CBD-180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium
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                                                                                                                                  2001-457121/49
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                                                                                     tion of a polysaccharide containing material having at least structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                        CBD TECHNOLOGIES LTD.
YISSUM RES DEV CO HEI
                                                                                                                        AAE05746
                                                                                                                                                    Nussinovitch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                      cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cellulovorans cellulose binding
                                                                                                                                                                                                                                    2000WO-IL00708
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99US-0166389.
                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "C
/note= "CDS
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
3..572
                                                                                                                                                                                                                                                                                                /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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                                                                                                                                                                                                                                                                                                      "Cellulose binding domain-180
DS does not include stop codon
                                                                                                                                                   Shoseyov
                                                                                                                                                                       HEBREW UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽P
                                                                                                                                                                         JERUSALEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain-180 (CBD-180) DNA.
                                                                                                                                                                                                                                                                                                               _protein"
                                                                                              least one
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The present invention relates to methods and compositions for cross-linking and/or modifying the properties of polysaccharide materials. The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and

ior cross-

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RESULT 6
AADI10104
ID 10ADI
XX AADI
XX AADI
XX Clos
DT 24-s
DT Clos
XX POll
KW VART
KW WET
KW WET
KW CEB
OS Clos
XX KEPT
CDS
FT CDS
FT CDS
FT CDS
FT TT
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         penetrate paper.
The present sequence is a DNA encoding Clostridium cellulovorans cellulose binding domain (CBD)-180. CBD-180 contains 180 amino acids Clostridium cellulovorans CBD (CBDclos) of cellulose binding protein
                                                                                                                                                                                                                                                                                                                                                                          Clostridium
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     02-NOV-2000; 2000WO-IL00708.
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linking and/or modifying the properties of polysaccharide materials.
The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and
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18-NOV-1999;
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Cellulose binding domain

05-JUN-1995

(first entry)

AAQ72917

standard;

DNA;

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                            C AAQ72917/R63634 is a novel isolated cellulose binding domain. It pref. C binds crystalline with a Kd ranging from 1.5 microM - 0.5 microM, C pref. with a Kd of <1.2 microM, esp. <1.0 microM. The protein and C comprising DNA are claimed, as is a CBD fusion protein (FP) C emprising the CBD and a second protein. The second protein is pref. C Protein A, heparinase, a hormone or an enzyme capable of degrading C an environmental pollutant, or an HSP, HSP antibody, cross-reactive MSP-related protein or an antigenic portion of this. The CBD and FP cellingues. CBD nucleic acid may be used in drug delivery, affinity sepns. and diagnostic techniques. CBD nucleic acid may be obtd. from a variety of cell cources that produce CBDs that bind with high affinity and in a reversible manner or that produce CBD encoding mRNA. The preferred xxx
                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                   181
                                                                                                                                               121 TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Fig 1; 125pp; English.
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                                              GCAAGCCCAACATCAACCTATGATACATATCTGGA 275
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                                                                                              TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA
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                                                                                                                                                                                                ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAAGTTAGATAT 120
                                                                                                                                                                                    ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT
                                                                                                                                                                                                                                                                                               al Similarity
272; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIV CALIFORNIA.
YISSUM RES & DEV
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                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                          BP; 194 A; 89 C; 79 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellulovorans.
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98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain and fusion proteins - with ug delivery, affinity separations. and
                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                    Score 270.2; DB 1
Pred. No. 5.7e-69;
                                                                                                                                                                                                                                                                                            Mismatches
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QY

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121 TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGGTGCATTA

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Вb
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                                                                                                 Matches
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Best Local
                                                                                                                                                       CbpA protein of Clostridium cellulovorans. The sequence is used the construction of a fusion protein which can be used in diagnostic immunoassays, e.g. to detect heat-shock proteins (HSP) and their cross-reactive proteins, antigenic fragments or HSP-specific antibodies (which indicate insulin-dependent diabetes mellitus, or susceptibility to it. The CBD, has very high affinity for cellulose (including crystalline forms) and chitin (dissociation constant 0.8-1.4 mu M), but has almost no cellulolytic or amorphogenic activities. The CBD binds ove a wide pH range and is not released from cellulose by washing with water
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                            Detection of a specific analyte by reaction with binding agent fused to cellulose binding domain - and subsequent treatment with cellulose and reaction of insoluble product with a label specific for the analyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-1994;
14-APR-1993;
14-APR-1994;
                                                                                                                                                                                                                                                          This sequence encodes a cellulose binding domain (CBD) derived
                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC
                                                                                                                                                                                                                                                                                                                                                                                                      Doi RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigenic fragment; antibody; insulin-dependent diabetes mellitus; cellulose; chitin; cellulolytic; amorphogenic; ds
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ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT 120
                                                         1999-105130/09
DB; AAW90077.
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                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV CALIFORNIA.
YISSUM RES & DEV
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                                                                                                                                                                                                                                                                                                                                                                                                   Goldstein MA,
                                                                                             Conservative
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93US-0048164.
94WO-US04132.
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                                                                                                                                      194 A; 89 C; 79 G; 124 T; 0 other;
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98.9%;
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Pred. No. 5.7e-69;
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                                                                                                              Length 486;
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RESULT 9
AAX24930
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                                                                                                                                                                                                                                the cbpA procein of Clostridium cellulovorans. It was obtained by PCR amplification (see also AAX2495-3), and was used in the construction of binary vector pCCl, in which cbd was joined to the promoter and signal region of the novel endo-1.4-beta-glucanase cell gene (see AAX24923) of Arabidopsis thaliana. Expression of cbd in transgenic tobacco plants modulated their growth. The cell promoter can provide expression of any protein in elongating tissue. CBD is an example of a cell wall modulation transgene used to alter the structure or morphology of a plant. Transgenic plants of the invention may have altered biomass, growth, yield, greater or less resistance to biodegradation, be more or less digestible by ruminants, have altered cellulose content, larger or smaller leaves, etc., when compared to non-transgenic plants of the
                                                                     Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This DNA fragment encodes the cellulose binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellulose content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic plants expressing cell-value altered morphology, e.g. increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JAN-1998;
27-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       morphology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cellulose binding domain; CBD; cbpA; endo-1,4-beta-glucanase; Arabidopsis thaliana; transgenic plant; crop improvement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium
                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YISS ) YISSUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX24930 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256
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                                                                                                                  Match
species
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                                                                                                 Similarity
                                                                                                                                                                    499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 134; 144pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cellulovorans
                                                                          Conservative
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97IL-0121404.
98US-0006632.
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98.9%;
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                                                                                                                                                                    C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell-wall modulating protein reased growth, modified fiber
                                                                     Score 270.2; DB 20 Pred. No. 5.8e-69; 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                    82
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                                                                                                                                                                    <u>د:</u>
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                                                                                                                                                                    other;
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                                                                     Gaps
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The present invention relates to methods and compositions for cross-linking and/or modifying the properties of polysaccharide materials. The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide materials such as paper, yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD
                                                                                                                                                                                                                                             (YISS
                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                                                                                                                               08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polysaccharide modification; polysaccharide binding domain; PBD; pyarn; fiber; textile; biological crosslinker; mechanical property; Clostridium cellulovorans cellulose binding domain; wet strength;
                                                                                                                 Example 1.1;
                                                                                                                                                               Preparation of a
                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                            (CBDT-)
                                                                                                                                                                                                                                                                                                                02-NOV-2000; 2000WO-IL00708
                                                                                                                                                                                                                                                                                                                                        17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                              WO200134091-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 durability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAAGCCCAACATCAACCTATGATACATATGTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tion of a polysaccharide containing material having at least one structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                             CBD TECHNOLOGIES LTD
YISSUM RES DEV CO HE
                                                                                                                                                                                       AAE05745
                                                                                                                                                                                                                      Nussinovitch
                                                                                                                                                                                                                                                                                                                                                                                                                                            cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elasticity; CBDclos; cellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cellulovorans
                                                                                                                   Page 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                               99US-0164140.
99US-0166389.
                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 3..494
                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                      A,
                                                                                                                   121pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              507
                                                                                                                                                                                                                      Shoseyov
                                                                                                                                                                                                                                              HEBREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cellulose
                                                                                                                                                                                                                                                                                                                                                                                   "CBDclos protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                 English
                                                                                                                                                                                                                                              VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CBDclos)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 272;
    WO200134091-A2
                                                                                                                                                                                             Chimeric -
Chimeric -
                                                 misc_feature
                                                                                  misc_feature
                                                                                                                                                                                                                             Polysaccharide modification; polysaccharide binding domain; PBD; papyarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CBD; chimeric protein; S peptide-cellulose binding domain-S protein;
                                                                                                                                                                                                                                                                                               Chimeric
                                                                                                                                                                                                                                                                                                                                                               AAD11046 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains the fine fibers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                           261
                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a DNA encoding Clostridium cellulovorans cellulose binding domain (CBDclos) of cellulose binding protein A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                GCAAGCCCAACATCAACCTATGATACATATCTGGA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S peptide-cellulose binding domain-S protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                         Clostridium cellulovorans Bos \operatorname{sp}.
                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                          /*tag= b
/note= "This
652..981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                             /partial 68..624
                                                                                              /product= "Spep-CBD-Sprot protein"
/transl_except= "(pos: 979...981, aa:Xaa)"
/note= "Xaa corresponds to in-frame stop codon"
CDS does not include start and stop codon"
                    'notẽ= "This region is
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 A; 94 C; 84 G; 129 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.2%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                984
                                                                                                                                                                                                                                                                                                                                                               ВP
                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 270.2; DB 2
Pred. No. 5.8e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                       is
                     derived
                                                     derived
                                                                                         and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                   from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
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                                                 cellulovorans"
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RESULT
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                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to methods and compositions for cross-
CC linking and/or modifying the properties of polysaccharide materials.
CC The method involves treating the polysaccharide structure with a
CC polysaccharide binding domain (PBB) fusion protein. The method is
CC used to alter the structural, chemical, physical, electrical and
CC warns, fibers and textiles, using biological crosslinking agents.
CC The polysaccharide containing materials have improved mechanical
CC properties such as wet strengths, durability and elasticity. The PBD
CC which eliminates the sizing step. The use of a biological crosslinker
CC improves the recyclability of paper products. The PBD reagent maintains
CC the fine fibers in a slurry therefore resulting in better recovery of
CC caw materials. The PBD molecules are eluted by strong alkaline conditions
CC content a policy of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                   Matches
                                         343
                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a DNA encoding S peptide-cellulose binding domain-S protein (Spep-CBD-Sprot), a fusion protein derived from Clostridium cellulovorans and bovine.
                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                           103
                                                                                                                                                                                                                 61 ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT 120
                                                                                                                                                                                                                                                                                                                   Local
272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 4b-4g; 121pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparation of a desired structura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                           Levy I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-NOV-2000; 2000WO-IL00708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAY-2001
                               GCAAGCCCAACATCAACCTATGATACATATGTTGA
                                                GCAAGCCCAACATCAACCTATGATACATATCTGGA
                                                                                  TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA
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                                                                                                 TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA 240
                                                                                                                                           TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA
                                                                                                                                                                                                   ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tion of a polysaccharide containing material having at least one structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                      984 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nussinovitch
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0164140.
99US-0166389.
                                                                                                                                                                                                                                                                                                                                                                             325 A; 240 C; 193 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       35.2%;
98.9%;
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                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                      Score 270.2; DB : Pred. No. 8.3e-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
                                                                                                                                                                                                                                                                                                                        Mismatches
                                   377
                                                                                                                                                                                                                                                                                                                                               22; Length
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                     342
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AAZ27550 ID AAZ2 XX

AAZ27550 standard; DNA; 1146

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                                                                                                                                                                                                                                                            Renilla and Ptilosarcus green fluorescent protein (GFP) nucleic acids and C proteins. The luciferases and GFPs can be used in C bioluminescence-generating systems, assays, screening methods, diagnostic method and articles of manufacture. They can be expressed using c.g. bacterial, yeast, fungal, plant, insect or animal cells. The Renilla cmullerl, Gaussia and Pleuromamma lucifers or Renilla or Ptilosarcus GFPs can be used in e.g. toys, cosmetics, fountains, personal care items, fairy dust, beverages, soft drinks, foods, textile products, bubbles, the or paper products. In particular, they can be used in e.g. squirt guns, personal items, dentrifrices, soaps, body paints, bubble bath, inks, pellet guns, finger paints, foot bags, greeting cards, slimy play material, clothing, bubble making toys, bath powders, cosmetics, body commeters, body powders, body creams, toothpastes, mouthwashes, cospass, body paints, bubble bath, inks, wrapping paper, gelatins, icings, frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes, teacher, fish and later.
                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-1998;
15-JUN-1998;
01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 222-223; 233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Luciferase; green fluorescent protein; GFP; screening assay; diagnosis; bioluminescence-generating system; toy; cosmetic; fairy dust; beverage; body paint; squirt gun; balloon; slimy play material; soap; toothpaste; fusion protein; ds.
                                                                                                                                                                                                                          Sequence 1146 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a luciferase of the invention. The invention relates to Renilla mulleri, Gaussia and Pleuromamma luciferase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated
Renilla and F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-1999;
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                                                                                                                                                                                                                                                     transgenic
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                                                                                                                                                                    Local Sinhes 272;
                            121
                                                        61
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                                                                                                                                         <u>بـ</u>
                                                                                                                                         1999-580443/49
DB; AAY39952.
TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA
                                                      ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROLUME
BRYAN B
                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                     fish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Szent-Gyorgyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ptilosarcus green
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Renilla mulleri,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0079624.
98US-0089367.
98US-0102939.
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                                                                                                                                                                                                                          396 A; 222 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion
                                                                                                                                                                                                                                                    plants.
                                                                                                                                                                                35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein coding
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                                                                                                                                                                 Pred. No. ye-
0; Mismatches
                                                                                                                                                                                 Score 270.2; DB Pred. No. 9e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaussia and Pleuromamma luciferase fluorescent protein nucleic acids -
                                                                                                                                                                                                                          247
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••
                                                                                                                                                                                                                          0 other;
                                                                                                                                                                    Indels
                                                                                                                                                                                              Length
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                                                                                                                                                                   Gaps
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÕ
The patent discloses sea pansy (Renilla reniformis) green fluorescent proteins (GFP) and their corresponding polynucleotides. The invention also relates to sequences of the bioluminescence generating system (e.g. luciferase). R. reniformis GFP are used in diagnostic methods and in the production of novelty items such as toys (e.g. squirt gun, pellet gun, toy "Halloween" eggs, toy cigarettes, board/card game toys), finger paints, slimy play material, bubbles in bubble making toys, fishing lures, dolls, sparklers, mayic wand toys, balloons, personal care item (e.g. cosmetic, bath powders, body creams, tooth pastes, mouth wash, soaps, body paints, bubble bath), ornamental transgenic plants, fountain, fairy dust, food (gelatins, icings, frosting, beers, wine, champagne, milk, soft drinks, ice cubes, ice, dryice, beverage), textile (foot bag, clothing) and/or paper product (greeting cards, wrapping paper). The present sequence is a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Green fluorescent protein; GFP; bioluminescence generating system; luciferase; finger paint; slimy play material; fishing lure; sparkl doll; balloon; personal care item; cosmetic; bath powder; body cree tooth paste; mouth wash; soap; body paint; cramental transgenic pl bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage, wine; textile; clothing; paper product; greeting card; wrapping
                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2000; 2000US-189691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2001; 2001WO-US08277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200168824-A2
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                                                                                                                                                                                                                                                                                                                                                      2002-010561/01
                                                                                                                                                                                                                                                                                                                                                                                     ВJ,
                                                                                                                                                                                                                                                                                     in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                   PROLUME
BRYAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                     acids encoding Renilla reniformis green fluorescent proteins, in diagnostic bioluminescence procedures -
                                                                                                                                                                                                                                                                                                                                     AAE13383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp.
                                                                                                                                                                                                                                                                                                                                                                                   Szent-Gyorgyi C,
                                                                                                                                                                                                                                                   Page 162-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Gaussia CBD-luciferase fusion protein"
/note= "CDS does not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..1146
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                                                                                                                                                                                                                                                                                   procedures
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encoding

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RESULT 14
AAD11045
AAD111045
AXX AAD11
AXX AAD11
AXX AAD11
AXX AAD11
AXX POLys
COLost
AXX POLYs
KW Yarn;
KW Wet s
XXX POLOSt
XXX POLOSt
FT CDS
FT CDS
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XX PAN (CBD)
PAN (CBD)
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(CBDT-) CBD TECHNOLOGIES LTD.
(YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                       08-NOV-1999;
18-NOV-1999;
                                                                     02-NOV-2000; 2000WO-IL00708
                                                                                               17-MAY-2001.
                                                                                                                     WO200134091-A2
                                                                                                                                                                 misc_feature
                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                    Clostridium cellulovorans.
                                                                                                                                                                                                                                                                                                                                       Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; protein A-cellulose binding domain; ProtA-CBD; ds.
                                                                                                                                                                                                                                                                                                                                                                                         Clostridium cellulovorans protein A-cellulose binding domain DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD11045 standard; DNA; 1288
                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD11045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 98.972; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaussia species CBD-luciferase fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1146 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                     99US-0164140
99US-0166389
                                                                                                                                                                                                          /partial 3..791
                                                                                                                                                                                                                        /product= "Protein A-cellulose binding domain protein" /transl_except= "(pos: 1281..1283, aa:Xaa)" /note= "xaa corresponds to in-frame stop codon; CDS does not include stop codon"
                                                                                                                                                               cloning vector 795..1280
                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                  /note= "This region
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 A; 222 C; 247 G; 281 T; 0 other;
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"This region is
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                                                                                                                                                                                  is
                                                                                                                                   derived from cbp A
                                                                                                                                                                                derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Query Match

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The present invention relates to methods and compositions for cross-CC linking and/or modifying the properties of polysaccharide materials. The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) fusion protein. The method is composition of the structural, chemical, physical, electrical and composition proteins of polysaccharide materials such as paper, compositions, fibers and textiles, using biological crosslinking agents. CC The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD creagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker cc improves the recyclability of paper products. The PBD reagent maintains in the fine fibers in a slurry therefore resulting in better recovery of craw materials. The PBD molecules are eluted by strong alkaline conditions nemerate names.
Sequence 1288 BP; 523 A; 267 C; 202 G; 296 T; 0 other;
                                                                             Protein
                                                                                             The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1.3; Fig 3b-3g; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preparation of a polysaccharide containing material having at least desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-457121/49
                                    sent sequence is a DNA encoding Clostridium cellulovorans A-cellulose binding domain (ProtA-CBD). This sequence coof cbpA gene and a part of pRIT2T vector sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nussinovitch A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shoseyov
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                                                      This sequence contains
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д Q DЬ Qγ DЬ Qy DЬ Qy рЬ Qy Best Loc Matches 1050 241 GCAAGCCCAACATCAACCTATGATACATATCTGGA 275 990 181 121 TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA 180 810 870 Local GCAAGCCCAACATCAACCTATGATACATATGTTGA TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA Similarity Conservative 35.2%; 98.9%; 0; Score 270.2; DB 22, Pred. No. 9.6e-69; 0; Mismatches 3; DB 22; Length 0; Gaps 929 120 869 0

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RESULT 15
AAF86254/c
ID AAF862
XX
AAF862
XX
AC AAF862
XX
DT 11-JUL
XX
DE PCR pr
XX
DE PCR pr
XX
DE PCR pr
XX
Vaccin
KW Poikil
KW Vaccin
XX
XX
SRS; 1
                                                     PCR primer #4 used in cloning
                                                                                  11-JUL-2001
                                                                                                             AAF86254;
                                                                                                                                AAF86254 standard; DNA; 118
                                                                                (first entry)
                                                an optimisation of OspA gene
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Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct; PCR primer; ss.

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Search completed: October 27, 2002, 16:40:50 Job time: 198.984 secs
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                                                                                                                                                                                          Query Match 15.4%; Score 118; DB 22; Length 118; Best Local Similarity 100.0%; Pred. No. 1e-24; Matches 118; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis: The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly polkilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of the P. salmonis OspA gene. The OspA gene is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                                                                            Sequence 118 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 4B; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-316844/34.
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                                                                                                                              118
                                                                                                                                                                                                                                                                                              invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1999;
                                                                                                                                                               493
                                                              58
                                                            GGTCAGAGCATGGACCAGCAGGATAAAATCAAACTGAACCAGTCTCTGGAAAAAGTGAAA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99CA-2281913
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                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                            A; 32 C;
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                                                                                                                                                                                                                                                            28 G; 37 T; 0 other;
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Title:
Perfect score:
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SUMMARIES

19

BASE COUNT ORIGIN KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION RESULT 1 AX252413 REFERENCE FEATURES VERSION 000 a O a Ω Q a a a TITLE JOURNAL AUTHORS source 295 270.2 43.8 43.8 42.8 42.8 42.8 45 44.4 44.4 51 47.4 46.6 46.8 489 bp Sequence 5 from Patent W00168865. AX252413 Piscirickettsia salmonis. Piscirickettsia salmonis Fish vaccine against piscirickettsia Patent: WO 016865-A 5 20-SEP-2001; Aqua Health (Burope) Limited (GB)
Location/Qualifiers Burzio, L. 1 (bases 1 to 489) Simard,N., Brouwers,H., Jones,S.F., Griffiths,S., Piscirickettsia. 1 (bases 1 to 489) AX252413.1 GI:15985721 Bacteria; Proteobacteria; gamma 139 a /organism="Piscirickettsia salmonis" /db_xref="taxon:1238" 79 c 144 g 127 t . 489 AR096204 AR151733 AX250579 CLOCBP AB004845 CCU404845 AR129965 CTCIPBA CLOCIPA AE007606 AF155197 CTLOFEEGASE CTH275974 CSCELYZ RPXX04 CTH420770 AXZ51295 AX251295 AX2092545 AF429315 AF6429315 AC023433 AC064865 AP000982 AL603865 AC104102 AL646071 AX252413 AF184152 AR001083 AR001083 AR027448 AR027449 AR058257 AR058257 118514 CTCHIAGEN AX345104 CSCELZ RIR17KGCA 166614 166615 188789 **I88790** ALIGNMENTS subdivision; Piscirickettsia DNA salmonis linear AR027448 Sequence
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                                                                                                                                                                                                                       Submitted (10-SEP-1999) Biochemistry & Victoria, Petch Building, PO Box 3055, Location/Qualifiers
1. .4983
                                                                                                                                                                                                                                                                                                                                                     Identification of a genus-common Rickettsial surface salmonid pathogen Piscirickettsia salmonis Unpublished
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                                                                                                                                                                                                                                                                                              2 (bases 1 to 4983)
Kuzyk, M.A. and Kay, W.W.
Direct Submission
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MEVANYSSWTASVRAYIHTLLNTHNAYQALRDLRAHMRANHQDVSAFKLAEGLTAYSIK
                                                                                                                                                                                                                                                                          /organism="Piscirickettsia
/strain="LF-89"
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                                                                                                                                                      /gene="tnpA"
                                                                                                                                                                                                                                   /db_xref="taxon:1238"
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LFGKGSGRVAMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ospA"
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1373. .2743
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/transl_table=11
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/product="BAX"
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GCCAGCAATATTGTCGAGAATTTCAGCAAAAGGCGATGATTGCAGGGCAGAAGCAAGAGA
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EIMTIMIYFHKSMYRNFKMYYLHVIKGSMVKYFNSVSYNRFVELMPSTILLPLCFFIA
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MKNKLMIDKILKKRGIIA"
                                                                                               /organism="unknown"
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Location/Qualifiers
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Patent: 1
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Shoseyov,O.
Kits and methods of detection
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TITLE
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Matches 272; Conser
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                                          ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT 120
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                                 ATCAAAATTACTAACACATCTGACAGTGATTTAAAATTTAAATGACGTAAAAAGTTAGATAT
product
Patent: US 5856201-A 1 05-JAN-1999;
Location/Qualifiers
1. .486
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Patent:
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Shoseyov,O., Shpiegl,I., Goldstein,M.A.
Methods of detection using a cellulose
                                                                                                                                                                                                                                          Unclassified.

1 (bases I to 486)
Shoseyov,O., Shpiegl,I., Goldstein,M.A. and Doi Methods of detection using a cellulose binding
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                                                                                                                                                                                                                                                                                                                                   Sequence 3
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1 (bases 1 to 486)
Shoseyov,O., Shpiegl,I., Goldstein,P
Cellulose binding domain proteins
Patent: US 5837814-A 1 17-NOV-1998;
Location/Qualifiers
                Unclassified.

1 (bases 1 to 486), Goldstein, Shoseyov,O., Shpiegl,I., Goldstein, Cellulose binding domain proteins Patent: US 5837814-A 3 17-NOV-1998; Location/Qualifiers
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Shoseyov,O., Shpiegl,I., Goldstein,M.A. and Nucleic acids encoding a cellulose binding Patent: US 5496934-A 1 05-MAR-1996;

Location/Qualifiers

1. 486
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1 Nucleic acids encoding a cellulose in Nucleic acids encoding a cellulose in Patent: US 5496934-A 3 05-MAR-1996;
Location/Qualifiers
1. 486
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Shoseyov,O., Shpiegl,I., Goldstein,M.A.
Methods of use of cellulose binding doma
Patent: US 5670623-A 1 23-SEP-1997;
Location/Qualifiers
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Shoseyov,O., Shpiegl,I., Goldstein,M.A. and Doi,R. Methods of use of cellulose binding domain protein Patent: US 5670623-A 3 23 SEP-1997;
Location/Qualifiers
                                                         Sequence 1 from I88789
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Shoseyov,O., Shpiegl,I., Goldstein,M.A. and Doi,R. Cellulose binding domain fusion proteins
Patent: US 5719044-A 3 17-FEB-1998;
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Shoseyov,O. and Shani,Z.
Arabidopsis thaliana endo-1,4-.beta.-glucanase gene and promoter
Patent: US 6005092-A 5 21-DEC-1999;
Location/Qualifiers
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Unpublished (2000)
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AV760726.1
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Cohinese National Human Genome Center at Shanghai
S51 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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clone is available at CHGC
Location/Qualifiers
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/cell_type="CD34" hematopoietic stem/progenitor cell"
/lab_host="MM25.8"
/note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIE
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                                                                                                                                in Shanghai.
DB
                            Site_1: sfiIA; Site_2: sfiIB"
9
Length 709
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AV763598 AV763598
AW068733 cn24c11.x
BM309775 sak66e03.
A1478023 fb50d08.x
AI678459 tu82f07.x
BM381932 MEST542-A
AW658421 94440 MAR
AI637152 603001096
BM335231 MEST147-F
BG924401 HNC26-1-1
BH381604 AG-ND-132
AI267409 aq64e09.x
BH151293 602917270
AW167360 x974h05.x
BM35033 MEST264-C
BI868632 60399555
BH524872 BOGFY559F
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AU135371
AL303076 Tetraodon
BG715056 602673281
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391 bp DNA linear GSS 10-OCT-1998
HS_3029_A2_D03_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3029 Col=6 Row=G, DNA sequence.
AQ252889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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                                                                                                     AQ518147 516 bp DNA linear GSS 05-MAY HS_5090_A1_F08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=666 Col=15 Row-K, DNA sequence.
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                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                              Homo sapiens
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    mmalia; Eutheria;
(bases 1 to 516)
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E-Coli DH10B"
3 73 c 85 g 156 t
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3029 Col=6 Row=G"
/clone_lib="CIT Approved Human Genomic Sperm Library
                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
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                                                                                            GI:4743329
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296 GCCTGCAGGGCAGCTCTCTG 315
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 666 row: K column: 15
Seq primer: T7
Class. T3
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9380589
Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
Oniversity of Washington
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Fax: (206) 616-3887
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Location/Qualifiers
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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156 c 129 g 104 t 5 others
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/db_xref="taxon:9606"
/clone="plate=666 Col=15 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                      Email: dpomp@unl.edu
Oligo-dT track not found, Not I si
is likely internal to the message.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Pomp, D
Department of Animal Science
University of Nebraska, Linco
                                                                                                                                                                                                                                                                                                                                                                                                                   Lincoln, NE 68583-0908,
Tel: 402 472 6416
Fax: 402 472 6362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caetano, A.R., Johnson, R.K. and Pomp, D. Generation and sequence characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa
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/lab_host="DH108" (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified 
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified 
polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN 
library is a normalized library representing portine 
ovarian follicles, ranging between 2.0 to 10.0 mm in 
diameter, collected during 7 days of the follicular pha 
of the pig estrous cycle. This library was derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                            /clone="UNL-P-FN-cf-b-07-0-UNL"
/clone_lib="UNL-P-FN"
                                                                                                                                                                                                                     Lines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
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/clone="IMAGE:3597462"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="FVB/N"
                                                                                                                                          /dev_stage="ADULT"
                                                                                                                                                                                                                                    /organism="Sus scrofa"
/strain="University of Nebraska, Lincoln
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Texas Children's Cancer Center and Human Genome at Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric Leukemia cDNA Sequencing Project
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TCBAP2E5356 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5356, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: clones@txccc.org
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                                                  Conservative
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3 272 c 231 g
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full-length cDNA by improved biotinylated cap trapper., DNA Res 4:\ 1,\ 61-6, Feb 28,\ 1997)"
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/dev_stage="pediatric 2 years"
/lab_nost="DH10B"
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/db_xref="taxon:9606"
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Primates;
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/db_xref="taxon:31033"
/clone_lib="cosmid 072L05"
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/clone="072L05aB5"
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-CIO136-021100-670-dl1&t3=2000-11-02&t4=1)
Seq primer: puc 18 forward
                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                   Brazi
                                                                                                                                                 Rua Prof. Antonio Prudente
                                                                                                                                                               Laboratory of Cancer Genetics Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
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BF803712
BF803712 GI:12132701
                                                                              Email: asimpson@ludwig.org.br
                                                                                                                                                                                                 Contact: Simpson A.J.G
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
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/clone="IMAGE:2972613"
/clone_lib="NCI_CGAP_GUI"
/tissue_type="2 pooled high-grade transitional cell tumors"
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Technologies. "
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mRNA sequence.
AA909847
                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 528 Std Error: 0.00
Seq primer: 40ml3 fwd. ET from Amersham
High quality sequence stop: 210.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. " 41 c 42 g 63 t
                                                                                  /note-"Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and
                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1522242"
/clone_lib="MCI_CGAP_Lu5"
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/db_xref="taxon:9606"
/clone_lib="CI0136"
                                                                                                                                                                                               /tissue_type="carcinoid"
/lab_host="DH10B"
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sapiens cDNA clone IMAGE:1522242 3',
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Matches 19
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l Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-1yd07
Seq primer: (-21)M13_universal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genexpress@genethon.fr
Single read.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1, rue de l'Internationale,
Tel: 33169472800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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Auffray, C., Behar, G.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                   isolate=muscular atrophy patient; tissue_type=total brain total mRNA was oligo-(dT) primed and directionally cloned 5′ -> 3′ into the HindIII -> NotI Sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press*

a 43 c 48 g 89 t 9 others
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                                                                                                                                                                                                                                                                                                 /tissue_type="total brain"
/tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/site_2: NotI; sex=Female; dev_stage=3 months old;
Site_2: NotI; sex=Female; dev_stage=3 months old;
                                                                                                                                                                                                                                                                                                                                                                                                    /clone="c-lyd07"
/clone_lib="normalized infant brain cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
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mes 19; Conserv
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Indiminate, Townson, Marra, M., Bowles, M., Dietrich, N., Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris
                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                         AI182462
AI182462.1 GI:3733100
                                                                                                                                                                    uc26h10.r1 Soares_mammary_gland_NbMMG Mus musculus IMAGE:1399171 5', mRNA sequence.
                                                                                                               house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:2413408"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                  2.5%;
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                                                                                                                                                                                                                                                                                                                                                                 Score 19;
Pred. No.
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sapiens cDNA clone IMAGE:2413408 3',
                                                                                                                                                                                                                                                                                                                                                                 DB 9;
53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                              Length 283;
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                                                                                                                                                                                                       linear
                                                                                                                                                                                    EST 08-OCT-1998
CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         pT7T3 vector.
by Bento
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                                                                                                                                                                                                  SOURCE
ORGANISM
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D51829/c
                                           COMMENT
                                                                                                                                                     REFERENCE
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                                                                                                                                    AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                 sapiens cDNA
D51829
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    Pharmaceutical Co., Ltd
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135 TGGTACACAAGGACAAACT 153
                                          Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 335)
Fujiwara; T. Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)
Unpublished (1995)
                           Contact: Tsutomu Fujiwara
                                                                                                                                                                                                                                                                                                                                                                            JOIR29 ... 335 bp mRNA linear
HUM053G02B Clontech human fetal brain polyA+ mRNA
sapiens cDNA clone GEN-053G02 5', mRNA sequence.
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free th
TMAGE Consortium (info@image.lln1.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 303.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schellenberg,K., Steptoe,M.,
Theising,B., Wylie,T., Lennon
Waterston,R.
The WashU-HHMI Mouse EST Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
  GEN Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adaptors (Pharmacia), digested the Not I and Eco RI sites of t RNA provided by Dr. Minoru Ko, W constructed and normalized by Be Bonaldo."

95 g 79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:1399171"
/clone_1ib="Soares_mammary_gland_NbMAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 double-stranded cDNA was ligated to Eco RI
'S (Pharmacia), digested with Not I and cloned into
I and Eco RI sites of the modified pT7T3 vector.
Institute
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus"
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Bento Soares
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BE246888/c
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DEFINITION
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Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 ACAGTGATTTAAATTTAAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 ACAGTGATTTAAATTTAAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 2.5%; So 19: Ch 2.5%; So 19: Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Citation: Carninci,P. and Hayashizaki,Y. High efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Seg primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 336)

Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,I., Bouck,J., Gibbs,R.A. and Margolin,J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE246888 336 bp mRNA linear EST 03-OCT-2 TCBAP1E5756 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5756; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Texas Children's Cancer Center and Human Genome Sequencing Center at Baylor College of Medicine 1102 Bates, MC3-3320 Houston, TX 77030, USA Tel: 832-824-4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Dr. Judith F. Margolin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: clones@txccc.org
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/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; /note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored xhoI-oligo(dT) primer [5'GAGAGGGCGCGCAGGAGGAGGAGT)VN 3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand was primed with a BamHI-dC primer [5'AGAGAGCTCGGAGTCCGCGGCCGCAATAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamHI and xhoI and directionally cloned into the BamHI and salI sites of lambda pSB vector. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"GEN-053G02"
/_clone_lib-"Clontech human fetal brain polyA+ mRNA (#6535
                                                                                                                                                                                                                                                         /tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
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1. .335
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                                                                                                                                                                                                                                                                                                                                                                               leukemia Baylor-HGSC project-TCBA"
                                                                                                                                                                                                                                                                                                                                                                                                  /clone="TCBAP5756"
/clone_lib="pediatric pre-B cell acute lymphoblastic
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/db_xref="taxon:9606"
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Pred. No.
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BASE COUNT ORIGIN 99 D Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper., DNA Res 4: 1.61-6, Feb 28, 1997)"

a 43 c 56 g 138 t of

Query Match
Best Local Similarity
Matches 19; Conserv 2.5%; Score 19; pred. No. DB 10; Length 336; 55;

QY g

Conservative

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Mismatches

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Search completed: October 27, 2002, 22:36:47 Job time: 1544.65 secs

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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-672-211-3
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US-09-070-716-21

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US-08-468-164A-3
US-08-460-462-3
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ALIGNMENTS	US-08-858-207A-210	US-09-249-448-37	US-09-249-461-37	US-08-809-455-37	US-09-249-451-37	US-09-249-472-37	US-09-249-471-37	US-08-634-641-37	US-08-461-965-37	US-08-486-399-37	US-08-486-397-37	US-08-465-380-37	US-09-042-071-49	US-09-229-059-1	US-08-699-103B-1	US-08-553-888A-2	US-08-553-888A-1	US-09-541-941B-26
	Sequence 210, App	Sequence 37, Appl	Sequence 37, Appl	Sequence 37, Appl	Sequence 37, Appl	-	Sequence 37, Appl	•	•	•	Sequence 37, Appl	Sequence 37, Appl		Sequence 1, Appli	Sequence 1, Appli		Sequence 1, Appli	Sequence 26, Appl

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RESULT 1
US-08-048-164A-1
; NAME/KEY:
; LOCATION:
US-08-048-164A-1
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                                                                                                                                                                                                                                                                                       SOFTWARE: PATENTIN Release #10, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/048,164A
FILING DATE: 14-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
                                                                                                                                                                     TELEFAX: (212) 869-88 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shoseyov, Oded
APPLICANT: Shpiegl, Ital
APPLICANT: Goldstein, Marc
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: CELLULO
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENLE & EDMONDS
STREET: 1155 Avenue of the /
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 78 TELECOMMUNICATION INFORMATION:
                                                   FEATURE:
                                                                   MOLECULE TYPE:
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CITY: New York
STATE: New York
                                                                                   STRANDEDNESS:
TOPOLOGY: unl
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OPERATING SYSTEM: PC-DOS/MS-DOS
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(212) 869-8864/9741
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Query Match 33.2%; Sometime 100.0%; 18est Local Similarity 100.0%; 19est Matches 255; Conservative 0;

Score 255; DB 1; L; Pred. No. 5.5e-124; 0; Mismatches 0;

Length 486; 4; ; Indels

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                                                                 Query Match
Best Local Similarity
Matches 255; Conserv
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APPLICANT: Shoseyov, Oded
APPLICANT: Shpiegl, Itai
APPLICANT: Goldstein, Marc A.
                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                  TOPOLOGY: unknown
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 780:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                              MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Doi,
271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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Pred. No. 5.5e-124;
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                                                                   Mismatches
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Patent No. 5670623
GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 255; Conserv
                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/048,164
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                         FILING DATE: 14-APR-1993 ATTORNEY/AGENT INFORMATION:
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                                                                                                        FEATURE:
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                                                                                                                      MOLECULE TYPE:
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STATE: New Y
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                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 ACCTATGATACATAT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 14-APR-1993
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(212) 869-8864/9741
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Shpiegl, Itai
Goldstein, Marc A.
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100.0%; P
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                Score 255; DB 1; L Pred. No. 5.5e-124;
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US-08-460-462-3/c
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                                                                                                              US-08-460-462-3
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                                                                              Query Match
                                                 Matches
                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 780-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 01 FILING DATE: 14-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/460,462
FILING DATE: concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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ADDRESSEE: PENNIE & EDMONDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTILE OF INVENTION: METHODS OF USE OF CELLULOSE BINDING DOMAIN PROTEINS NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOG ""
SOFTWARE: PA+--'
TRAFAUT
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16 TACAACTCTAACAAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC 75
                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
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                                                                Local
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                                                                Similarity
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Goldstein, Marc A
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                                                            33.2%;
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                                          Score 255; DB 1; ...

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                                                                             Length 486
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US-08-460-457-1
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   Query Match
Best Local :
                                                                                                                                                                                              TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                 MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
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CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: concurr
CLASSIFICATION: 435
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ZIP: 10036
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                                                                                                                                               STRANDEDNESS:
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33.2%; Score 255; DB 1; L
100.0%; Pred. No. 5.5e-124;
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               Length 486;
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Local Similarity hes 255; Conserv

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GENERAL INFORMATION:
                                   Query Match
Best Local Similarity
Matches 255; Conserv
                                                                                                                                                                                TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 486 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 780
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STATE: New York
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16 ТАСААСТСТААСАААТСАGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC 75
                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                    nucleic acid
DEDNESS: double
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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Shpiegl, Itai
                                   Conservative :
                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                   concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELLULOSE BINDING DOMAIN FUSION PROTEINS
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                                   0;
                                                   Score 255;
Pred. No.
                                     Mismatches
                                                   5.5e-124;
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                                                                  Length 486;
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US-08-460-458-1
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                                                                   US-08-460-458-1
 Matches
                                Query Match
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                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Shosey
                                                                                                                                                                                                                 TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STREET: New York
CITY: New York
STATE: New York
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                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
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                                                                                                                                   MOLECULE TYPE:
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SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/460,458 FILING DATE: concurrently herewith
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                                                                                                                                                     TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                         NAME:
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IBM PC comparible
SYSTEM: PC -DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                 Score 255; DB 1; L. Pred. No. 5.5e-124;
 Mismatches
 0;
                                Length 486;
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US-08-460-458-3/c
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; MOLECULE TYPE:
US-08-460-458-3
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                                                                                                                                     Query Match
                                                                                                         Matches
                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/048,164 FILING DATE: 14-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/460,458 FILING DATE: concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                 76
                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
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ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTACACAAGTGAT 135
                                              ACCTATGATACATAT 270
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100.0%; Pr
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Pred. No. 5.5e-124;
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                                                                                         Query Match
Best Local
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,87
REFERENCE/DOCKET NUMBER: 7
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                  FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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(212) 869-8864/9741
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Pred. No. 5.5e-124;
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                                                                                                       Matches
                                                                                                                                    Query Match
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Shpieg1, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Boi, Roy H.
TITLE OF INVENTION: CELLULOSE
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APPLICATION NUMBER: US 08
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    TELEFOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: PENNIE & EDMONDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/460,455 FILING DATE: concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1155 AV
CITY: New York
STATE: New Yor)
76 ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTATTACACAAGTGAT 135
                                                                                                   Local Similarity es 255; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                      LENGTH:
                                     ACCTATGATACATAT 270
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                                                                      TACAACTCTAACAAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC 75
                                                                                                                                                                                                                                   nucleic acid
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                                                                                                       Conservative
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                                                                                                                                                                                                                         double
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                                                                                                                   33.2%; Score 255; DB 2; L
100.0%; Pred. No. 5.5e-124;
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                                                                Matches
                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/
FILING DATE: 27-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CIP OF
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-90
TELEFAX: (212) 869-8864
TELEX: 6441 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS OF DETECTION USITITLE OF INVENTION: CELLULOSE BINDING DOMAIN NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                         FEATURE:
                                                                                                                                                                                         MOLECULE TYPE:
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COMPUTER: IBM PC
OPERATING SYSTEM:
Local Similarity
nes 255; Conserv
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ZIP: 10036
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                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                        TYPE:
                                                                                                                                           LOCATION:
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Goldstein, Marc A.
                                                                Conservative
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SYSTEM: PC-DOS/MS-DOS
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55 AVENUE OF THE AMERICAS
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100.0%; Pred. No. 5.5e-124;
tive 0; Mismatches 0;
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                                                                                             Length 486
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                                                             Matches
                                                                                      Query Match
                                                                                                                                                                                                               TELEFAX: (212) 869-886
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: CIP
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/330,394A FILING DATE: 27-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
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                                                                                                                                        MOLECULE TYPE:
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                                                   Local 255;
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456 TACAACTCTAACAAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC
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            16 TACAACTCTAACAAATCAGCACAAACTAAACTCAATTACACCAATAATCAAAATTACTAAC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                STRANDEDNESS: double
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                                                                          Similarity
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                                                             Conservative
                                                                                                                                                    unknown
                                                                                                                                                                                                                                                            (212) 790-9090
12) 869-8864
                                                                          33.2%;
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                                                                        Score 255;
Pred. No.
                                                             0;
                                                             Mismatches
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US-09-006-636-5
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US-09-006-636-5
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Best Local Similarity
Matches 255; Conserv
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                                                                                                                                                                                                                                                                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ARABIDOPSI TITLE OF INVENTION: GLUCANASE UMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shoseyov, (APPLICANT: Shani, Ziv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
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136 GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT 195
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                                                                                                          16 TACAACTCTAACAAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
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                                                                                           36 TACAACTCTAACAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP STREET: 1155 Avenue of the Amer
                                                                                                                                                                                                                                                                                                LENGTH:
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                               ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTATTACACAAGTGAT
                                                            ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTATTACACAAGTGAT
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                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                   TYPE: DNA
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US-09-006-632-5
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                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Shpigel, Etai
TITLE OF INVENTION: TRANSGENIC
TITLE OF INVENTION: MORPHOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
196 GTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACAGCAAGCCCAACATCA 255
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                  156 GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT
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                                                                  136 GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT 195
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                                                                                                                  76 ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTATTACACAAGTGAT 135
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                                                                                                                                                                                  16 TACAACTCTAACAAATCAGCACAAACAAACTCAAATTACACCAATAATCAAAAATTACTAAC 75
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TOPOLOGY: li
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 790-9090
(212) 869-8864
                                                                                                                                                                                                                                  Conservative
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Pred. No. 5.5e-124;
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Search completed: October Job time: 63.0363 secs
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US-09-277-716-21
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Best Local Sim
Matches 255;
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No. 6232107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 21
LENGTH: 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS,
TITLE OF INVENTION NUMBER: US/09/277,716A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 60/079,624
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER FILING DATE: 1998-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/277, CURRENT FILING DATE: 1999-03-26 EARLIER APPLICATION NUMBER: 60/102,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence: fusion construct {\tt FEATURE}:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                      ACCTATGATACATAT
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100.0%;
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Perfect score:
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AAQ72917
AAV74072
AAX24930
AAD11042
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DNA sequence of cl
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Clostridium cellul
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Cellulose binding
C. cellulovorans C
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Chimeric S peptide
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herichia coli	8135	22	3741		18	5
encoding	3	23	3684		18	44
73	AAD16584	22	1903		18	Ω
DNA encoding novel	37	23	1623		18	12
DNA encoding novel	AAS77372	23	1445		18	11
Propionibacterium	AAS59780	23	1356		18	0
Arabidopsis thalia	AAC39312	21	1353	٠	18	39
rotei	AAT66951	18	1300		18	38
DNA encoding novel	AAS94517	23	1237	٠	18	37
m tub	AAH52010	22	1029		18	36
polynucleot	AAI58573	22	6382		19	35
	AAI58574	22	6304		19	34
Human polynucleoti	AAI58572	22	6223	٠	19	33
æ	AAT86625	19	5562	٠	19	32
cDNA enco	AAS25994	22	4283		19	31
secreted	AAS02416	22	2878	٠	19	30
	AAF32744	22	2735		19	29
polynu	AAI59154	22	2562	٠	19	28
NA sec	AAH16496	22	2042	2.5	19	27
tate lyase CBD	AAZ31562	20	1482		19	26
	AAX90978	20	1482		19	25
	AAZ45336	21	1438		19	24
A clone	AAH07401	22	892	٠	19	23
℧	AAV28688	19	808		19	22
mela	ABL02577	23	3833		20	21
smid pET-RI-	AAV74089	20	26		20	20
primer for	AAA27285	21	38		34	19
primer #6	AAF86256	22	110	5.2	40	18
primer #3	625	22	94		75	
primer #1	625	22	111		87	
primer #5	AAF86255	22	102	ω.	102	
primer #2	625	22	110	13.5	104	14
primer #	AAF86254	22	118	ŗ	118	13
ridium cellu	1104	22	1288	33.2		12
sia species C	AAD22201	24	1146	ω.		Ξ
Gaussia luciferase	AAZ27550	20	1146	ω.	5	10

ALIGNMENTS

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XX AAP862
AC AAF8
XX DA AAP86
XX DO DNA
XX POIK
KW Vacc
KW SRS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct; ds.
                                                   CA2281913-A1
                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                              misc_feature
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                                                                                                                                                                                                                      /note= "DNA encoding undefined N-terminal fusion partner" 286..768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..768
                                                                                                                                                                                                                                                                                                                                                                                          /partial
/product= "C17E2 OspA with N-terminal
/note= "No stop codon is given"
                                                                                                                                  /note= "Optimised OspA construct c17E2"
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a possible salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen particularly poikilothermic fish, against the bacterial pathogen particularly poikilothermic fish, against the bacterial pathogen prickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents P. salmonis OspA DNA termed C17E2 optimised for expression in Escherichia coli fused to DNA encoding an undefined N-terminal fusion partner. The protein encoded by this fusion construct is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KAYW/)
(BURI/)
(KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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GGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGATAAAATCAAACTGAACCAGTCTCTG
                            CGCCAGGAAGTTGGCGCGCCACCGGTGCCGGTTGTTGGGGCGGTGTTGCCGGCCAGCTGTTC
                                                                                                          CAGGGCAGCTCTCTGATCATTATCTCTGTTTTCCTGGTGGGTTGCGCCCAGAACTTCAGC
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BURIAN J.
KUZYK M A
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                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 0;
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                                                                                                                                                                                          (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M I
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poikilothermic vaccine; OspA; SRS; 17E2; ds.
This invention relates to a method for the protection against infection of a poikliothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals
                                                                                        Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis -
                                                                                                                                                                     Kay WW,
                                                                                                                                                                                                                                                                                                          CA2281913-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                    Example
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/note= "Genus spe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rickettsial p
a; rickettsial
                                                                                                                                                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogen;
al disease;
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RESULT 3
AAD11043
ID AAD11
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XX AAD1
XX AAD1
XX POly
KW Poly
KW Yarn
KW Clos
KW Clos
KW CBD-
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                                                            Clostridium durability; cBD-180; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmo rickettsial septicaemia (SRS) and other rickettsial diseases. The resequence represents DNA which has been optimised for expression in Escherichia coll to encode the P. salmonis OspA protein. An OspA protein an N-terminal fusion partner is used in a vaccine to create an
                                            Clostridium
                                                                                             Polysaccharide modification; polysaccharide binding
                                                                                                               Clostridium
                                                                                                                                 24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-OspA antibody response.
                                                                                      yarn;
                                                                                                                                                  AAD11043;
                                                                                                                                                                  AAD11043 standard;
                                                                                                                                                                                                             481
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                                                                                                                                                                                                                                                                                                                GAAATCTACGGCACCGCGTGCCCTCAGCCGGATGGCCGCTGGCAGGTGATTAGCACCGAA
                                                                                                                                                                                                                                                                               CGCCGTCAGCAGTACTGCCGCGAATTTCAGCAGAAAGCCATGATCGCAGGTCAGAAACAG
                                                                                                                                                                                                                                                                                                                                                           CTGAACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGTAATCCGGAC
                                                                                                                                                                                                                                                                                                                                                                                              CTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGATAAAATCAAA
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                                                                                                                                                                                                                                                                                                                                                   CTGAACCAGTCTCTGGAAAAAGTGAAAGCCGGCCAGGTTACTCGTTGGCGTAATCCGGAC
                                                                                                                                                                                                                                                                                                                                                                                     CTGGGCGGTCTGATTGGCTCTAAAATCGGTCAGAGCATGGACCAGCAGGATAAAATCAAA
                                                                                     fiber;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483
                                                                                                                                                                                                             483
                                                                   ; textile; biological crosslinker; mechanical property; cellulovorans cellulose binding domain; wet strength; elasticity; CBDclos; cellulose binding protein A; CBP
                                                                                                               cellulovorans cellulose
                                            cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP;
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/*rag= a
/product=
                  Location/Qualifiers 3..572
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          /*tag=
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                                                                                                                                                                   573
"Cellulose binding
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Pred. No.
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                                                                                                                                                                  ВP
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                                                                                                              binding domain-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 T;
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 domain-180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 483;
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                                                                                             domain;
                                                                                                               (CBD-180)
                                                                                              PBD;
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18-NOV-1999;
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          243
                                                                             123
                                           183
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                                                                                                               63
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                                                                                                                                                                                           Local Similarity
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DB; AAE05746.
                                                                                                                                                                                  270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBD TEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                structural,
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RES
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99US-0166389
                                                                                                                                                                                                                     215
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                                                                                                                                                                                          35.2%;
100.0%;
                                                                                                                                                                                                                     A; 112
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The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.

The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide materials such as paper, fibers and textiles, using biological crosslinking agents.

The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains the fibers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a DNA encoding Clostridium cellulovorans cellulose binding domain (CBD)-180. CBD-180 contains 180 amino acids Clostridium cellulovorans CBD (CBDclos) of cellulose binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1.2; Fig 1e-1g; 121pp; English
                                                                                                                                                                                                                TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA
                                                                                                                                                                                                                                                                                                                                       ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAAGCCCAACATCAACCTATGATACATAT
                                                                                      TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA
                                                                                                                                                                                TATTACACAAGTGATGGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTA
                                                             TTAGGAAATAGCTATGTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACA
                                                                                                                                                                                                                                                                                                           ATCAAAATTACTAACACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "CDS does not include stop codon"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polysaccharide containing material having at least one al, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEBREW UNIV JERUSALEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 270; DB; Pred. No. 1e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 G;
270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
1e-130;
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                                                                                                                   240
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Matches 270;
                        Query Match
Best Local S
                                                                                                                    polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural chemical, physical, electrical and mechanical properties of polysaccharide materials such as paper, it bers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker the fine fibers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                  Sequence
                                                                                          cellulose binding
                                                                                                                                                                                                                                                                        The present invention relates to methods and compositions for cross-linking and/or modifying the properties of polysaccharide materials. The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) fusion protein. The method is
                                                                                                                                                                                                                                                                                                                                                      Example 1.2;
                                                                                                                                                                                                                                                                                                                                                                                   Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-NOV-2000; 2000WO-IL00708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polysaccharide modification; polysaccharide binding domain; yarn; fiber; textile; biological crosslinker; mechanical pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yarn; fiber; textile; bio]
wet strength; durability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-457121/49
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                        Similarity
                                                                  1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nussinovitch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linker protein;
          Conservative
                                                                                        sequence is a DNA e
inding domain (CBD)
                                                                                                                                                                                                                                                                                                                                                   Fig 2b-2e; 121pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellulovorans.
                                                                В₽;
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99US-0166389.
                                                              402 A;
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/product= "CCP protein"
/transl_except= "(pos:
/note= "CDS does not in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
3..1028
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100.0%; Pred. No.
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                                                              195 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elasticity;
CCP; ds.
          0;
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does not include stop codon"
                                                                                        encoding Clostridium cellulovorans
) cross linker protein (CCP).
                                                                                                                                                                                                                                                                                                                                                 English
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       Mismatches
                                                            166 G;
                                                            267 T; 0
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                                  DB 22;
        0,:
                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mechanical property
                               Length 1030;
                                                                                      (CCP).
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RESULT 5
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comprising the CBD and a second protein. The second protein is pref. Protein A, heparinase, a hormone or an enzyme capable of degrading an environmental pollutant, or an HSP, HSP antibody, cross-reactive HSP-related protein or an antigenic portion of this. The CBD and FP may be used in drug delivery, affinity sepns. and diagnostic techniques. CBD nucleic acid may be obtd. from a variety of cell sources that produce CBDs that bind with high affinity and in a
                                                                                  AAQ72917/R63634 is a novel isolated cellulose binding domain. It is binds crystalline with a Kd ranging from 1.5 microM - 0.5 microM, pref. with a Kd of <1.2 microM, esp. <1.0 microM. The protein and the encoding DNA are claimed, as is a CBD fusion protein (FP)
                                                                                                                                                 Claim 10; Fig 1; 125pp; English.
                                                                                                                                                                                                                                                                                   (REGC )
                                                                                                                                                                          applications. including diagnostic techniques
                                                                                                                                                                                Isolated cellulose binding domain and fusion proteins - with applications. including drug delivery, affinity separations.
                                                                                                                                                                                                                                                                                                                      14-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                             14-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ72917;
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YISSUM RES & DEV
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Matches
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                                                                                                                                                                                  27-OCT-1994;
14-APR-1993;
14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoassay; heat-shock protein; cross reactive protein; detection antigenic fragment; antibody; insulin-dependent diabetes mellitus; cellulose; chitin; cellulolytic; amorphogenic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cellulose binding domain; CBD; CbpA; fusion protein; diagnosis; HSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. cellulovorans CbpA CBD DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-1999
Detection of a specific analyte by reaction with binding agent fused to cellulose binding domain - and subsequent treatment with cellulose and reaction of insoluble product with a label specific
                                                                                                                                                                                                                                                                              05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV74072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV74072 standard;
                                                                                                                                                                                                                                                                                                          US5856201-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reversible manner or that produce CBD encoding mRNA. The source of CBD encoding nucleic acid is \mathbb{C}. cellulovorans.
                                                                                                         Dol RH,
                                                                                                                                      (REGC ) UNIV CALIFORNIA.
(YISS ) YISSUM RES & DEV
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DB; AAW90077.
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255; Conserv
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                                                                                                         Goldstein MA,
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93US-0048164.
94WO-US04132.
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Best Local
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                                                                                          13-JAN-1998;
27-JUL-1997;
13-JAN-1998;
   WPI; 1999-180488/15
                                                                                                                                                                                                                                                                        Arabidopsis morphology;
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX24930
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                               Shani Z,
                                                            (YISS
                                                                                                                                                                                                                                                                                                                                                                     21-JUN-1999
                                                                                                                                                      26-JUL-1998;
                                                                                                                                                                                    18-FEB-1999
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                                                            MUSSIA
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This sequence encodes a cellulose binding domain (CBD) derived from the CbpA protein of Clostridium cellulovorans. The sequence is used the construction of a fusion protein which can be used in diagnostic immunoassays, e.g. to detect heat-shock proteins (HSP) and their cross-reactive proteins, antigenic fragments or HSP-specific antibodies (which indicate insulin-dependent diabetes mellitus, or susceptibility to it. The CBD, has very high affinity for cellulose (including crystalline forms) and chitin (dissociation constant 0.8-1.4 mu M), but has almost no cellulolytic or amorphogenic activities. The CBD binds over a wide pH range and is not released from cellulose by washing with water.
                                                                                                                                                                                                                                                                                  Clostridium celulovorans.
                                                                                                                                                                                                                                                                                                                                                            Cellulose binding domain; CBD;
                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium cellulovorans cbpA cellulose binding domain DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7.2.1; Fig 1A-B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 BP; 194
Shoseyov 0,
                                                                                                                                                                                                                                                                                                        thaliana; transgenic plant; crop improvement cell wall; ds.
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ilarity 100.0%;
Conservative (
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                                                                            98US-0006636.
97IL-0121404.
98US-0006632.
                                         RES
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                                         δ.
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Pred. No. 7e-123;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 G;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
WO200134091-A2
                                                                                                                                         Polysaccharide modification; polysaccharide binding domain; PBD; yarn; fiber; textile; biological crosslinker; mechanical property Clostridium celluloyorans cellulose binding domain; wet strength;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the cbpA protein of Clostridium cellulovorans. It was obtained by PCR amplification (see also AAX24952-53), and was used in the construction of binary vector pCCl, in which cbd was joined to the promoter and signal region of the novel endo-1,4-beta-glucanase cell gene (see AAX24923) of Arabidopsis thaliana. Expression of cbc in transgenic tobacco plants modulated their growth. The cell promoter can provide expression of any protein in elongating tissue. CBD is an example of a cell wall modulation transgene used to alter the structure or morphology of a plant. Transgenic plants of the invention may have altered biomass, growth, yield,
                                                                                                  Clostridium
                                                                                                                              durability;
                                                                                                                                                                                                        Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   greater or less resistance to biodegradation, be more or less digestible by ruminants, have altered cellulose content, larger smaller leaves, etc., when compared to non-transgenic plants of
                                                                                                                                                                                                                                                                                            AAD11042 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic plants expressing cell-wall modulating protein have altered morphology, e.g. increased growth, modified fiber length or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 134; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACAACTCTAACAAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC 75
                                                                                                                                                                                                                                                                                                                                                                                        ACCTATGATACATAT 270
                                                                                                                                                                                                                                                                                                                                                                                                                             GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTATGGAAATAGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTATTACACAAGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACAGCAAGCCCAACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACAACTCTAACAAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA fragment encodes the cellulose binding domain (CBD) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            content
                                                                                                  cellulovorans
                                                                                                                                                                                                    cellulovorans cellulose binding domain
                                                                                                                              elasticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.2%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                  (first entry)
                          /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 93 C; 82 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                             507
                                                                                                                             CBDclos; cellulose binding
                        "CBDclos protein"
                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 255; DB 20;
Pred. No. 7e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                             protein A;
                                                                                                                                                                                                     (CBDclos) DNA
                                                                                                                                                        property;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
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                                                                                                                                                                      paper;
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RESULT 9
AAD11046
ID AAD1
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AAD11046 standard;

DNA;

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                                                                                                                                                                                                                                                                                                    QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to methods and compositions for cross-
CC linking and/or modifying the purperties of polysaccharide materials.
CC The method involves treating the polysaccharide structure with a CC polysaccharide binding domain (PBD) fusion protein. The method is CC used to alter the structural, chemical, physical, electrical and CC mechanical properties of polysaccharide materials such as paper, CC yarns, fibers and textiles, using biological crosslinking agents.
CC The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD CC reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker CC improves the recyclability of paper products. The PBD reagent maintains CC in ine fibers in a slurry therefore resulting in better recovery of CC raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to CC cenetrate paper.
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                   penetrate paper.
The present sequer cellulose binding
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CBDT-)
   276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1.1; Page 111; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-1999;
18-NOV-1999;
                                 256
                                                                  216
                                                                                                                                    156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001.
                                                                                                   196
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                                                                                                                                                                                                                                                                     36 TACAACTCTAACAAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC
                                                                                                                                                                                                                                                                                                      16 TACAACTCTAACAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC
ACCTATGATACATAT
                                                                                 GTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACAGCAAGCCCAACATCA
                                                              GTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACAGCAAGCCCAACATCA
                                                                                                                                  GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT
                                                                                                                                                  GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT 195
                                                                                                                                                                                                                    ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTATTACACAAGTGAT 135
                                 ACCTATGATACATAT 270
                                                                                                                                                                                                   ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTATTACACAAGTGAT
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DB; AAE05745.
                                                                                                                                                                                                                                                                                                                                       255;
                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is a DNA encoding Clostridium cellulovorans .nding domain (CBDclos) of cellulose binding protein .
                                                                                                                                                                                                                                                                                                                                                                                                       вP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-IL00708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0164140.
99US-0166389.
                                                                                                                                                                                                                                                                                                                                                                                                       200
                                                                                                                                                                                                                                                                                                                                                     33.2%;
                                                                                                                                                                                                                                                                                                                                                                                                      A; 94 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoseyov 0;
                                                                                                                                                                                                                                                                                                                                     Score 255; DB; Pred. No. 7e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                      84 G;
                                                                                                                                                                                                                                                                                                                                                                                                      129
                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 507; 7e-123;
                                                                                                                                                                                                                                                                                                                                                                                                      T; 0 other;
                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                               255
                                                                                                                                                                                                   155
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                                                                                                                                                                                                                                                                                                    75
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Chimeric
Chimeric
                                                              yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains the fibers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide materials such as paper,
                                                                                                                                                                                                                             The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.
The method involves treating the polysaccharide structure with a
polysaccharide binding domain (PBD) fusion protein. The method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polysaccharide modification; polysaccharide binding domain; PBD; pyarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CB chimeric protein; S peptide-cellulose binding domain-S protein;
                                                                                                                                                                                                                                                                                                                               property
                                                                                                                                                                                                                                                                                                                                              Preparation
desired stru
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CBDT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-NOV-2000; 2000WO-IL00708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spep-CBD-Sprot; bovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric
                                      penetrate paper.
The present sequence is a DNA encoding S
                                                                                                                                                                                                                                                                                                   Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Levy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200134091-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                     2001-457121/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBD TEC
                                                                                                                                                                                                                                                                                                                                           tion of a polysaccharide containing structural, chemical, physical, elu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                          protein (Spep-CBD-Sprot), a
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nussinovitch
                                                                                                                                                                                                                                                                                                 Fig 4b-4g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide-cellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TECHNOLOGIES LTD
             cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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99US-0166389
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/note= "This
652..981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Spep-CBD-Sprot protein"
/transl_except= "(pos: 979..981, aa:Xaa)"
/note= "Xaa corresponds to in-frame stop codon;
CDS does not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "This region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ,>
                                                                                                                                                                                                                                                                                                 121pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                Shoseyov 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEBREW UNIV JERUSALEM
                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region
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             bovine
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                          fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 derived
                                        peptide-cellulose binding
                                                                                                                                                                                                                                                                                                                                             g material having at least
lectrical and/or mechanical
                          protein derived from
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RESULT 10
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DЪ
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                                                                                                                                                                       27-MAR-1998;
15-JUN-1998;
01-OCT-1998;
                                                                                                                                                                                                                                                                                 bioluminescence-generating system; toy; cosmetic; faile body paint; squirt gun; balloon; slimy play material;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                          Disclosure;
                                                                                                             WPI; 1999-580443/49
                                                                                                                             Bryan BJ, Szent-Gyorgyi
                                                                                                                                             (PROL-)
(BRYA/)
                                                                                                                                                                                                                                          W09949019-A2
                                                                                                                                                                                                                                                           Gaussia
                                                                                                                                                                                                                                                                                                                     Gaussia luciferase
                                                                                                                                                                                                                                                                                                                                       13-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                       AAZ27550
                                                                          New isolated Renilla mulleri,
Renilla and Ptilosarcus green
                                                                                                                                                                                                         26-MAR-1999;
                                                                                                                                                                                                                         30-SEP-1999
                                                                                                                                                                                                                                                                            fusion
                                                                                                                                                                                                                                                                                                    Luciferase;
                                                                                                     P-PSDB; AAY39952
                                                                                                                                                                                                                                                                                                                                                                                                                  358
                                                                                                                                                                                                                                                                                                                                                                                                                                  256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACAGCAAGCCCAACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTATTACACAAGTGAT
                                                                                                                                                                                                                                                                          protein;
                                                                                                                                             PROLUME
BRYAN B
                                                                                                                                                                                                                                                         sp.
                                                                                                                                              BRYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            984
                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                          Page
                                                                                                                                                                                                                                                                                                    green fluorescent protein; GFP; screening assay; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                               98US-0079624
98US-0089367
                                                                                                                                             J.
                                                                                                                                                                        98US-0102939
                                                                                                                                                                                                         99WO-US06698
                                                                                                                                                                                                                                                                            sb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325
                                                          222-223;
                                                                                                                                                                                                                                                                                                                   fusion protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Α.
                                                                                                                                                                                                                                                                                                                                                                                                                  372
                                                                                                                                                                                                                                                                                                                                                                                                                                  270
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                                                         233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ç;
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                                                                         Gaussia and fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
7e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ţ,
                                                                                   Pleuromamma luciferase and
                                                                           protein nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 984;
                                                                                                                                                                                                                                                                                            fairy dust;
                                                                                                                                                                                                                                                                                   soap;
                                                                           acids
                                                                                                                                                                                                                                                                                   t; beverage;
toothpaste;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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This sequence encodes a luciferase of the invention. The invention relates to Renilla mulleri, Gaussia and Pleuromamma luciferase and Renilla and Ptilosarcus green fluorescent protein (GFP) nucleic aci proteins. The luciferases and GFPs can be used in bioluminescence-generating systems, assays, screening methods, diag method and articles of manufacture. They can be expressed using

assays, screening methods, diagnostic

acids

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Qy
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밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFPS can be used in e.g. toys, cosmetics, fountains, personal care items, fairy dust, beverages, soft drinks, foods, textile products, bubble shalloons, personal items, dentriffices, scaps, body paints, bubble bath, ink or paper products. In particular, they can be used in e.g. squirt guns, pellet guns, finger paints, foot bags, greeting cards, slimy play material, clothing, bubble making toys, bath powders, cosmetics, body lotions, gels, body powders, body creams, toothpastes, mouthwashes, scaps, body paints, bubble bath, inks, wrapping paper, gelatins, icings, frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes, ice, dry ice or fountains. The nucleic acids can also be used to produce
                                                                                                                                                                                                                                        Green fluorescent protein; GFP; bioluminescence generating system; toy; luciferase; finger paint; slimy play material; fishing lure; sparkler; doll; balloon; personal care item; cosmetic; bath powder; body cream; tooth paste; mouth wash; soap; body paint; ornamental transgenic plant; bubble bath; fountain; fairy dust; food; gelatin; icing; frosting; beer; wine; champagne; milk; soft drink; ice cube; ice; foot bag; beverage; dry ice; textile; clothing; paper product; greeting card; wrapping.paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1146 BP; 396 A; 222 C; 247 G; 281 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic fish and plants.
                                                                                                                                                                                           Gaussia
                                                                                                                                                                                                                                                                                                                                                                         Gaussia species CBD-luciferase fusion protein encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD22201 standard; DNA; 1146
               20-SEP-2001.
                                              WO200168824-A2
                                                                                                                                                                                                                          fusion protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacterial, yeast, fungal, plant, insect or animal cells. The Renilla
eri, Gaussia and Pleuromamma luciferase or Renilla or Ptilosarcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTATGATACATAT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGATAACACTAGCAAAGTGACAGCAAACTTCGTTAAAGAAACAGCAAGCCCAACATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATCTGACAGTGATTTAAATTTAAATGACGTAAAAGTTAGATATTATTACACAAGTGAT
                                                                                                                                                                                          фs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                             ds.
                                                                                                                                          Location/Qualifiers
1..1146
                                                                                            /*tag= a
/product= "Gaussia CBD-luciferase fusion protein"
/note= "CDS does not include start and stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
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RESULT 12
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       KWWXEXTXCX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses sea pansy (Renilla reniformis) green fluorescent proteins (GFP) and their corresponding polynucleotides. The invention calso relates to sequences of the bioluminescence generating system (e.g. luciferase). R. reniformis GFP are used in diagnostic methods and in the production of novelty items such as toys (e.g. squirt gun, complete gun, toy "Halloween" eggs, toy cigarettes, board/card game covs), finger paints, slinny play material, bubbles in bubble making toys, fishing lures, dolls, sparklers, magic wand toys, balloons, compared to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the major to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding Renilla reniformis green useful in diagnostic bioluminescence procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2000; 2000US-189691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 162-163; 175pp; English.
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Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fibor; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; protein A-cellulose binding Anmain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1146 BP; 396 A;
                                                                                           Clostridium
                                                                                                                                                                                                                            AAD11045 standard; DNA;
                                                                                                                                        24-SEP-2001
                                                                                                                                                                                                                                                                                                                                             256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-010561/01:
                                                                                                                                                                                                                                                                                                                                                                                                                               GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Szent-Gyorgyi
                                                                                         cellulovorans protein A-cellulose binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 C; 247 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 255;
Pred. No.
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                                                                                                                                                                                                                                 ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 T; 0 other;
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7e-123;
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domain;

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                                                                                                                                                                                                     The present invention relates to methods and compositions for cross-
CC linking and/or modifying the polysaccharide structure with a
CC linking and/or modifying the polysaccharide structure with a
CC polysaccharide binding domain (PBD) fusion protein. The method is
CC polysaccharide binding domain (PBD) fusion protein. The method is
CC used to alter the structural, chemical, physical, electrical and
CC mechanical properties of polysaccharide materials such as paper,
CC yarns, fibers and textiles, using biological crosslinking agents.
CC The polysaccharide containing materials have improved mechanical
CC properties such as wet strengths, durability and elasticity. The PBD
CC reagent is applied in the forming stage in fluting paper manufacture
CC which eliminates the sizing step. The use of a biological crosslinker
CC improves the recyclability of paper products. The PBD reagent maintains
CC the fine fibers in a slurry therefore resulting in better recovery of
CC raw materials. The PBD molecules are eluted by strong alkaline conditions
CC which enhances the ability of the alkaline glue used in binding to
                                                           Matches
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YISS )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium cellulovorans
                                                                                                                                             The present sequence is a DNA encoding Clostridium cellulovorans Protein A-cellulose binding domain (ProtA-CBD). This sequence co a part of cbpA gene and a part of pRIT2T vector sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1.3;
                                                                                                                    Sequence 1288
                                                                                                                                                                                             penetrate paper.
 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-457121/49
DB; AAE05748.
TACAACTCTAACAAATCAGCACAAACAAACTCAATTACACCAATAATCAAAATTACTAAC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CBD TECHNOLOGIES LTD.
YISSUM RES DEV CO HEBREW UNIV JERUSALEM
                                                                          Similarity
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                                                                                                                    BP;
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99US-0166389.
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/note= "This region i
cloning vector"
795...1280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Protein A-cellulose binding domain protein"
/transl_except= "(pos: 1281.1283, aa:xaa)"
/note= "Naa corresponds to in frame stop codon;
CDS does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      3b-3g; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                    523 A; 267 C; 202 G; 296 T; 0 other;
                                                                        33.2%;
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                                                                                      Score 255;
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                                                                                     Length 1288;
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RESULT 13
AAF86254/c
ID AAF862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ф
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                                                                         This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of the P. salmonis OspA gene. The OspA gene is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1005
                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for protecting polkilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KAYW/)
(BURI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF86254 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1065 ACCTATGATACATAT 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Кау ₩₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen;
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR primer #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCTATGATACATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTACACAAGGACAAACTTTCTGGTGTGACCATGCTGGTGCATTATTAGGAAATAGCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAY W W.
BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                    3; Fig 4B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KUZYK M A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burian J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OspA; salmonid rickettsial septicaemia; rickettsial disease; 2; fusion construct; PCR primer; ss.
     118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in cloning an optimisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99CA-2281913
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        21
                                                                                                                                                                                                                                                                                                                                                                                    35pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuzyk MA;
  ?
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        32 C;
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        0 other;
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Query Match Best Local : Matches 11:

Local Similarity les 118; Conser

15.4%;

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Mismatches

Score 118; Pred. No.

DB 22; 2.4e-51

Length 118; Indels

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RESULT 14
AAF86252
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                      δÃ
                                                   Вр
                                                                           Qy
밁
                                                                                                                    Query Match
Best Local
                                                                                                         Matches
                                                                                                                                                                                              This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a P. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen particularly poikilothermic fish, against the bacterial pathogen salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRB) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of the P. salmonis OspA gene. The OspA gene is used in the method of the
                                                                                                                                                                                                                                                                                                                                                                            Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poikilothermic fish; Piscirickettsia vaccine; OspA; salmonid rickettsial s SRS; 17E2; fusion construct; PCR prim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer #2 used in cloning an optimisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF86252 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-316844/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   493
                                                                                                                                                            Sequence 110
                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 4B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KUZY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAYW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BURI/)
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61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCAGAGCATGGACCAGCAGGATAAAATCAAACTGAACCAGTCTCTGGAAAAAAGTGAAA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGTTGCGCCCAGAACTTCAGCCGCCAGGAAGTTGGCGCCGGCCACCGGTGCGGTTGTGG 397
GCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTG
               GCGGTGTTGCCGGCCAGCTGTTCGGTAAAGGCTCTGGTCGTGTG
                                                                                                          104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAY W W.
BURIAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KUZYK M A.
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burian J,
                                                                                                          Conservative
                                                                                                                                                             BP; 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99CA-2281913.
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                                                                                                                                                                                                                                                                                                                                                      35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuzyk MA;
                                                                                                                                                                A; 28 C;
                                                                                                                      13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rickettsial septicaemia; rickettsial disease;
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                                                                                                         Score 104; DB; Pred. No. 4.8
                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer; ss.
                                                                                                                                                                45 G;
                                                                                                                                                                24 T;
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                                                                                                                                                                0 other;
                                                                                                                                        DB 22;
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                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rickettsial pathogen;
                                                                                                                                       Length 110;
                               441
                                                                                                             Indels
     104
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Search completed: October 27, Job time: 197.542 secs

2002,

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RESULT 15
AAF86255/c
ID AAF86252X
XX AAF862
XX POOK!
AAF862
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XX POOK!
XX POOK!
XX POOK!
XX POOK!
XX POOK!
XX POOK!
XX PISCIT
XX POOK!
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XX WPI; 2
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XX Method
PT VACCIN
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                                                                                                                                                                                                                                                                                                           This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a p. salmonis specific antigen termed OspA, or an immunogenic fragment of OspA in the form of a vaccine. The method is used for protecting animals, particularly poikilothermic fish, against the bacterial pathogen p. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents a PCR primer used in the cloning and optimisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KAYW/) KAY W W.
(BURI/) BURIAN J.
(KUZY/) KUZYK M P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer #5
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                                                                                                                                                                                                                             Sequence 102 BP; 14 A; 23 C; 30 G;
                                                                                                                                                                                                                                                                                 sequence represents a PCR primer used in the cloning and optimisation the P. salmonis OspA gene. The OspA gene is used in the method of the
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Query Match Best Local	BASE COUNT ORIGIN	JOURNAL FEATURES	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AROO1082 LOCUS DEFINITION
Query Match Best Local Similarity	/orç	proteins Patent: US 5738984-A 1 14-APR-1998; Location/Qualifiers 1 486	Unclassified. 1 (bases 1 to 486) Shoseyov,O. Kits and methods of detection using cellulose binding domain fusion	AR001082 AR001082.1 GI:3963149 Unknown. Unknown.	AR001082 486 bp Sequence 1 from patent US 5738984.
33.2%; 100.0%;	c u	S 5738984-A 1 14-AP Location/Qualifiers	o 486) nods of de	31:3963149	com patent
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Shoseyov,O.
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1 (bases 1 to 486)

1 (bases 7)

Shoseyov,0., Shpieg1,I., Goldstein,M.A. and Doi,R.H. Methods of detection using a cellulose binding domain
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1 (bases 1 to 486)
Shoseyov,O., Shpiegl,I., Goldstein,M. a Cellulose binding domain proteins Patent: US 5837814-A 1 17-NOV-1998;
Location/Qualifiers
1. 486
1. 486
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Unclassified
1 (bases 1 to 486)
Shoseyov,O., Shpiegl,I.,
Cellulose binding domain
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Best Local Similarity 100.
Matches 255; Conservative
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Best Local Similarity 100.0%;
Matches 255; Conservative
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I18514
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1 (bases 1 to 486)
Shoseyov,O., Shpiegl,I., Goldstein,
Nucleic acids encoding a cellulose
Patent: US 5496934-A 1 05-MAR-1996;
Location/Qualifiers
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Location/Qualifiers
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         255;
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Sequence :
166614
166614.1
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Sequence
I18515
                                                                              Shoseyov,O., Shpiegl,I., Goldstein,M.A. and Doi,R. Methods of use of cellulose binding domain protein Patent: US 5670623-A 1 23-SEP-1997;
Location/Qualifiers
1. .486
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Nucleic acids encoding a cellulose binding
Patent: US 5496934-A 3 05-MAR-1996;
Location/Qualifiers
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1 (bases 1 to 486)
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166615
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Shoseyov,O., Shpiegl,I., Goldstein,M.A. and Doi,R. Methods of use of cellulose binding domain protein Patent: US 5670623-A 3 23-SEP-1997;
Location/Qualifiers
1. .486
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Shoseyov,O., Shpiegl,I., Goldstein,M.A. (
Cellulose binding domain fusion proteins
Patent: US 5719044-A 3 17-FEB-1998;
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AR151733
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Sequence 21
AR151733
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Sequence
AR096204
        l (bases 1 to 1146)
Bryan, B.J. and Szent-Gyorgyi, C.
Luciferases, fluorescent proteins, nucl
luciferases and fluorescent proteins an
diagnostics, high throughput screening
Patent: US 6232107-A 21 15-MAY-2001;
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Shoseyov,O. and Shani,Z.
Arabidopsis thaliana endo-1,4-,beta.-glucanase
Patent: US 6005092-A 5 21-DEC-1999;
Location/Qualifiers
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1146 bp
Sequence 21 from Patent W00168824.
AX250579
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Bryan, B.J., Szent-Gyorgyi, C. and Szczepaniak, W.
Renilla reniformis fluorescent proteins, nucleic acids encoding fluorescent proteins and the use thereof in diagnostics, high throughput screening and novelty items
Patent: WO 0168824-A 21 20-SEP-2001;
Patent: WO 0168824-A 21 20-SEP-2001;
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/PICTEIN_IG="CAC93785.1"
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/translation="MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKPRYYYYTS
/translation="MSVEFYNDNYSFYNDYSFYTYDTYVEFGFASGAATL
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GLVPRGSTAIGKKETAAAKFERQHMDSSDLGTDDDKMGVKVLFALICIAVAEAKPTE
NNEDENITVAVAANFATTPIDAADRKELPGKLPGKLPLEVLKEMEANARKAGGTRGCLICLSH
IKCTPKNKKFIPGRCHTYEGDKESAQGGIGEAIVDIPEIPGFKDLEPMEQFIAQVDLC
VDCTTGCLKGLANVQCSDLLKKWLPQRCATFASKIQGQVDKIKGAGGD"
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/db_xref="taxon:32644"
/note="Gaussia"
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                                                                                                                                                                                                                                                                                        /note="Nucleotide sequence encoding a CBD-Gaussia
luciferase fusion protein"
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Search completed: October 27, 2002, 21:53:00 Job time: 1490.04 secs

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length: 2000000000
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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RESULT 2
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; Sequence 2, Application US/08048164A
; Patent No. 5495934
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
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1 1 61 61 118 121	LENGTH: 38 TYPB: PRT ORGANISM: FEATURE: OTHER INFO 09-277-716 Ouery Match Best Local s Matches 107	RESULT 1 US-09-277-716- Sequence 22, Patent No. 6 GENERAL INFO APPLICANT: APP		44444333333333333333333333333333333333
MSVEFYNSNKSAQTNSITPIIKITNT	Ar Ar 22 Sim	ULT 1 09-277-716-22 equence 22, Applic equence 22, Applic eneral information applicant: Bryan, applicant: Bryan, Applicant: Bryan, Applicant: PROLUME TITLE OF INVENTION CURRENT FILING DAT EARLIER APPLICATIO EARLIER APPLICATIO EARLIER APPLICATIO EARLIER APPLICATIO EARLIER FILING DAT EARLIER FILING		
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KSAQTNSITPIIK KSAQTNSITPIIK KSAQTNSITPIIK SKVTANFVKETAS SKVTANFVKETAS -EVGAATGATVGG : : : FDASSSTPVVNPK	ATION: Cellulose Bi ation: Sequence: 36.0%; Silarity 62.6%; F	16-22 22, Application US/09277716 222, Application US/09277716 NFORNATION: UT: Bryan, Bruce UT: Srent-Cyorgyi, Christoph UT: PROLUME, LTD. INVENTION: LUCIFERASES, FL APPLICATION NUMBER: US/09/2 FILING DATE: 1999-03-26 FILING DATE: 1998-10-01 FILING DATE: 1998-10-01 FILING DATE: 1998-06-15 APPLICATION NUMBER: 60/079, FILING DATE: 1998-03-27 FILING DATE: 1998-03-27 FILING DATE: 1998-03-27 FILING DATE: 1998-03-27 FILING DATE: 1998-03-27 FILING DATE: 1998-03-27 FILING DATE: 1998-03-27 FILING DATE: 1998-03-27 FIEDO ID NOS: 32 :: Patentin Ver. 2.0		597 599 599 599 613 613 739 781 781 781 781 790 970 970 970 970 971 971 973 973 973 973
PIIK PIIK ETAS ETAS ETAS	quenc ulose ulose 2.6%;	\$/0927 Chris Chris R: USE R: USE R: 60/ -03-26 R: 60/ -06-15 R: 60/ -03-27		4545444444444444
SDSDLNLNDVKVRYYYT	e: fusion protein Binding Domain (CBD)-G Score 480.5; DB 4; Pred. No. 4.1e-41; 10; Mismatches 33;	09277716A hristopher hases, FLUORESCENT PROTEINS, US/09/277,716A 3-26 60/102,939 0-60/102,939 0-60/102,939 5-15 6-15 6-15	ALIGNMENTS	US-08-867-611-16 PCT-US92-06965A-21 US-08-867-611-18 PCT-US92-06965A-23 US-08-867-611-49 US-08-867-611-49 US-08-444-818-30 US-08-444-818-54 US-08-467-611-52 US-08-467-611-53 US-08-867-611-54 US-08-464-818-54 US-08-464-818-54 US-08-464-818-56
SDGTQGQTEWCDHAGAL 60	aussia luciferase fusion prote Length 382; Indels 21; Gaps 4;	, NUCLEIC ACIDS ENCODING THE		Sequence 16, Appl Sequence 21, Appl Sequence 23, Appl Sequence 23, Appl Sequence 44, Appl Sequence 4, Appl Sequence 4, Appl Sequence 4, Appl Sequence 7, Appl Sequence 7, Appl Sequence 7, Appl Sequence 5, Appl Sequence 53, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 66, Appl Sequence 68, Appl Sequence 68, Appl

APPLICANT:
APPLICANT:

Shpiegl, Itai Goldstein, Marc A

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shoiegl, Itai
APPLICANT: Goldstein, Marc A.
APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, ROY H.
TITLE OF INVENTION: METHODS OF USE OF CELLULOSE BINDING DOMAIN PROTEINS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 869-8864/9
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
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REFERENCE/DOCKET NUMBER: 780;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9741
TELEPAX: (212) 869-8864/9741
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: Floppy Compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 97.8 es 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 65
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                                                                                                       COUNTRY:
                                                                                                                              STATE:
                                                                                                                                                                 STREET:
                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                          New York
                                                                                           10036
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1155 Avenue of the Americas
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                                                                                                                                                                 1155 Avenue of the Americas
                                                                                                             U.S.A.
                                                                                                                                                                                   PENNIE & EDMONDS
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97.8%;
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pred. No. 2.7e-41;
2; Mismatches 0
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US-08-460-457-2
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Best Local Similarity 97.8
Matches 90; Conservative
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 01 FILING DATE: 14-APR-1993 ATTORNEY/AGENT INFORMATION:
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TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
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                                                                                                                                                                                                                                                                                                                                      STREET: LL. STREET: New York
CITY: New York
TO S.A.
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APPLICANT: Shpiegl, Itai
APPLICANT: Goldstein, Marc A.
                                                                                                                             FILING DATE: concurrently herewith CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/048,164
APPLICATION NUMBER: US 08/048,164
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                              FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Doi, Roy H.
TITLE OF INVENTION: CELLULOSE BINDING DOMAIN FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/460,462 FILING DATE: concurrently herewith CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
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                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                REGISTRATION NUMBER: 18
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                APPLICATION NUMBER: US/08/460,457
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amino acid
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1155 Avenue of the !
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97.8%;
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pred. No 2.7e-41;
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Matches
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                                                           Matches
                                                                                      Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                      NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 780
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,164
FILING DATE: 14-APR-1993
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                          Local
                                                                                                                                               TOPOLOGY:
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TELEPAX: (212) 869-8864/9741
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/460,458 FILING DATE: concurrently herewith
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            1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
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                                                           Conservative
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                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KITS AND METHODS OF DETECTION USING CELLULOSE BINDING DOMAIN
                                                                        35.7%;
97.8%;
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                                                                       Score 477; DB 1; Length 162; Pred. No. 2.7e-41;
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                                                          Mismatches
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US-08-330-394A-2

Sequence 2, Application US/08330394A Patent No. 5856201

GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT:

Shoseyov, Oded Yosef, Karmey Shpiegl, Itai

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US-08-460-455-2
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GENERAL INFORMATION:
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                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-8864/9
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 01 FILING DATE: 14-APR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 781
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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APPLICANT: Doi, Roy H.
TITLE OF INVENTION: CE
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            61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD
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                                                                                                                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                        1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
LGNSYVDNTSKVTANFVKETASPTSTYDTYVE
                                                          MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 65
                                                                                                                    90;
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(212) 869-8864/9741
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                                                                                                                    Conservative
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                                                                                                                                Score 477; DB 2; Pred. No. 2.7e-41;
                                                                                                                    Mismatches
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Best Local Similarity 9/.u
                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09006636 Patent No. 6005092
                                      ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Component
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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TITLE OF INVENTION: M
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                         APPLICANT:
SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         TITLE OF INVENTION: ARABIDOPSIS THALIANA ENDO-1,4-BETA-TITLE OF INVENTION: GLUCANASE GENE, PROMOTER AND PROTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING DATE: 14-APR-1994
                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                               OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                    New York
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1155 Avenue of the Americas
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1155 AVENUE OF THE AMERICAS
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                                               IBM Compatible
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Pred. No. 2.7e-41;
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RESULT 9
US-09-006-632-7
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Best Local Similarity
                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
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NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809-019
TELECOMMUNICATION INFORMATION:
                                                                                                                                REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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APPLICANT: Shani,
                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: TRANSGENIC PLANTS OF ALTERED
TITLE OF INVENTION: MORPHOLOGY
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STRANDEDNESS:
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(212) 869-8864
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Shani, Ziv
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Pred. No. 2.7e-41;
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US-08-330-394A-29
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Best Local Similarity
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APPLICATION NUMBER: US/08/330,394A
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CIP OF PCT/US94/04132
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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                                                                                                                                                                                                                                                                      TELEFAX: (212) 869-
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 10036
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GNSYVDNTSKVTANFVKETASPTSTYDTYLD
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                                              SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL
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Shpiegl, Itai
Goldstein, Marc A.
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Conservative
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97.8%;
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Pred. No. 8.2e-41;
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Pred No. 2.7e-41;
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RESULT 11
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GENERAL INFORMATION:
APPLICANT: Yeda F
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Best Local :
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APPLICATION NUMBER: CIP OF
EILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REFERENCE/DOCKET NUMBER: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 APPLICANT:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                   APPLICANT:
                                                      APPLICANT:
                                                                    APPLICANT:
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TELEFAX: 66441 / TEX: 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1155 A
CITY: NEW YORK
STATE: NEW YOR
                                                                                                                                                                                                                       35.4%;
Local Similarity 97.8%;
les 89; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 27-OCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                       61 GNSYVDNTSKVTANFVKETASPTSTYDTYVE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                       1 SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL 60
                                                                                                                                                                                                                                                                                        2 SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL 61
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                                                                                                                  Application PC/TUS9513813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 amino acids
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Shpiegl, Itai
                                               Yeda Research and Development Co. Ltd. Ramot University Authority for Applied Research and Industrial Development Ltc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoseyov,
Bayer, Edward A.
Morag, Ely
                                   Technion Research and Development Foundation Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENNIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               METHODS OF DETECTION USING
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                                                                                                                                                                                                                                                                                                                                      Score 472; DB 2;
Pred. No. 8.4e-41;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7809-005
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NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS TITLE OF INVENTION:

Shoham,

MODIFIED CELLULOSE-BINDING DOMAIN (CBD)
PROTEINS AND USE THEREOF
: 9

Raphael

ADDRESSEE:

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APPLICANT: Longe, Niels Erik K.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Schnorr, Kirk
TITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
TITLE OF INVENTION: Licheniformis
FILE REFERENCE: 5377.200-US
CURRENT APPLICATION NUMBER: US/09/198,956
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: 1344/97
EARLIER APPLICATION NUMBER: 60/067,240
EARLIER APPLICATION NUMBER: 60/067,240
EARLIER APPLICATION DATE: 1997-12-02
NUMBER OF SEO ID NOS: 26
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US-09-198-956-10
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TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.4%;
Best Local Similarity 51.5%;
Matches 53; Conservative 16
                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09198956 Patent No. 6165769
                                                                                                                                                                                                                                                                                                                                                   GENERAL
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                          APPLICANT: Andersen, Lene N
APPLICANT: Schulein, Martin
                 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIA RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 41. _
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US95/13813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHA-AI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGSNGSYNGITSNVKGTFVKMSSS-TNNADTYLEISFTGGTLE 109
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419 Seventh Street N.W., Ste. 300
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; LENGTH: 493
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-198-956-10
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US-09-198-955A-12
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TYPE: PRT
CORGANISM: Clostridium thermocellum
US-09-198-955A-12
RESULT 15

US-09-136-574A-43

; Sequence 43, Application US/09136574A

; Patent No. 6294366
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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PRIOR EPLICATION NUMBER: 60/067.2
PRIOR FILING DATE: 1997-12-02
PRIOR FILING DATE: 1997-12-02
PRIOR FILING DATE: 1997-12-02
PRIOR APPLICATION NUMBER: 60/067.2
PRIOR FILING DATE: 1997-12-02
PRIOR FILING DATE: 1997-12-02
PRIOR FILING DATE: 1997-12-02
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PRIOR FILING DATE: 1998-11-02
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PRIOR FILING DATE: 1998-05-06
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: ||||||| | | ||| | |:||| | ::|: ::||||| ||: ||
                                                                                                                                                                                                                                                                                                                                          335 LKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHA-AI 393
                                                                                                                                                                                                       394 IGSNGSYNGITSNVKGTFVKMSSS-TNNADTYLEISFTGGTLE 435
                                                                                                                                                                                                                                                                     61 LGN--SYVDNTSKVTANEVKETASPTSTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 18.4%; Score 245; DB 4; Length 493; Local Similarity 51.5%; Pred. No. 8.3e-17; Local Similarity 16; Mismatches 30; Indels 16; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatches 10; Mismatche
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Schnorr, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glad, Sanne O. S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bjornvad, Mads E
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N: No. 6187580el Pectate Lyases
5378.200-US
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Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 245; DB 4;
Pred. No. 8.3e-17;
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6294366e
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-136-574A-43
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Search completed: October 27, 2002, 11:00:30 Job time: 15.2642 secs
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                                                                                                                                                                                                                                                                                                                                       Ouery Match 11.2%; Score 149.5; DB 4; Length 1426; Best Local Similarity 32.9%; Pred. No. 2.4e-06; Matches 50; Conservative 16; Mismatches 35; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Farrington, Grah
Anderson, Paige
Gibbs, Moreland
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-9200
TELEFAX: 215-540-5818
                                                                                      496
                                                                                                              119 FSRQEVGAATGAVVGGVAGQLF-GKGSGRVSM 149
                                                                                                                                                                     474 A-----SNVTFNFVK-LSSGVSGADYYL----
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MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COPERATING SYSTEM: DOS
CURRENT APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

CRESIFICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                              59 ALLGNSYDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Daniels, Roy
Morgan, Hugh W.
Williams, Diane P.
TITLE OF INVENTION: Compositions and Methods for
Treating Cellulose Containing Fabrics Using Truncated
Cellulase Enzyme Compositions
                                                                               ----EVGFSSG-----AGQLQPGKDAGDIQV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                         Gaps
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       October 27, 2002, 10:55:57; Search time 34.487 Seconds (without alignments) 824.509 Million cell updates/sec
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1335
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62.3
61.0
36.5
36.5
36.5
36.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1980_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1980_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1990_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1991_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1993_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1993_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1993_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1995_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1995_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1997_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1998_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA1999_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA2000_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA2000_DAT:*

JSIDSI/gcgdata/geneseq/geneseqp-embl/AA2000_DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _Geneseq__032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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                                                                                                                                                                                                                                                               Length DB
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AAB81128
AAB81127
AAG81126
AAB81126
AAE05746
AAE05749
AAE05747
AAR65747
AAR65747
AAR65747
                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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                                                                               OspA antigen amino Clostridium cellul Chimeric S peptide Clostridium cellul Callula Chimeric Strain cellul
                                                                                                                                                                                                                                                            Description
                                         Clostridium cellul
Cellulose binding
Clostridium cellul
                    Clostridium
                                                                                                                                                                        Optimised OspA pro
Piscirickettsia sa
                                                                                                                                                                                                                      C17E2 OspA constru
    Gaussia luciferase
                         cellul
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AAB81128 RESULT 1

AAB81128 standard; Protein;

11-JUL-2001 (first entry)

AAB81128;

	ALIGNMENTS					
Human secreted pro Human protein HP10	AAY73440 AAG93288	22	285 285	6. 9	91.5 91.5	4 4 5
Human signal pepti	AAY87280	21	285		91.5	43
Human PRO polypept	AAU29025	22	285		92	42
PRO284	AAB44244	21	285	6.9	92	41
Human PRO284 prote	AAY41688	20	285		92	40
Drosophila melanog	ABB66232	22	2309		95	39
Novel human diagno	ABG15906	22	309	7.1	95	38
	AAY95548	21	922	7.3	98	37
Chlamydia pneumoni	AAW88419	20	922	7.3	98	36
Chlamydia pneumoni	AAY34597	20	922	7.3	98	35
Novel endoglucanas	AAR13227	12	700		100.5	34
PBOMP-2 gene prod.	AAR05799	11	154		101.5	33
Cellulase AE-1. A	AAR15625	12	782	7.6	102	32
Porphorymonas ging	AAY34362	20	230		102.5	31
Porphorymonas ging	AAY34487	20	223	7.7	102.5	30
Moraxella catarrha	AAB20105	22	224		111	29
OspA B-cell epitop	AAB81130	22	20		112	28
NK-1 cellulase. B	AAR42122	14	499		113.5	27
Corrected Bacillus	AAW18790 .	18	551		122.5	26
Amino acid sequenc	AAG63963	22	1350	9.5	126.5	25
Amino acid sequenc	AAG63962	22	1352		127.5	24
	AAY13493	20	1751		148.5	23
	AAY13494	20	616		148.5	22
Truncated cellulas	AAY13492	20	1426	11.2	149.5	21
C. thermocellum ce	AAW43108	19	1853	18.4	245	20
din pro	AAW15238	18	531	18.4	245	19
	AAY43218	20	493	18.4	245	18
Pectate lyase-link	AAY28850	20	493		245	17
A mannanase-linker	AAY54123	21	476		245	16
еl	AAR95080	17	167		245	15
	AAW90080	20	156	35.4	472	14
•	AAW90081	20	154		472	13
. cellulovorans	AAW90077	20	162	35.7	477	12

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Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct.
                  17-SEP-1999;
                                    17-SEP-1999;
                                                                         CA2281913-A1
                                                                                                                                      Key
Region
                                                                                                                                                                             Piscirickettsia
                                                                                                                                                                                                                                  C17E2 OspA construct with N-terminal fusion partner
(KAYW/) KAY W W.
                                                      17-MAR-2001.
                                                                                                                      Region
                                                                                                                                                                    Synthetic
                   99CA-2281913
                                     99CA-2281913.
                                                                                                                                                                             salmonis.
                                                                                                                     /label= Undefined_N-terminal_fusion_partner
                                                                                         /label= C17E2_OspA
/note= "Product of OspA gene optimised for expression in
Escherichia coli"
                                                                                                                                                 Location/Qualifiers
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QΥ
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RRESULT 2
AABBILT 7
ID AABB
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a palmonis specific antigen termed OspA, or an immunogenic fragment of pospA in the form of a vaccine. The method is used for protecting animals, OspA in the form the interface of the particularly polkilothermic fish, against the bacterial pathogen particularly polkilothermic fish, against the bacterial pathogen in the protecting animals, as almonis. The method is also useful for protecting against salmonid protecting. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents the amino acid sequence of C17E2, a p. salmonis OspA construct optimised for expression in Escherichia coii, fused to an undefined N-terminal fusion partner. The fusion protein is used in a vaccine to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BURI/) BURIAN J. (KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for protecting polkilothermic fish against salmonid rickettsial septiloaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAF86248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                AAB81127 standard; Protein; 161
                                                                                                                                                         Optimised
                                                                                                                                                                                      11-JUL-2001
                                                                                                                Poikilothermic vaccine; OspA;
                                                    Synthetic
                                                                   Piscirickettsia
                                                                                                                                                                                                                                                                                                                                                         241
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        Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAONFS 120
                                                                                                                                                                                                                                                                                                                                                                                   RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                           ACPOPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                    ACPOPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burian J,
                                                                                                                                                         OspA protein 17E2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                         (first entry)
                                                                                                                fish; Piscirickettsia salmonis; rickettsial pathogen; salmonid rickettsial septicaemia; rickettsial disease
                                                                    salmonis
            Location/Qualifiers 109..128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kuzyk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1335; DB 22;
Pred. No. 1.5e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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(BURI/) BURIAN J.
(KUZY/) KUZYK M A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a method for the protection against infection of a polkilothermic fish by the bacterial pathogen, Pisciriokettsia salmonis. The method comprises administering an immunogenic amount of a salmonis specific antigen termed OspA, or an immunogenic fragment of p. salmonis specific antigen termed OspA, or an immunogenic fragment of p. salmonis polkilothermic fish, against the bacterial pathogen particularly polkilothermic fish, against the bacterial pathogen particularly. The method is also useful for protecting against salmonid p. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettsial diseases. The present sequence represents optimised p. salmonis OspA protein 17E2. The DNA sequence represents optimised p. salmonis OspA protein 17E2. The DNA encoding OspA 17E2 (AARB6247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is Ecsherichia coli. An OspA protein with an N-terminal fusion partner is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                           AAG78025 standard; Protein;
                                                                                                 Piscirickettsia salmonis polypeptide P10.6.
                                          septicaemia;
ATCC VR-1361
                                                       piscirickettsia salmonis; piscirickettsiosis; salmonid rickettsial;
septicaemia; SRS; surface antigen; vaccine; antibacterial; fish;
                                                                                                                               15-JAN-2002
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              Piscirickettsia salmonis
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KUZYK M A.
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61; Conservative
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Pred. No. 1.6e-73;
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RRESULT 4
AAB81126
IID AAB8
XX AAB6
AC AAB6
XX AAB6
XX AAB6
XX AAB6
XX PO11-J
XX PO19
KW VACC
KW SRS.
XX P1sc
XX P1sc
XX P1sc
XX Reg T
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FT Reg T
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XX CA22
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Best Local
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01-JUL-2000;
01-JUL-2000;
29-JUL-2000;
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Burzio
                                                    Key
Region
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                                                                                                                Poikilothermic vaccine; Ospa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acids encoding an amino acid sequence homologous to surface antigen present on Piscirickettsia salmonis are useful t protect fish against piscirickettsiosis
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N-PSDB; AAH79040.
                                                                                   Piscirickettsia
                                                                                                                                               OspA antigen
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                                                                                                                                                                                                            AAB81126 standard;
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2000GB-0016080.
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2000GB-0018599.
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                                                                                                                fish; Piscirickettsia salmonis; r
salmonid rickettsial septicaemia;
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                                                                                   salmonis
                                                    Location/Qualifiers
                                           /label=
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98.8%;
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                                          B_cell_epitope
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a; rickettsial disease
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RRESULT 5
AAE057AC
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AC AAE0
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(BURI/)
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                                                                                                                          Clostridium
                                                                                                                                                                                                  durability;
                                                                                                                                                                                                                            Clostridium
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DB; AAF86246.
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                                                                                                                                                                                                                          fiber; textile; biological crosslinker. man
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KUZYK M
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                                                                                                                                                                                                ; textile; biological crosslinker; mechanical property cellulovorans cellulose binding domain; wet strength; elasticity; CBDclos; cellulose binding protein A; CBF
                                                                                                                          cellulovorans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99CA-2281913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.0%;
98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 815; DB Pred. No. 7.6e 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
1.6e-72;
                                                                                                                                                                                                                                                                                                                               domain-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                              domain;
                                                                                                                                                                                                                                                                                                                               (CBD-180).
                                                                                                                                                                                                                                                    property;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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                                                                                                                                                                                                                                                                              paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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02-NOV-2000;

2000WO-IL00708

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RESULT 6
AAE05749
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                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to methods and compositions for cross-cc linking and/or modifying the properties of polysaccharide materials. CC The method involves treating the polysaccharide structure with a cpolysaccharide structure with a cc polysaccharide binding domain (PBD) fusion protein. The method is cc used to alter the structural, chemical, physical, electrical and cc mechanical properties of polysaccharide materials such as paper, cc yarns, fibers and textiles, using biological crosslinking agents. CC The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD cc properties such as wet strengths, durability and elasticity. The PBD cc properties such as set the sizing step. The use of a biological crosslinker cc improves the recyclability of paper products. The PBD reagent maintains ct the fine fibers in a slurry therefore resulting in better recovery of the fine fibers in a slurry therefore resulting in better recovery of c which enhances the ability of the alkaline glue used in binding to remembrate names.
DXAXE
                                                                                                                                                                           QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is Clostridium cellulovorans cellulose binding domain (CBD)-180. CBD-180 contains 180 amino acids of C. cellulovorans CBD (CBDclos) of cellulose binding protein A (CBP A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1.2; Fig 1e-1g; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           penetrate paper.
        24-SEP-2001
                                                                       AAE05749 standard; Protein;
                                       AAE05749;
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                                                                                                                                                    154
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                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                   2001-457121/49
                                                                                                                                                                      GTACPQPD 246
                                                                                                                                                                                                                                                                                                        RQEVGAATGAVVGGVAGQLEGKGSGRVSMATGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                         LGNSYVDNTSKVTANFVKETASPTSTYDTYVE-----
                                                                                                                                                                                                                                                                                                                                                          LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                    GTA-PGPD 160
                                                                                                                                                                                                                                            EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
         (first entry)
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99US-0166389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.5%;
                                                                                                                                                                                                                                                                                 FGFASGRATL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                          328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 487; DB 22;
Pred. No. 1.4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                          A
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                                                                                                                                                                                                                                                                                  KKGQFITIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                      -KVTGYIGGAK--VL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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The present invention relates to methods and compositions for cross-
Clinking and/or modifying the properties of polysaccharide materials.
Clinking and/or modifying the properties of polysaccharide materials.
Clinking and/or modifying the properties of polysaccharide structure with a
Clinking and involves treating the polysaccharide structural. The method is
Clinking poperties of polysaccharide materials such as paper,
Clinking in the structural properties of polysaccharide containing materials have improved mechanical
Clinking polysaccharide containing materials have improved mechanical
Clinking polysaccharide containing materials have improved mechanical
Clinking polysaccharide containing materials have improved mechanical
Clinking polysaccharide containing materials have improved mechanical
Clinking polysaccharide the strengths, durability and elasticity. The PBD
Clinking polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide polysaccharide pol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric S peptide-cellulose binding domain-S protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200134091-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Fig 4b-4g; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levy I,
Sequence
                                                                                                                                                                                                                                                      The present sequ
                                                                                                                                                                                                                                                                                                                            which enhances the ability of the alkaline
                                                                                                                                                                                                                Spep-CBD-Sprot), a
                                                                 ID NO: 10
                                                                                                               ID NO:
                                                                                                                                                                                     bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-457121/49.
                                                                 This sequence is stated to be the same as that shown as D NO: 10 in the sequence listing of the specification. He sequence has 2 additional residues at its C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD11046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium cellulovorans.
   328
                                                                                                                                                                                                                    sequence is S peptide-cellulose binding domain-S prot), a fusion protein derived from Clostridium c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-IL00708
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e 327..328
/note= "These res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gg.
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99US-0166389.
   AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "This region is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "These residues are absent in the sequence ID NO: 10 in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoseyov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bу
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                                                                                                                                                                                                                                                                                                                                           glue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain; PBD; paper;
                                                                                                                                                                                                                                       cellulovorans
                                                                                                                                   However
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Query Match

36.5%;

Score

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 46.8 Matches 116; Conservative
                                                                                                                                                    WPI;
                                                                                                                                                                                                           (CBDT-)
                                                                                                                                                                                                                                                       08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CBD; CBD cross linker protein; CCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium
 The present invention relates to methods and compositions linking and/or modifying the properties of polysaccharide
                                                                                       Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                              17-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                                                                                                                                                                                                                                                                                                 02-NOV-2000; 2000WO-IL00708
                                                                                                                                                                                                                                                                                                                                                           WO200134091-A2
                                             Example 1.2; Fig 2b-2e; 121pp; English.
                                                                                                                                                                               Levy I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 GTA-PGPD 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cross linker protein;
                                                                                                                                                  2001-457121/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGNSYVDNTSKVTANFVKETASPTSTYDTYVE----
                                                                                                                                                                                                           CBD TECHNOLOGIES LTD.
YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                               Nussinovitch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRITKSDWSNYTQTNDYSFDASSSTPVVNP-----KVTGYIGGAK--VL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellulovorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellulovorans CBD cross linker protein
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                                                                                                                                                                                                                                                      99US-0164140.
99US-0166389.
                                                                                                                                                                                                                                                                                                                                                                                                                   341
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 340..341
                                                                                                                                                                                                                                                                                                                                                                                      /note= "This residue is absent
as SEQ ID NO: 6 in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FGFASGRATL------KKGQFITIQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                              "Encoded by CCATAGGAT"
                                                                                                                                                                              Shoseyov 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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2; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                     sequence
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for cross-
materials.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                        RESULT 8
AAR63634
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide materials such as paper, yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains the fine fibers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is Clostridium cellulovorans cellulose binding domain (CBD) cross linker protein (CCP).

Note: This sequence is stated to be the same as that shown as SEQ ID NO: 6 in the sequence listing of the specification. However this sequence has an additional residue at its C-terminal.
   Doi RH,
                                                                                                                                                                                            Clostridium cellulovorans
                                                                                                                                                                                                                      Cellulose binding domain;
                                                                                                                                                                                                                                                   Cellulose binding domain.
                                                                                                                                                                                                                                                                                 05-JUN-1995
                                                                                                                                                                                                                                                                                                              AAR63634;
                                                                                                                                                                                                                                                                                                                                          AAR63634 standard; Protein; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                             (REGC ) UNIV CALIFORNIA. (YISS ) YISSUM RES & DEV
                                                                                                      14-APR-1994;
                                                                                                                                   27-OCT-1994
                                                                                                                                                                WO9424158-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                  154 GTA-PGPD 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTACPQPD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNSYVDNTSKVTANFVKETASPTSTYDTYVE---
   Goldstein MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 AA;
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                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                      94WO-US04132
                              & DEV CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -FGFASGRATL------KKGQFITIQ------
 Shoseyov 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 487; DB 22; Pred. No. 3.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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 Shpiegl I;
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-KVTGYIGGAK--VL

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Length 341; Indels

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Gaps

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60 60

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AAAAA72917/R63634 is a novel isolated cellulose binding domain. It pref. Collinds crystalline with a Kd ranging from 1.5 microm. 0.5 microm. Collings pref. with a Kd of <1.2 microm, esp. <1.0 microm. The protein and Collings pref. With a Kd of <1.2 microm, esp. <1.0 microm. The protein and Collings pref. Comprising the CBD and a second protein. The second protein is pref. Comprising the CBD and a second protein. The second protein of degrading Comprising the CBD and a second protein. The second protein of degrading Comprising the CBD collings. Constructive of the collings of this. The CBD and FP CHSP-related protein or an antigenic portion of this. The CBD and FP CHSP-related protein or an antigenic portion of this. The CBD and FP CHSP-related protein or an antigenic portion of this. The CBD and FP CHSP-related protein call disprostic may be used in drug delivery, affinity sepns. and diagnostic cell collings. CBD nucleic acid may be obtd. from a variety of cell Conversible manner or that produce CBD encoding mRNA. The preferred CRSP cource of CBD encoding nucleic acid is C. cellulovorans.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-341767/42.
N-PSDB; AAQ72917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE05745 standard; Protein; 163
                                                                                                                                                                                                                                                                                                                                                                                polysaccharide modification; polysaccharide binding domain; PBD; polysaccharide modification; polysaccharide; mechanical property; yarn; fiber; textile; biological crosslinker; mechanical property; Clostridium cellulovorans cellulose binding domain; wet strength; durability; elasticity; CBDclos; cellulose binding protein A; CBP l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium cellulovorans cellulose binding domain
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                                                                                                                                                                                                                                                                                                               Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                       durability;
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                                                  08-NOV-1999;
18-NOV-1999;
                                                                                                                                   02-NOV-2000; 2000WO-IL00708
                                                                                                                                                                                                 17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 51.7 ges 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GRITKSDWSNYTQTNDYSFD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGNSYVDNTSKVTANFVKETASPTSTYDTYVE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                        99US-0164140.
99US-0166389.
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51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -FGFASGRATL---
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ug delivery, affinity separa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 483; DB 15;
pred. No. 2.7e-39;
9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oteins - with separations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CBDclos).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116
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The present invention relates to methods and compositions for cross-cC linking and/or modifylng the properties of polysaccharide materials. CC The method involves treating the polysaccharide structure with a CC polysaccharide binding domain (PBD) fusion protein. The method is CC mechanical properties of polysaccharide materials such as paper. CC mechanical properties of polysaccharide materials such as papers. CC yarns, fibers and textiles, using biological crosslinking agents. CC yarns, fibers and textiles, using biological crosslinking agents. CC properties such as wet strengths, durability and elasticity. The PBD CC properties such as wet strengths, durability and elasticity. The PBD CC properties such as wet strengths, because in fluting paper manufacture reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker cc improves the recyclability of paper products. The PBD reagent maintains cc improves the recyclability of paper products. The pBD reagent maintains the fibers in a slurry therefore resulting in better recovery of the fine fibers in a slurry therefore resulting in better recovery of competence and the pBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to consider the pBD molecules are eluted by strong alkaline conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                            RESULT 10
AAE05748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DЬ
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Query Match
Best Local S
Matches 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Levy I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1.1; Page 111-112; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             penetrate paper.
The present sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain (CBDclos) of
                                                                                                                                                                                                                                           AAE05748 standard; Protein; 428
                                                                Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; protein A-cellulose binding domain;
                                                                                                                                                                                                           AAE05748;
                                                                                                                                        Clostridium
                                                                                                                                                                       24-SEP-2001
               Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                       118
                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSVEFYNSNKSAQTNSTTPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-457121/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106;
                                                                                                                                                                                                                                                                                                                                                                       EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGNSYVDNTSKVTANFVKETASPTSTYDTYVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBD TECHNOLOGIES LTD.
YISSUM RES DEV CO HEBREW UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nussinovitch
                                                                                                                                                                                                                                                                                                                                       -GRITKSDWSNYTQTNDYSFD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is Clostridium cellulovorans cellulose binding :los) of cellulose binding protein A (CBP A).
                                                                                                                                       cellulovorans protein A-cellulose binding domain
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               -----FGFASGRATL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoseyov 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 483; DB 22;
Pred. No. 2.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                           ₿
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                          --KKGOFITIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                   Query Match
                                                                                                             Matches
                                                                                                                                                                                                                                                                                       polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide materials such as paper, yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains the fibers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CBDT-)
                                                                                                                                                                                            binding domain (ProtA-CBD). This sequence contains a part of CBP A protein and a part of protein A derived from PRIT2T vector sequence Note: This sequence is stated to be the same as that shown as SEQ ID NO: 8 in the sequence listing of the specification. However this sequence has 2 additional residues at its C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1999;
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                 penetrate paper.
The present sequence is Clostridium cellulovorans Protein A-cellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Levy I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W0200134091-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                       270
 330
                          61
                                                    present invention relates to methods and compositions for cking and/or modifying the properties of polysaccharide mater method involves treating the polysaccharide structure with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-457121/49
DB; AAD11045.
              LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                             106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CBD TECHNOLOGIES LTD.
YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                            Similarity 51.7
06; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nussinovitch
                                                                                                                                                                   428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 3b-3g; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-IL00708
                                                                                                                                                                   Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0164140
99US-0166389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- CBP_A_protein 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Unknown
/note= "Encoded by
427..428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Protein_A
/note= "This region is
265..426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                         36.2%;
51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "These residues are abser ID NO: 8 in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shoseyov
                                                                                                             9:
                                                                                                                     Score 483; Db 2.
                                                                                                          Pred. No. le-3
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are absent in the sequence listing"
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                                                                                                                                        22;
                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from pRIT2T vector"
                                                                                                                                     Length 428;
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              materials.
                                                                                                            76;
                                                                                                          Gaps
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361
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-1998;
15-JUN-1998;
01-OCT-1998;
                                       bioluminescence-generating systems, assays, screening methods, diagnostic method and articles of manufacture. They can be expressed using e.g. bacterial, yeast, fungal, plant, insect or animal cells. The Renilla mulleri, Gaussia and Pleuromamma luciferase or Renilla or Ptilosarcus GrPs can be used in e.g. toys, cosmetics, fountains, personal care items, fairy dust, beverages, soft drinks, foods, textile products, bubbles bath, ink or paper products. In particular, they can be used in e.g. squirt guns, pellet guns, finger paints, foot bags, greeting cards, slimy play material, clothing, bubble making toys, bath powders, cosmetics, body lotions, gels, body powders, body creams, toothpastes, mouthwashes, soaps, body paints, bubble bath, inks, wrapping paper, gelatins, icings, frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes, ice, dry ice or fountains. The nucleic acids can also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bioluminescence-generating system; toy; cosmetic; fairy dust; beverage; body paint; squirt gun; balloon; slimy play material; soap; toothpaste; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaussia sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY39952;
                                                                                                                                                                                                                                               Renilla and Ptilosarcus green fluorescent protein (GFP) nucleic proteins. The luciferases and GFPs can be used in
                                                                                                                                                                                                                                                                            This sequence represents a luciferase of the invention. The invertates to Renilla mulleri, Gaussia and Pleuromamma luciferase
                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                               New isolated Renilla mulleri, Gaussia and Pleuromamma luciferase and Renilla and Ptilosarcus green fluorescent protein nucleic acids - \,
                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ27550.
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-580443/49
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ВJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROLUME
BRYAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Szent-Gyorgyi
                              fish
 382
                                                                                                                                                                                                                                                                                                                      Page 222-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0079624.
98US-0089367.
98US-0102939.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.
                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
                            plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                      C;
                                                                                                                                                                                                                                                                                                                     233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KKGQFITIQ---
                                                                                                                                                                                                                                                                                          The invention
                                                                                                                                                                                                                                                               acids and
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Query Match Best Local Similarity

36 62 . 6%;

Score Pred.

480.5; DB 20; No. 1.6e-38;

Length

Sequence

В

<u>_</u> μ.

61

61

δÃ

Matches

107;

Conservative

10;

Mismatches

33;

QΥ 밁 Q

118

NFSRQ---

Вþ

121 NYTOTNDYSFDASSSTPVVNPKVTGY-----

RESULT 12 AAW90077 ID AAW9(

AAW90077

standard; Protein; 162

C. cellulovorans CbpA CBD protein.

Clostridium cellulovorans

05-JAN-1999 US5856201-A.

27-OCT-1994;

94US-0330394

09-MAR-1999 AAW90077;

(first entry)

```
Cellulose binding domain; CBD; CbpA; fusion protein; diagnosis; HSP; immunoassay; heat-shock protein; cross reactive protein; detection; antigenic fragment; antibody; insulin-dependent diabetes mellitus; cellulose; chitin; cellulolytic; amorphogenic.
                                                                                                                                This sequence represents a cellulose binding domain (CBD) derived from the CbpA protein of Clostridium cellulovorans. The sequence is used the construction of a fusion protein which can be used in diagnostic immunoassays, e.g. to detect heat-shock proteins (HSP) and their cross-reactive proteins, antigenic fragments or HSP-specific antibodies (which indicate insulin-dependent diabetes mellitus, or susceptibility (which indicate insulin-dependent for the cellulose (including to it. The CBD, has very high affinity for cellulose (including to it. The CBD) and chitin (dissociation constant 0.8-1.4 mu M), but crystalline forms) and chitin (dissociation constant 0.8-1.4 mu M), but crystalline forms) and chitin (dissociation activities. The CBD binds over has almost no cellulolytic or amorphogenic activities. The CBD binds over has almost no cellulolytic or amorphogenic activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of a specific analyte by reaction with binding agent fused to cellulose binding domain - and subsequent treatment with cellulose and reaction of insoluble product with a label specific
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AAW90AW99
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14-APR-1994;
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                                                                                                                                                                                                                                                                                                                                           This sequence represents a fusion protein (CBD-Kpn1) composed of the Cbf protein cellulose binding domain (CBD) from Clostridium cellulovorans protein cellulose binding domain (CBD) from Clostridium cellulovorans from the protein sused in diagnostic immunoassays, e.g. to detect the constant of the constant constant constant constant constant constant constant constant constant constant constant constant constant to it. The CBD has very high affinity for cellulose (including crystalline forms) and chitin affinity for cellulose (including crystalline forms) and chitin constant 0.8-1.4 mu M), but has almost no cellulolytic or (dissociation constant 0.8-1.4 mu M), but has almost no cellulolytic or composed cactivities. The CBD binds over a wide pH range and is not camorphogenic activities. The CBD binds over a wide pH range and is not released from cellulose to cellulolytic or released from cellulose to cellulolytic constant 0.8-1.4 mu M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-1994;
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(YISS ) YISSUM RES & DEV
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                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                               amorphogenic activities. The CBD binds over a amorphogenic activities by washing with water released from cellulose by washing with
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                                               5; Column 55-56; 63pp; English.
                                                                                                                                                              1 Similarity 97.4
89; Conservative
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97.8%;
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                                                                                                                                                                       ; Score 472;
pred. No. 3;
2; Mismatch
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(REGC) 14-APR-1994;

UNIV CALIFORNIA.

DEV CO

94US-0330394. 93US-0048164. 94WO-US04132.

Doi RH,

Goldstein MA,

Shoseyov

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Shpiegl I;

1999-105130/09

AAV74072

Claim 3;

Fig 1A-B;

63pp; English.

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Matches Query Match Best Local S

Similarity

35.7%;

Score 477; DB 20 pred. No. 1e-38; 2; Mismatches

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                                                                                                                                                                                             shock protein (HSP) fragment. This protein is used in diagnostic immunoassays, e.g. to detect heat-shock proteins (HSP) and their cross-reactive proteins, antigenic fragments or HSP-specific antibodies (which indicate insulin-dependent diabetes mellitus, or susceptibility to it. The CBD has very high affinity for cellulose (including crystalline forms) and chitin (dissociation constant 0.8-1.4 mu M), but has almost no cellulolytic or amorphogenic activities. The CBD binds over
                                                                                                                                                                                                                                                                            This sequence represents a fusion protein composed of the CbpA protein cellulose binding domain (CBD) from Clostridium cellulovorans and a he shock protein (HSP) fragment. This protein is used in diagnostic
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14-APR-1993;
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             GNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                 SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL
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 GNSYVDNTSKVTANFVKETASPTSTYDTYVE 91
                                                 SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL
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                                                                                                                    Similarity
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Pred. No. 3e-38;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cellulose binding domain; CBD; hapten; moiety; biotin; avidin; streptavidin; affinity chromatography; cell separation, cell immobilisation; protein immobilisation; enzyme immobilisa multienzyme reactors; signal immunoassays; drug delivery; pest cellulose. Chitia
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Search completed: October Job time: 36.487 secs

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054381 rickettsia
09f9f2 rickettsia
09f9f2 rickettsia
05252 rickettsia
09k2n6 male-killin
031065 rickettsia
09k4w8 male-killin
045996 clostridium
053154 rickettsia
09f9g9 rickettsia
09f9g7 rickettsia
09f9g7 rickettsia
09f0g1 rickettsia
052637 rickettsia
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052830 clostridium
0977y4 clostridium
031208 rickettsia
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
17 KDA COMMON-ANTIGEN (FRAGMENT).
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Bacteria; Proteobacteria; alpha subdivision;
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID-789;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-MAR-2001 (TrEMBLrel. 19, Last annotation
01-DEC-2001 (TrEMBLREL. 19, Last annotation
17 KDA GENUS-COMMON ANTIGEN
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Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AAC28452.1;
CENTIFICE 159 AA; 16497 MW; 34C5B020AF470A1F
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-2117364; PubMed-11321078;
MEDLINE-2117364; PubMed-11321078;
Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,
Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
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                             SSLIIISV---FLVGC--AQNESRQEVGAATGAVVGGVAGQLEGKGSGRVSMAIG-GAVL 156
SKIMITALAASMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL 63
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61; Conservative
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Pred. No. 2.2
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ith papaya bunchy top disea
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Best Local S
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"Molecular characterization of a novel spotted fever group
species from Ixodes scapularis in Texas.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF031534; AAB95267.1; -
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Rickettsiaceae; Rickettsieae; Rickettsia
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17 KDA ANTIGEN (FRAGMENT).
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01-JUN-1998
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
17KDA ANTIGEN (17 KDA ANTIGEN) (FRAGMENT).
male-killing Rickettsia from Adalia bipunctata.
mate-killing Rickettsia; alpha subdivision; Ricket
Bacteria; Proteobacteria; alpha subdivision; Ricket
Rickettsiaceae; Rickettsiaee; Rickettsia.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,

Schulenburg H.J.G.V.D., Majerus M.E.N.;

Bertrand D., Hurst G.D.D., Majerus M.E.N.;

On the evolution of male-killing: Monophyletic origin and horizontal transfer of male-killing Rickettsia (a-Proteobacteria) from two contensions of male-killing Rickettsia (a-Proteobacteria) from two congeneric ladybirds, Adalia bipunctata L. and A. decempunctata L.

(Coleoptera: Coccinellidae).";

(Coleoptera: Coccinellidae).";
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1 (TrEMBLrel. 19,
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Last annotation update)
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RESULT
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Q9K4W8;
Q9K4W8;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spotted fever in Australia.";
Int. J. Syst. Bacteriol. 48:1399-1404(1998)
EMBL; AF027124; AAB81846.1;
EMBL; AF060706; AAD20231.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stenos J., Roux V., Walker D., Raoult D.;
Rickettsia honei sp. nov., the aetiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Billings A.N., Yu X.-J.,
Submitted (SEP-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-TT-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 KDA ANTIGÉN (17 KDA PROTEIN) (FRAGMENT). RICKETLSIA honei. Bacteria; Proteobacteria; alpha subdivision Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99045882; PubMed=9828442;
Stenos J., Roux V., Walker D., Raoult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                        QEIYGTACPQPD 246
                                                                                                                                                                                                                                           QEIYGTACPOPD
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                                                                                                                                                        QKAYGNACROPD 135
                                                                                                                                                                                                                                                                                           NKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALLGAVLGGQIGAGMDEQDRRLAEL
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(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 19,
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eae; Rickettsia.
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 Last sequence update)
Last annotation update)
                                   Created)
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Pred. No. 3.1
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Best Local :
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                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
STRAIN=ATCC 35319;
MEDLINE=99173902; Po
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01-NOV-1996
01-MAR-2001
01-JUN-2001
SCAFFOLDING
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MEDLINE-20575219; PubMed-11133455;

Schulenburg H.J.G. V.D., Habig M., Sloggett J.J., Webberley M.K.,

Schulenburg H.J.G. V.D., Majerus M.E.N.;

Bertrand D., Hurst G.D.D., Majerus M.E.N.;

"Incidence of male-killing Rickettsia spp. (alpha-Proteobacteria)

"Incidence of male-killing Rickettsia decempunctata L. (Coleoptera:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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male-killing Rickettsia from Adalia decempunctata.
Bacteria: Proteobacteria: alpha subdivision; RicketRickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=120393;
                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium celluloly Bacteria; Firmicutes; Clostridium.
                                                                                 "Sequence analysis of scaffolding protein CipC and ORFXp, a new cohesin-containing protein in Clostridium cellulolyticum: comparison of various cohesin domains and subcellular localization of ORFXp."; J. Bacteriol. 181:1801-1810(1999).
                                                                                                                                                                                                                                                      "Interaction between the endoglucanase CelA and the scaffol protein CipC of the Clostridium cellulolyticum cellulosome. J. Bacteriol. 178:2279-2286(1996).
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Appl. Environ. Microbiol. 67:270-277(2001).
EMBL; AJZ69516; CAB96381.1; -.
 Reverbel-Leroy Belaich J.;
                                 SEQUENCE FROM N.A. STRAIN-ATCC 35319;
                                                                                                                                                      Pages S., Bel
Belaich J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     cellulolyticum.
irmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 01, Created)
(TrEMBLrel. 16, Last sequence up
(TrEMBLrel. 17, Last annotation
PROTEIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                         Α.,
                                                                                                                                                                  PubMed=10074072;
A., Fierobe H.P.,
                                                                                                                                                                                                                                                                                                                       PubMed=8636029;
A., Tardif C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
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                   Tardif
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Pred. No. 3.7
                 Belaich
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                 A.,
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                                                                                                                                                                                                                                                                                                                       С.,
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Best Local S
Matches 72
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                                     Matches
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EMBL; U40345; AAC28899.2;
HSSP; Q06851; INBC.
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Pfam; pF00963; Cohesin; 8.

ProDom; pD001947; CBD_3; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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Belaich J.P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003880; Phosphopant_attach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002102;
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                                                                                                                        Baird R.W., Lloyd M., Stenos J., F. "Characterization and comparison o group rickettsiae.";
J. Clin. Microbio
                                                                                                                                                                                                                                                                         Q53154 PRELIMINARY; PKT; 134 AA.
Q53154;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1998 (TrEMBLrel. 08, Last annotation update)
QCLONE PRB FISF 1), 5' END CDS (FRAGMENT).
                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                        NON_TER
                                                                                                                                                                                                                                                                Rickettsia sp.
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                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           198
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                                                                                                                                                                                                                       NCBI_TaxID=789;
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             103
                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSVQFNNGSSPASSNSIYARFKVTNTSGSPINLADLKLRYYYTQDADKPLTFWCDHAGYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NESRQEVGAATGAVVGGVAGQLEGKGS----GRVSWAIGGAVLGGLIGSKIGQSMDQQDK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSNYIDATSKYTGSF-KAYSPAYTNADHYLEVALNSDAGSLPAGGSIEIQTRFARNDWS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                  IKLNQSLEKVKAG-----QVTRWRNPDTGNSYS
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                                                                                                                                                                                                                                                                                                                                                                                                          -TINPTSISAKAGSFADTKITLTPNGNTFNGIS
SSLIIISV---FLVGC--AQNESRQEVGAATGAVVGGVAGQLEGKGSGRVSMAIG-GAVL 156
                                                                                                                 in. Microbiol. 30:2896-
M99391; AAA73386.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
72; Conserv
                                       l Similarity
55; Conserv
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1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                          154 AA;
                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                        154
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 POTENTIAL.
1546 SCAFFOLDING PROTEIN.
A; 158748 MW; F8651504EC27809F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cohesin
                                                                                                                                   30:2896-2902(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reverbel C.,
                                                                                             15849 MW;
                                           18.3%; Score 244; DB 2;
35.3%; Pred. No. 1.7e-12;
Live 31; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 249;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                               F5C35855EDB439D2 CRC64;
                                                                                                                                                              Ross B.C., Stewart R.S., Dwyer B.; of Australian human spotted fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tardif C.,
                                                                                                                                                                                                                                                                                                                                                  154
                                                                                                                                                                                                                                                                                                                                                                                                                 229
                                                                                                                                                                                                                                                                                                                                                                                                                                         201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; I
1.3e-11;
hes 81;
                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fierobe H.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     databases
                                                                                                                                                                                                                                                          Rickettsiales;
                                              54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1546;
                                                                     Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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OpFOQ1;
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17 KDA PROTEIN (FRACKENT).
Rickettsia sp. California 2.
Bacteria; Proteobacteria; alp)
Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
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STRAIN=CALIFORNIA 2;
ROUX V., RAOULT D.;
Submitted (DEC-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       υ
                                                                                                                                                                                                                                                           Raoult D.;
"A new SFG rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=147259;
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                                                                                                                                      SEQUENCE FROM
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SEQUENCE 131 A
O91522 PRELIMINARY; PRT; 131 AA.
091522; PRELIMINARY; PRT; 131 AA.
0915252;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
17 KDA SURFACE ANTIGEN (FRAGMENT).
Rickettsia peacockii.
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Majerus M.E.;
"Rickettsial relative associated "Rickettsial relative associated";
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SEQUENCE FROM N.A.
MEDLINE-94117373; PubMed-8288533;
MEDLINE-94117373; PubMed-8288533;
                                                                                                                                                                                                                                                                                                                                                 beetle (Adalia bipunctata).";
J. Bacteriol. 176:388-394(1994).
EMBL; U04162; AAA19235.1; -.
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NCBI_TaxID=789;
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17 KDA ANTIGEN (FRAGMENT).
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131 AA;
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eae; Rickettsia.
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Last sequence up
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                      Kakiuchi M., Isui A., Suzuki K., Fujino T., Fujino E., Kimura T., Karita S., Sakka K., Ohmiya K.;
"Cloning and DNA sequencing of the genes encoding Clostridium josui scaffolding protein CipA and cellulase CelD and identification of their gene products as major components of the cellulosome.";
J. Bacteriol. 180:4303-4308(1998).
                                                                                                                                                                                   Pfam; PF00942; CBD_3; 1.
Pfam; PF00963; Cohesin; 6.
ProDom; PD001947; CBD_3 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_5.
SEQUENCE 1162 AA; 120229 MW; 95F02DDD27ADFBA2
                                                                                                                                                                                                                                                                                                        InterPro; IPR001956; CBD_3.
InterPro; IPR002102; Cohesin
InterPro; IPR003880; Phosphor
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Bacteria; Firmicutes;
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98361925; PubMed-9696784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=47589;
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                      MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKAYGNAC
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  ISVQFNNGSSPTSSSSIYARFKVTNTSGSPINLADLKLRYYFTQDENKQMTFWCDHAGYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF260571; AAF69012.1;
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49; Conserv
                                                                                              Similarity
66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 08, (TrEMBLrel. 08, TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN
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38.3%;
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                                                                                              31;
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Last sequence up
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Pred. No. 6.7e
24; Mismatches
                                                                                            Score 233.5;
Pred. No. 1.6e
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228C020550CAA9D0 CRC64;
                                                                                            1.6e-10;
.ches 74;
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                                                                                              Indels
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RESULT 15
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RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Rennett G.N., Koonin E.V., Smith D.R.,
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Rennett G.N., Smith D.R.,
Rennett G.N., Smith D.R.,
Rennett G.N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q977Y4
Q977Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2001 (TremBLrel. 18, Created)
01-OCT-2001 (TremBLrel. 18, Last sequence update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
PROBABLY CELLULOSOMAL SCAFFOLDING PROTEIN, SECRETED,
CELLULOSE-BINDING AND COHESIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE-21359325; PubMed-11466286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome: SEQUENCE 1483 AA; 154444 MW; A74808E396AA9807 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGNNYMDVTSKVSGTF-NEVSPAVTNADHYLEVALSSDAGSLPAGGSIEIQTRFARNDWS 151
                                                                                                                                                                                                                                                                                                                                                NGYNYQTITSNVVGTFV-AMDNATATADHYLEISFSNG
                                                                                                                                                                                                                                                                     RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                           EKVKAGQVTRWRNPDTGNSYS 201
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                                                                                                                     -WSNYDQSNDYS 164
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Title:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 20
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1335
1 MSVEFYNSNKSAQTNSITPI.....IYGTACPQPDGRWQVISTEK
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RESULT 2
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AC P16624
DT 01-AUG
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17 kba surface antigen precursor.
0MP OR RP833.
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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STRAIN-MADRID E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G., "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson B.E., Tzianabos T.;
"Comparative sequence analysis of a gene.";
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                                                                                                                                                                                                                                                                                                                                                                                    the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
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                                                                                                                                                                                                                                                                                                                                              EMBL; M28482; AAA26378.1; ALT_SEQ.
                                                                                                                                                                                                                             Outer membrane; Lipoprotein; SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                     EMBL; AJ
                                                                                                                                                           SEQUENCE
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                 103 SSLIIISV---FLYGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                                     LIPID
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159 AA;
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N-ACYL DIGLYCERIDE (PROBABLE).
; A33D404B65EEB071 CRC64;
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Antigen; Signal; Complete
                                                                                                    Score 288;
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Q52764;
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Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95229950; PubMed-7714214; Furuya Y., Katayama T., Yoshida Y., Kaiho I.; "Specific amplification of Rickettsia japonic specimens by PCR.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 kDa surface antigen precursor.
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                                                                                                                                                                                                                                                      Outer membrane; Lipoprotein; Antigen; Signal.

SIGNAL 1 19 BY SIMILARITY.

CHAIN 20 159 17 KDA SURFACE ANTIGEN.

LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).

SEQUENCE 159 AA; 16554 MW; CDDCE7CEBDCD6B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Clin. Microbiol. 33:487-489(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  EMBL; D16515; BAA03965.1; -. PROSITE; PS00013; PROKAR_LIE
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17KD_RICCN
P05372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGLIGSKIGOSMDQODK----IKLNQSLEKVKAGQVTEWRNPDTGNSYSVEPVRTYQRYN
                                                                                                                  64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                anchor (Probable).
                                                                                                                                                               GGLIGSKIGQSMDQQDK----IKLNQSLEKYKAGQYTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                  GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
                                                                   -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN
                                                                                         KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35, Last sequence up 35, Last annotation
               STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35, Created)
                                                                                                                                                                                                                                                                                                                         PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                            21.4%;
                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                              Score 286; DB 1
Pred. No. 1.1e-1
                   PRT;
                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                             DB 1;
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Rickettsia conorii, and
Rickettsia rickettsii.
Bacteria; Proteobacteria; a
Rickettsiaceae; Rickettsiea
NCBI_TaxID=781, 783;
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01-AUG-1990
01-MAR-2002
17 kDa surfa
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 kDa surface antigen precursor. OMP OR RC1287.
                                                                                                                       EMBL;
EMBL;
PIR;
PIR;
                                                                                                                                                                     EMBL;
EMBL;
                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content
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J. Bacteriol. 170:4493-4500(1988)
-:- SUBCELLULAR LOCATION: Attached to the outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=R.conoril; STRAIN-Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fo
Samson D., Roux V., Cossart P., Weissenbach
                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                Anderson B.E., Baumstark B.R., Bellir "Expression of the gene encoding the Rickettsia rickettsii: transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson B.E., Regnery R.L., Carlone G.M., Tzian
Fu Z.Y., Bellini W.J.;
"Sequence analysis of the 17-kilodalton-antigen
                                                          Outer membrane;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-R.rickettsii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87222152; PubMed-3108232; Anderson B.E., Regnery R.L., Carlone G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=R.conorii, and R.rickettsii; MEDLINE=89359171; PubMed=2768201; Anderson B = m-1-1
                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89008059;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-30 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=R.rickettsii;
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                                                                                              BL; M28479; AAA26379.1; -.
BL; M28480; AAA26376.1; -.
BL; AE008675; AAL03825.1; -.
BL; M16486; AAA26381.1; -.
BL; J03371; -; NOT_ANNOTATED_CDS.
R; A325972; A25972.
R; A33971; A33971.
R; B33971; B33971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 169:2385-2390(1987).
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                                                                                                                                                                                                                                                                                                                    anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lsms of evolution in Rickettsia 293:2093-2098(2001).
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                                                                                    PS00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 09, Created)
(Rel. 15, Last sequence up)
(Rel. 41, Last annotation
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146
153
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1 19
10 159
10 20
10 146
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783;
                                                                       PROKAR_LIPOPROTEIN;
ipoprotein; Antigen;
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eae; Rickettsia.
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        17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PRO
N -> D (IN REF. 3).
G -> E (IN REF. 3).
  206A2BBF74FCE169 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genus-common
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and posttranslational
                                                              1.
Signal; Complete
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ch J., Claverie v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tzianabos
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                                  (PROBABLE)
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Best Local S
Matches 55
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Best Local Similarity
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01-AUG-1991
01-OCT-1996
17 kDa surfa
                                                                                                                                                                                                                                          EMBL; M28481; AAA26377.1; --
PIR; C33971; C33971, PROKAR_LIPOPROTEIN; PROSITE; PS00013; PROKAR_LIPOPROTEIN; Outer membrane; Lipoprotein; Antigen; SIGNAL 1
                                                                                                                                                                                                                   CHAIN
LIPID
                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.";
J. Bacteriol. 171:5199-5201(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; alpi
Rickettsiaceae; Rickettsieae;
NCBI_TaxID=785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=89359171; Anderson B.E., Tzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P22882;
                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                          anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Attached to the
                                                                                                GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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                    QEIYGTACPQPDGRWQVIS
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                                                   TSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY - -
                                                                        KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         surface antigen precursor
                                                                                                                                                     . Similarity
55; Conser
                                                                                                                                                                                                       159
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(Rel. 19, Last sequence up
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ianabos T.;
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                                                                                                                                                              20.7%; Score 276.5; DB 1 39.6%; Pred. No. 6.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analysis of
 159
                         253
                                                                                                                                                                                                    17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBA
MW; 08973E2648FD8CD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha subdivision; Rickettsiales; eae; Rickettsia.
                                                                                                                                                      27;
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                                                                                                                                                                                                                                                       OPROTEIN; 1.
Antigen; Signal.
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                                                   -RNSTGQYCREYTQTVVIGGKQ
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RESULT 6
17KD_RICAU
RESULT 7
17KD_R
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CO Ricket
OC Ricket
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Best Local S
Matches 59
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
17 kba surface antigen precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baird R.W., Ross B., Dwyer B.;
Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rickettsia australis.
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                                                                                                                      17KD_RICPA Since...
17KD_RICPA Since...
17KD_RICPA Since...
195030;
101-0CT-1996 (Rel. 34, Last sequence update)
101-0CT-1996 (Rel. 34, Last annotation update)
101-0CT-1996 (Rel. 34, Last annotation update)
101-0CT-1996 (Rel. 34, Last annotation update)
101-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Outer membrane;
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                                                                                    Rickettsia parkeri.
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsiae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                             157
            STRAIN-MACULATUM; Pretzman C.I., St
                                                                    NCBI_TaxID=35792;
                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                               GGLIGSKIGOSMDQQDK----IKLNOSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                    SSLIIISV---FLVGCAQ--NFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
                                                                                                                                                                                                                                                                                         ----GQYCREYTQTVVIGGKQQKAYGNACRQPDGQ 154
                                                                                                                                                                                                                                                                                                                     KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M74042; AAA26394.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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BY SIMILARITY.
NACYL DIGLYCERIDE (PROBABLE).
20 N-ACYL DIGLYCERIDE (PROBABLE).
                  Stothard
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                     D.R.,
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                     Ralph
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                        Clark
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                                                                                                              Rickettsiales;
                          J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 154;
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                            Fuerst P.A.;
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                                          Outer membrane; SIGNAL 1 20 CHAIN 20
                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               Stothard D.R., Ralph D.A., Clark J.B., Submitted (AUG-1994) to the EMBL/GenBs of SUBCELLULAR LOCATION: Attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsia rhipicephali
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between the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                EMBL; U11020; AAB07706.1; -
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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-1996 (Rel. 34, Last sequence update)
-1996 (Rel. 34, Last annotation update)
surface antigen precursor (Fragment).
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LLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
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; Lipoprotein; 19
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                                                                                                                                                                                                                                                                                                                                                                                                         Clark J.B., Fuerst P.A., Pretzman C.;
e EMBL/GenBank/DDBJ databases.
Attached to the outer membrane by a lipid
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                              Antigen; Signal.
Antigen; Signal.
BY SIMILARITY.
17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE)
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-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
17 kDa surface antigen precursor (Fragment).
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Rickettsieae; Rickettsia.
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Pred. No. 2.9e-14
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No. 1.7e-14;
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SEQUENCE FROM STRAIN=YS;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pret Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases -i- SUBCELLULAR LOCATION: Attached to the outer membrane
                                                                                Clostridium thermocer
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
Outer membrane; Lipoprotein; Antigen; Signal.
SIGNAL 1 19 BY SIMILARITY.
CHAIN 20 >154 17 KDA SURFACE ANTIGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MO 85-1084;
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Rickettsiaceae; Rickettsieae;
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                                                                     Bacteria; F
Clostridium
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    Last sequence update)
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36.5%;
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eae; Rickettsia.
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Pred. No. 3.
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                                                                                     group; Clostridiaceae
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Gilbert H.J.
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Poole D.M., Morag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00963; Cohesin; 3.
Pfam; PF00404; Dockerin_1; 2.
ProDom; PD001947; CBD_3; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS000448; CLOS_CELLULOSOME_RPT;
PROSITE; PS00448; CLOS_CELLULOSOME_RPT;
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Pfam; PFO
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                                                            Q06851;
01-JUN-1994
01-NOV-1997
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S Microbiol. Lett. 78:181-186(1992).
S MICROBIOL. ACTS AS A SCAFFOLDING PROTEIN IN THE CELLULOSOME. IT PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE CELLULOLYTIC ENZYMES PROBABLY THROUGH THE BINDING OF THE NINE CELLULOLYTIC ENZYMES PROBABLY THROUGH THE BINDING OF THE NINE REPEATED DOMAINS WITH THE DUPLICATED SEGMENT OF 24 AMINO ACIDS PRESENT IN CATALYTIC SUBUNITS OF THE CELLULOSOME.
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Pro; IPR002105; Dockerin_1.
Pro; IPR002048; EF-hand.
Pr00942; CBD_3; 1.
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
1 scaffolding protein A precursor (Cellu
n S1/SL) (Cellulose integrating protein
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E., Lamed R., B
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PRO/THR-RICH.
CELLULOSE-BINDING
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (PARTIAL)
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                                                                                                                                                                                                                                                                           Mismatches
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InterPro;

IPR002102; Cohesin.
IPR002105; Dockerin_1. IPR001956; CBD_3

EF-hand

1NBC; 1AOH; 1ANU;

23-JUL-97. 08-JUL-98. 26-SEP-97.

InterPro; InterPro;

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rujino T., Beguin P., Aubert J.-P.;
"Organization of a Clostridium thermocellum gene cluster encoding the cellulosomal scaffolding protein CipA and a protein possibly involved in attachment of the cellulosome to the cell surface.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequencing of a Clostridium thermocellum gene (cipA) encodin cellulosomal SL-protein reveals an unusual degree of internal homology.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE STRAIN=ATCC 27405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; F. Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimon L.J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain: a general mechanism EMBO J. 15:5739-5751(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structure provides new ins
Structure 5:381-390(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 184-321
MEDLINE-97238934; PubMed=9083107;
                                                                                                                                                                                                                                                                                                                                                               J. MOI. Biol. 273:701-713(1997)
-i- FUNCTION: ACTS AS A SCAFFOLDING
PROMOTES BINDING OF CELLULOSE TO
CELLULOSTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98022914; PubMed=9402065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crystal structure of a bacterial family-III cellulose-binding
                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                        resolution.";
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PDB;
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                                                                                                                                                      entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                               EMBL;
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SUBCELLUAR LOCATION: CELL SURFACE.
DOMAIN: CONTAINS 9 COPIES OF A DOMAIN (COHESIN) OF ABOUT DOMAIN: CONTAINS 9 COPIES OF A DOMAIN BORN BY THE C RESIDUES THAT BINDS TO THE DOCKERIN DOMAIN BORN BY THE CELLULOSOME.
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L; X67506; CAA478
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01-FEB-1995 (Rel. 3
01-NOV-1995 (Rel. 3
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Pfam; PF00963; Cohesin; 9.

Pfam; PF00404; Dockerin 1; 2.

ProDom; PD001947; CBD_3; 1.

PROSITE; PS00018; EF_HAND; UNKNOWN_1.

PROSITE; PS00448; CLOS_CELLULOSOME_RPT; 2.

Cellulose degradation; Cell wall; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
SEQUENCE
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REPEAT
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DOMAIN
REPEAT
                                                J. Gen. Microbiol. 139:307-316(1993).

-I- FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF 1,4-B.
GLUCOSIDIC LINKAGES IN CELLULOSE, LICHENIN AND CEREAL BETA-I
GLUCANS. PRINCIPALLY ACTIVE AGAINST BARLEY BETA-GLUCAN.

-I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
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REPEAT
                                                                                          "Gene sequence and properties of Clostridium thermocellum.";
                                                                                                             Gilbert H.J.;
                                                                                                                   MEDLINE-93171873; PubMed-8436949; Hazlewood G.P., Davidson K., Laur
                                                                                                                                   SEQUENCE FROM N.A., AND STRAIN-NCIB 10682;
                                                                                                                                                            NCBI_TaxID=1515;
                                                                                                                                                                      Clostridium.
                                                                                                                                                                             Clostridium thermocellum.
Bacteria; Firmicutes; Bacillus/Clostridium
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                         linkages in cellulose.
PATHWAY: CELLULOSE DEGRADATION.
SIMILARITY: BELONGS TO CELLULASE
                 HYDROLASES).
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Last annotation update)
rsor (EC 3.2.1.4) (EGI)
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Best Local
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ACT_SITE
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SEQUENCE
and cellulose-binding domains.";
Mol. Gen. Genet. 223:258-267(1990)
-!- CATALYTIC ACTIVITY. F-3.
                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 26-36 STRAIN-NCIB 11745; MEDLINE-91066838; PubMed=2250652; Jauris S., Ruecknagel K.P., Schwarz W.H., Bronnenmeier K., Staudenbauer W.L.; "Sequence analysis of the Clostridium Ster
                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Endoglucanase Z precursor (EC 3.2.1.4) (Endo-
(Thermoactive cellulase) (Avicelase I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00942; CBD_3; 2. Pfam; PF00759; Glyco_hydro_9; 1. ProDom; PD001347; CBD_3; 1.
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the Euro
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01-NOV-1991
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prosite; ps00698; GLYCOSYL_HYDROL_F9_2; 1.
Cellulose degradation; Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                         Bacteria; F:
Clostridium
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                                                             a thermoactive cellulase (Avicelase
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                   Bacillus/Clostridium
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  Endohydrolysis
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CATALYTIC.
CELLULOSE-BINDING (
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Pred. No. 7.3
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  of 1,4-beta-D-glucosidic
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                                                               identification
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RESULT 15
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AC P50900
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DT 01-OCT
DT 01-OCT
DT 01-OCT
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CLLY
CS CLOST
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RN [1]
RP SEQUEN
RC STRAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X55299; CAA39010.1; ALT_SEQ.
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REPEAT
DOMAIN
              SEQUENCE FROM N.A.
STRAIN-NCIB 11754;
Bronnenmeier K., Kundt K., R
Staudenbauer W.L.;
Staudenbauer W.L.;
Submitted (FEB-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; p26221; 1TF4.
InterPro; IPR001956; CBD_3.
InterPro; IPR001701; Glyco_hydro_9.
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PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
Cellulose degradation; Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00942; CBD_3; 2.
Pfam; PF00759; Glyco_hydro_9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD001947; CBD_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Exoglucanase II precursor (EC 3.2.1.91) (Exocellobiohydrolase (1,4-beta-cellobiohydrolase II) (Avicelase II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                         Clostridium stercorarium.
Bacteria; Firmicutes; Bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSKADWTDYIQTNDYSFSTNTSYG-----SNDRITVYISGVLVSGI 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GSNNITGTFVK-MAEPKEGADYYLETGFTDGAGYLQPNQSIEVQ-----
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CONTAINS MULTIPLE CELLULOSE-BINDING SITES.
BELONGS TO CELLULASE FAMILY E (FAMILY 9 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                             the EMBL/GenBank/DDBJ databases
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DOMAIN B'.

DOMAIN B'.

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CELLULOSE-BINDING (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
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Pred. No. 9.2e
29; Mismatches
                                                                          Riedel K.,
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                                                                               Schwarz W.H.,
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Search completed: October 27, Job time: 11.7271 secs
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Best Local
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Bronnenmeier K., Rueckhagel K.P., Staudenbauer W.L.;

Purification and properties of a novel type of

"purification and properties of a novel type of

thermophile Clostridium stercorarium.";

Eur. J. Biochem. 200:379-385(1991).

Eur. J. Biochem. 200:379-385(1991).

-i- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages

-i- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages

reducing ends of the chains.

reducing ends of the chains.

-i- SIMILARITY: BELONGS TO CELLULASE FAMILY L (FAMILY 48 OF GLYCOSYL-HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
CHARACTERIZATION.
STRAIN=NCIB 11754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; pF00942; CBD_3; 1.
pfam; pF02011; Glyco_hydro_48; 1.
pRINTS; PR00844; GLHYDRLASE48.
proDom; pD001947; CBD_3; 1.
prodom; pD011903; Glyco_hydro_48; 1.
probom; pD011903; Glyco_hydro_lase; Glycosidase; Cellulose degradation; Hydrolase; Glycosidase; Glycolase; Glycosidase; Glycolase; Glycosidase; Glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z69359; CAA93280.1; -. HSSP; Q06851; INBC.
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InterPro; IPR000556; Glyco_hydro_48.
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A;Molecule type: genomic RNA
A;Residues: 1-1848 <SHO>
A;Cross-references: GB:M73817; NID:g144748; PIDN:AAA23218.1; PID:g144749
C;Genetics:
A;Gene: cbpA
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A;Title: Primary sequence analysis of Clostridium cellulovorans A;Reference number: A44140; MUID:92228810
A;Accession: A44140
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27-Jun-1994 #text_change 15-Oct-1999

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RESULT 2 D33971 D33971 rickettsial common antigen precursor - Rickettsia prowazekii N;Alternate names: 17kD surface antigen; outer membrane protein (omp); RP833 C;Species: Rickettsia prowazekii C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 03-Nov-2000 C;Accession: D33971; B71645 C;Accession: B.E.; Tzianabos, T. R;Anderson, B.E.; Tzianabos, T. J. Bacteriol. 171, 5199-5201, 1989	239 GTACPQPD 246 	181 EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238 :: :	121 ROEVGAATGAVVGGVAGOLFGKGSGRVSMAIGGAVLGGLIGSKIGOSMDOODKIKLNQSL 180	61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDDSHMRGCLQGSSLIIISVFLVGCAQNFS 120 	1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60 	Query Match 36.5%; Score 487; DB 2; Length 1848; Best Local Similarity 46.8%; Pred. No. 2.8e-32; Matches 116; Conservative 12; Mismatches 30; Indels 90; Gaps 7;

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J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a ger A;Reference number: A33971; MUID:89359171
A;Recession: B33971
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 < AND>
A;Cross-references: GB:M28479; NID:g152463. prov.
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A;Note: the sequence in GenBank entry RIRANT17KC, release 109.0, (PID:g152462) omits the R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-159 <AN2>
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A;Accession: B71645
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A;Experimental source: strain Madrid E
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Rickettsial common antigen precursor - Rickettsia conorii
C;Species: Rickettsia conorii
C;Species: 16 Mar-1990 #sequence_revision 16 Mar-1990 #text_C;Date: 16 Mar-1990 #sequence_revision 16 Mar-1990 #text_RANGERSON, B.E.; Tzianabos, T.
R;Anderson,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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:Superfamily: rickettsial common antigen
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                                                                                                                                                                                                                                                                                              103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
      120
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                       64
                                                                                                                                                                                                                                        5 SKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKQQL-VGVGVGALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKIMIIALAASMLQACNGQSGMNKQGTGTLLGGAGGALLGSQFGQGKGQL-VGVGVGALL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAYLGGQTGASMDEQDRRLLELTSQRALESAPSGSNTEWRNPDNGNHGYYTPNKTY----
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                                                          KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                                                                                                                       GGLIGSKIGQSMDQODK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                    GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
   -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
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nilarity 37.9%;
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pred. No. 6.3e-17;
2; Mismatches 52;
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RESULT C33971

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Rickettsial common antigen precursor - Rickettsia rickettsii
C:Species: Rickettsia rickettsii
C:Date: 16-Mar-1990 #text_change
C:Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change
C:Accession: A33971
R:Anderson, B.E.; Tzianabos, T.
R.Anderson, B.E.; Tzianabos, T.
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A33971
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A; Molecule type: DNA
A; Residues: 1-159 <AND>
                                                                                                                                                                                                                                                                                                                                                                                                                                 17K surface antigen precursor [imported] - Rickettsia conorii (strain Malish C.Specles: Rickettsia conorii c.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C.Accession: G97860 C.Accession: G97860 S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Sam R.Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Sam Science 293, 2093-2098, 2001 in Rickettsia conorii and Rickettsia prowaze A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowaze A;Reference number: A97700; MUID:21442074; PMID:11557893
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A;Molecule type: DNA
A;Molecule type: NA
A;Residues: 1-159 <KUR>
A;Cross-references: GB:AE006914; PIDN:AAL03825.1; PID:g15620425; GSPDB:GN00173
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                                                                                                             157
 120
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                                                                          64
                                                                                                                                             5 SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                       KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS
                                                                                                         GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                        GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
61;
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                                                                                                                                                                                                                             21.3%; Score 285; DE 37.9%; Pred. No. 1.1c tive 31; Mismatches
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1.1e-1<u>6</u>;
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Rickettsial common antigen precursor - RicketC; Species: Rickettsia typhi
C; Date: 16-Mar-1990 #sequence_revision 16-Ma
C; Accession: C33971
R; Anderson, B.E.; Tzlanabos, T.
J. Bacteriol. 171, 5199-5201, 1989
A; Title: Comparative sequence analysis of a A; Reference number: A33971; MUID:89359171
A; Accession: C33971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17K antigen precursor - Rickettsia rickettsii
C;Species: Rickettsia rickettsii
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change
C;Accession: A25972
R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.;
J. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen gene fr
A;Reference number: A25972; MUID:87222152
scaffolding protein CipC precursor - Clostridium cellulolyticum (fragment)
C:Species: Clostridium cellulolyticum
C:Date: 17-Aug-1990 #sequence_revision 16-Aug-1996 #text_change 13-Nov-1998
C:Accession: PC6006
C:Accession: PC6006
R:Pages, S.; Belaich, A.; Tardif, C.; Reverbel-Leroy, C.; Gaudin, C.; Belaic
J. Bacteriol. 178, 2279-2286, 1996
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C;Superfamily: rickettsial
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A;Cross-references: GB:M28481; NID:g152459; PIDN:AAA26377.1; PID:g152460 C;Superfamily: rickettsial common antigen
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A; Residues: 1-159 < AND>
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A; Residues: 1-159 < AI
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                                                                                                                                                                                                            -RNSTGQYCREYTQTVVIGGKQQKAYGDACRQPDEQWQVVN 159
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1615,1617-1854 <GE2>
A;Residues: 1-1615,1617-1854 <GE2>
A;Cross references: EMBL:108665
R;Fujino, T.; Beguin, P.; Aubert, J.P.
FEMS Microbiol. Lett. 94, 165-170, 1992
A;Title: Cloning of a Clostridium thermocellum
A;Reference number: $25767
A;Accession: $25767
                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-1854 <ER>
A; CROSS-references: EMBL:LO8665
A; CGOSS- U.T.; Romaniec, M.P.M.; Kobayashi, T.; Huskisson, Mol. Microbiol. 8, 325-34, 1993
Mol. Microbiol. 8, 325-34, 1993
A; Title: Sequencing of a Clostridium thermocellum gene (cipA) & A; Reference number: S33527; MUID:93302508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cipA protein - Clostridium thermocellum N;Alternate names: probable cellulosome C;Species: Clostridium thermocellum C;Date: 13-Jan-1995 #sequence_revision 1 C;Accession: S36859; S33527; S25767; S28 R;Gerngross, U.T.; Demain, A.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Gerngross, U.T.; Demain, submitted to the EMBL Data
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A; Residues: 1-586 < PAG>
                                          submitted to the EMBL Data Library,
                                                                                       A; Molecule type: DNA
A; Residues: 1216-1232,'Y',1234-1241,'T',1243-1319,'R',1321-1615,1617-1854
A; Cross-references: EMBL: X67406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S36859
A; Accession: S36859
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A; Reference number: A; Accession: S28659
                                                                       R;Beguin, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GSYMDWQKISAFVGGTLAYG--STPDGGNPPPQDP
                                          August 1992
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$28659; T18261
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A; Molecule type: DNA
A; Residues: 1216-1232/YY, 1234-1241, TY, 1243-1319, 'R', 1321-1615, 1617-1768,
A; Cross-references: EMBL:X67406
A; Cross-references: EMBL:X67406
R; Fujino, T.; Beguin, P.; Aubert, J.P.
R; Fujino, T.; Beguin, P.; Aubert, J.P.
J. Bacteriol. 175, 1891-1899, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1821-1854 <FU2>
A; Cross references: EMBL:X67506; NID:g296879; PID:g296880; C; Genetics:
A; Gene: cipA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: Z18847; MUID:93209931
A; Accession: T18261
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T30433
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                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: 220837; MUID:98361925
A;Accession: T30433
A;Status: preliminary; translated from GB,
A;Molecule type: DNA
A;Residues: 1-1162 <KAK>
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                            RESULT 11
C97012
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Best Local S
Matches 53
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probably cellulosomal scaffolding protein C; Species: Clostridium acetobutylicum
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Best Local
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                                                                                                                                                                                                    SGNNYMDVTSKVSGTF-NEVSPAVTNADHYLEVALSSDAGSLPAGGSIEIQTRFARNDWS
                                                                                                                                                                                                                             LGNSYVDNTSKVTANFVKETASPTSTYDTYLDP--SHMRGCL-QGSSLIIISVFLVGCAQ
                                                                                                                                                                                                                                                          NFDQSNDWSYTSA-
                                                                                                                                                                      NFSRQEVGAATGAVVGGVAGQLFGKGS----GRVSMAIGGAVLGGLIGSKIGQSMDQQDK 173
                                                                                        -KISPTSISAKQGQ
                                                                                                                IKLNQSLEKVKAGQ 187
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53; Conser
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34.0%;
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                                                                                                                                                                                                                                                                                                                    31;
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Pred. No. 5e-12;
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                                                                                                                                                                                                                                                                                                                   Score 233.5; DB 2
Pred. No. 2.6e-11;
1; Mismatches 74
                                                                                                                                               -GSYMDWQKIAAFVGGTLVYG--STPNGDDNPTQDP 197
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                    precursor,
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C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: C97012
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gib: Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing E A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001437; PIDN:AAK78886.1; A;Experimental source: Clostridium acetobutylicum C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1483 <KUR>
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A47704
A47704
A47704
endoglucanase I (EC 3.2.1.-) CelI - Clostridium thermocellum
C; Species: Clostridium thermocellum
C; Species: Clostridium thermocellum
C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C; Accession: A47704
C; Accession: A47704
C; Accession: A47704
C; Accession: A47704
C; Accession: A47704
C; Accession: A47704
R; Hazlewood, G.P.; Davidson, K.; Laurie, J.I.; Huskisson, N.S.; Gilbert, H.J.
R; Hazlewood, G.P.; Davidson, K.; Laurie, J.I.; Huskisson, N.S.; Gilbert, H.J.
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                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L04735; NID:g144807; PIDN:AAA20892.1; A;Note: sequence extracted from NCBI backbone (NCBIN:125637, C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA; p
A;Residues: 1-879 <HAZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Gen. Microbiol. 139, 307-316, 1993
A;Title: Gene sequence and properties of Cell, a family E endoglucanase A;Reference number: A47704; MUID:93171873
A;Accession: A47704
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                                                                                                                                                                                                         3 VEFYNSNKSAQTNSITBIIKITNTSDSDLNLNDVKVRYXYTSDGTQGQTFWCDHAGALLG
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                                                                                                                                             NSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFSRO 122
                                                                                                                                                                                     LQYANGNAGATSNSINPRFKIINNGTKAINLSDVKIRYYYTKEGGASQNFWCDWSSA--G
VKAGQVTRWRNPDTGNSYSVEPVRTYQR
                                                                     EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSLEK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
57; Conser
                                                                                                                                                                                                                                                               l Similarity
59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                               -SNVTGNFF-NLSSPKEGADT------
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                                                                                                                   14.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
                                                                                                                                                                                                                                                               ; Score 188.5; DB 2;
; Pred. No. 1.1e-07;
20; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
       210
                                                                                                                     -CL--
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ATCC824
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                                                 EVQIRFSKED
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NCBIP: 125638)
                                                                                                                                                                                                                                                                                                               879;
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                                                                                                                         821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostrid
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R:Morris, D.D.; Glbbs, M.D.; Ford, M.; Thomas, J.; Bergquist, P. submitted to the EMBL Data Library, December 1997
A;Description: Family 10 and 11 xylanase genes from Caldicellulc A;Reference number: 220972
A;Accession: T31085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gibate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997 G;Accession: S12021 R;Accession: S12021 R;Brandsel, K.P.; Schwarz, W.H.; Kratzsch, P.; Bronnenmeier, K.; Staudenba Mol. Gen. Genet. 223, 258-267, 1990 Mol. Gen. Genet. 223, 258-267, 1990 A;Title: Sequence analysis of the Clostridium stercorarium celZ gene encoding a thermoac A;Reference number: S12021; MUID:91066838 A;Accession: S12021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xylanase - Caldicellulosiruptor sp.
C;Species: Caldicellulosiruptor sp.
C;Species: C2-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31085
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S12021
thermoactive cellulase - Clostridium stercorarium
RESULT
A43802
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A; Residues: 1-1779 <
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Matches
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Best Local
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                                                                                                                                                                                                                                                                     1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHA--G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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                                                                                                                                                                                                                               LKVLYKNNETSASTGSIRPWFKIVNGGSSSVDLSRVKIRYWYTVDGDKPQSAVCDWAQIG 1173
                                                                                                                FSRQEVGAATGAVVGGVAGQLF-GKGSGRVSM 149
                                                                                                                                                                                        ALLGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGC--LQGSSLIIISVFLVGCAQN 118
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47; Conservative
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                                                                                                                                                                                                                                                                                                                               Similarity
                                                                            EVGFSSG----
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                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: AF036924;
                                                                                                                                                      -SNVTFNEVKLT-SGVSGADYYL--
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                                                                                                                                                                                                                                                                                                                             11.3%;
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                                                                          AGQLQPGKDTGDIQV 1217
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                                                                                                                                                                                                                                                                                                     Score 151.5; DB 2;
Pred. No. 0.00032;
""omatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 188; DB 2;
Pred. No. 1.4e-07;
9; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                        NID:g2760905; PID:g2760909;
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Search completed: October Job time: 19.3592 secs

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R;Saul, D.J.; Williams, L.C.; Grayling, R.A.; Chamley, L.W.; Love, Appl. Environ. Microbiol. 56, 3117-3124, 1990
A;Title: celB, a gene coding for a bifunctional cellulase from the A;Reference number: A43802; MUID:91136262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cellulase (EC 3.2.1.4) / cellulose 1,4-beta-cellobiosidase N;Alternate names: endo-1,4-beta-glucanase C;Species: Caldocellum saccharolyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: Streptomyces endo-1,4-beta-xylanase A homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;20-320/Domain: Streptomyces endo-1,4-beta-xylanase A homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 30-Jan-1993 #sequence_revision 30-Sep-1993 #text_change 10-Jul-1998 C;Accession: A43802
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A;Residues: 1-915 <SAU>
A;Cross-references: EMBL:X13602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Pathway: cellulose degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: hydrolysis of 1,4-beta-D-glucosidic linkages
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Best Local
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                                       238
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                                     YGTACPQPDGRWQVISTEK 256
                                                                                                                                                                                                         FSRQEVGAATGAVVGGVAGQLF-GKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLN 177
                                                                                                                        QSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEI 237
                                                                                                                                                                  ----EIGFKSG-----AGQLQPGKDTGEI---
                                                                                                                                                                                                                                                     A-----SNVTFKFVK-LSSSVSGADYYL-----
                                                                                                                                                                                                                                                                                             ALLGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQN 118
----PSTNDDWLYVSGNK
                                                                                                                                                                                                                                                                                                                                                                                                                          60;
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                                                                                 DWSNYNQGNDWSW--LQSMTSYGENEKVTAYI--
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23.2%;
512
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5;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 147; DB 2;
Pred. No. 0.00034;
5; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                          64;
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                                                                                 -DGVLVWGQE---
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                                                                                                                                                                  -QIRFN
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Perfect score:
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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1335
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    MSVEFYNSNKSAQTNSITPI.....IYGTACPQPDGRWQVISTEK 256
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/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-30-394A-2
US-09-006-632-7
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US-09-198-9574A-44
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CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/102,939
EARLIER FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER FILING DATE: 1998-06-15
EARLIER APPLICATION NUMBER: 60/079,624
EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 32
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US-08-048-164A-2
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi,
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFE
                                                                                                                                                                      121
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ALIGNMENTS

US/09277716A

Christopher

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Artificial Sequence: fusion protein
; FEATURE: INFORMATION: Cellulose Binding Domain (CBD)-Gaussia luciferase fusion prote
US-09-277-716-22
Sequence 2, Application US/08048164A Patent No. 5496934
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
                                                                                                                                                                                                                                                                                                                                     1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                        LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCL---QGSSLIIISVFLVGCAQ
                                                                                                                                                            NYTQTNDYSFDASSSTPVVNPKVTGY----
                                                                                                                                                                                NFSRQ----EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGA-VLGGLIGS 162
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                                                                                                                                                                                                                                     LGNSYVDNTSKVTANFVKETASPTSTYDTYVEFGFASGAATLKKGQFITIQGRITKSDWS
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Pred. No. 4.1e-41;
0; Mismatches 33
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APPLICANT: Doi, ROY H.
TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

Goldstein, Shpiegl, Itai

ADDRESSEE:

COUNTRY: U. ZIP: 10036 STREET: 1155 AV CITY: New York STATE: New Yor

New York

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Query Match 35.7%;
Best Local Similarity 97.8%;
Matches 90; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
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TypOLOGY: line
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                       APPLICANT: DOI, ROY H.
TITLE OF INVENTION: METHODS OF USE OF CELLULOSE BINDING DOMAIN PROTEINS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/00 FILING DATE: 14-APR-1993
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , Application US/08460462
5670623
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(212) 869-8864/9741
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Pred. No. 2.7e-41;
2; Mismatches 0
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           Version #1.25
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Best Local S
Matches 90
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/460,462
APPLICATION NUMBER: US/08/460,462
FILING DATE: concurrently herewith
FILING DATE: 435
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REFERENCE/DOCKET NUMBER: 780:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: Goldstein, Marc A.
APPLICANT: Doi, Roy H.
TITLE OF INVENTION: CELLULOSE BINDING DOMAIN FUSION PROTEINS
                                                                                                                                                                                                    FILING CALL
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,164
APPLICATION APPLICATION:
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                                                                                  REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                  FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 LGNSYVDNTSKVTANFVKETASPTSTYDTYVE 97
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: concur
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                                                                 TELEPHONE:
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shpiegl, Itai
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                                     : (212) 790-9090
(212) 869-8864/9741
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                                                                                                                                                                                                                                                                                                                concurrently herewith ON: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.7%;
97.8%;
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                                                                                                                                7809-008
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, MOLECULE TYPE: protein US-08-048-164A-2

TELEFAX:

TELEPHONE:

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US-08-460-462-2

Patent No.

APPLICANT: Shpieg

APPLICANT:

CITY: New York STATE: New York

ZIP: 10036 COUNTRY:

U.S.A.

STREET:

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; MOLECULE TYPE: protein US-08-460-457-2
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                                                              Matches
                                                                                           Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acid
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: concurrently/
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 14-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              TELEFAX: (212) 869-8864/9:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 70:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 11. CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                      TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                 LENGTH:
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              MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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                                                            Similarity 97.
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amino acid
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   amino acid
)GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shoseyov, Oded
VENTION: KITS AND METHODS OF DETECTION USING CELLULOSE BINDING DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                 concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                       protein
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                                                                           35.7%;
97.8%;
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Pred. No. 2.7e-41;
2; Mismatches 0,
                                                            Score 477; DB 1;
Pred. No. 2.7e-41;
2; Mismatches 0
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                                                            0;
                                                           Gaps
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US-08-330-394A-2

Sequence 2, Application Patent No. 5856201

US/08330394A

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GENERAL INFORMATION:

APPLICANT:

APPLICANT:

Shoseyov, Oded Yosef, Karmey Shpiegl, Itai Goldstein, Marc

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RESULT 6
US-08-460-455-2
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                                                                                                                                 Matches
                                                                                                                                                Best Local
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Goldstein,
APPLICANT: Doi, Roy H
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,455
FILING DATE: concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-APR-1993
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 10036
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CITY: New York
STATE: New Yor
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                              61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                              1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                                                                                                           LENGTH:
LGNSYVDNTSKYTANFYKETASPTSTYDTYVE
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                                                              MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 65
                                                                                                                               l Similarity
90; Conserv
                                                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: PENNIE & EDMONDS
1155 Avenue of the Americas
                                                                                                                                                                                                                                                               162 amino acids
                                                                                                                                                                                                                                                                                                                               (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goldstein,
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                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             concurrently herewith
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                                                                                                                                             35.7%;
97.8%;
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                                                                                                                                                                                                                                                                                                                                                                                            18,872
                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                               7809-009
                                                                                                                                              Score 477; DB 2; Pred. No. 2.7e-41;
                                                                                                                                 Mismatches
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 97
                                                                                                                                 0
                                                                                                                                                               Length 162;
                                                                                                                                 Indels
                                                                                                                               0;
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US-08-330-394A-2
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TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-006-636-7
US-09-006-636-7
; Sequence 7, Application US/09006636
; Sequence 7, Application US/09006636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DOI, ROY TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PATENTIA Release #1.0,
SOFTWARE: PATENTIA Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CIP
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1155 AVENUE OF THE AMERICAS CITY: NEW YORK
STATE: NEW YORK
COUNTRY: " " " "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 10036
                                                                                                                                                                                                                             TITLE OF INVENTION: ARABIDOPSIS THALIANA ENDO-1,4-BETA-TITLE OF INVENTION: GLUCANASE GENE, PROMOTER AND PROTEIN
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               APPLICANT: Shoseyov, Oded APPLICANT: Shani, Ziv
                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                             1 MSVEEYNSNKSAQTNSITDIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 MSVEFYNSNKSAQTNSTTPIIKITNTSDSDLNLNDVKVRYYTTSDGTQGQTFWCDHAGAL 65
COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0 JRRENT APPLICATION DATA:
                                                                                                                                              CITY: New York
                                                                                                                                                                 STREET:
                                                                                                                                                                                  ADDRESSEE:
                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 97.8
90; Conservative
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amino acid
DGY: linear
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                                                                                                    10036-2711
                                                                                                                                   ΝY
                                                                                                                                                                 E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                    USA
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                                       IBM Compatible
SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIP OF PCT/US94/04132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 477; DB 2;
pred. No. 2.7e-41;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09006632
Patent No. 6184440
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 163 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,232
REGISTRATION NUMBER: 78
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 190-909
TELEPHONE: (212) 790-909
TELEFAX: (212) 869-8864
                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ANAME: Baldwin, Geraldine F.
ANAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REGISTRATION NUMBER: 7809-018
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                             TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shoseyov, Oded
APPLICANT: Shani, Ziv
APPLICANT: Shpigel, Etai
TITLE OF INVENTION: TRANSGENIC PLANTS OF ALTERED
TITLE OF INVENTION: MORPHOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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les 90; Conserv
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CITY: New York
STATE: NY
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                  STRANDEDNESS:
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                                                                  ENGTH:
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66141 PENNIE
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linear
                                                  : 163 amino acids amino acid
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                                       single
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97.8%;
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Pred. No. 2.7e-41;
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Best Local S
                                                                                          Matches
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Best Local
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TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                    OFTWARE: Patent...
SOFTWARE: Patent...
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/330,394A
APPLICATION NUMBER: 27-0CT-1994
                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CIP
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
ANTERCOLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                        TOPOLOGY: 11
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS OF DETECTION USING TITLE OF INVENTION: CELLULOSE BINDING DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
               62
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
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                                                                                                                                                                                                LENGTH:
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GNSYVDNTSKVTANFVKETASPTSTYDTYLD
                                       SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL
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                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                154 amino acids
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1155 AVENUE OF THE AMERICAS
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                                                                                                                                                                                                                                                   : (212) 790-9090
(212) 869-8864
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Shpiegl, Itai
                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
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                                                                                          Conservative
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                                                                                                                                                                         linear
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                                                                                                       35.4%;
97.8%;
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                                                                                                     Score 472; DB 2;
Pred. No. 8 2e-41;
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Pred. No. 2.7e-41;
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                                                                                          Mismatches
               92
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                                                                                                                                 RESULT 12
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            APPLICANT:
APPLICANT:
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Query Match
Best Local Similarity
~~+~hes 89; Conserva
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                                                                                                                      Sequence 9, Application PC/TUS9513813 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 14-APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
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NAME: MISROCK, S. LESLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                2 SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL
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1155 AVENUE OF THE AMERICAS
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(212) 869-8864
                                                Yeda Research and Development Co. Ltd.
Ramot University Authority for Applied
Research and Industrial Development Ltd.
Technion Research and Development Foundation Ltd.
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Wilchek,
                Bayer, Edward
Morag, Ely
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CELLULOSE E
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Pred. No. 8.4e-41;
2; Mismatches 0
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APPLICANT: Andersen, Lene N.
APPLICANT: Andersen, Martin
APPLICANT: Lange, Niels Erik K.
APPLICANT: Lange, Niels Erik K.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Bjornvad, Mads E.
APPLICANT: Shonorr, Kirk
APPLICANT: Shonorr, Kirk
FITLE OF INVENTION: Pectin Degrading Enzymes From Bacillus
FITLE OF INVENTION: Licheniformis
FILE REFERNCE: 5377.200-US
FILE REFERNCE: 5377.200-US
FILER REPLICATION NUMBER: US/09/198,956
CURRENT APPLICATION UNUMBER: 1344/97
EARLIER FILING DATE: 1997-11-24
EARLIER PILING DATE: 1997-11-24
EARLIER APPLICATION NUMBER: 60/067,240
EARLIER FILING DATE: 1997-12-02
EARLIER FILING DATE: 1997-12-02
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US-09-198-956-10
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TITLE OF INVENTION: MODIFIED CELLULOSE-BINDING DOMAIN
TITLE OF INVENTION: PROTEINS AND USE THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      sequence 10, Application US/09198956
patent No. 6165769
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TELEX: 248633
TELEX: 2580 ID NO: 9:
SEQUENCE CHARACTERISTICS:
SEQUENCE TARACTERISTICS:
LENGTH: 167 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13813
SEO ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
                         NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: BAN
RECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Browdy, Roger L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LGN--SYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 IGSNGSYNGITSNVKGTFVKMSSS-TNNADTYLEISFTGGTLE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHA-AI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 Seventh Street N.W., Ste. 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.4%; Score 245; DB 5; Length 167; 51.5%; Pred. No. 1.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAYER=3
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, ORGANISM: Bacillus licheniformis US-09-198-956-10
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                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/198,955A
CURRENT FILING DATE: 1998-11-24
CURRENT FILING DATE: 1998-11-24
PRIOR APPLICATION NUMBER: 1343/97
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 1344/97
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-12-02
PRIOR FILING DATE: 1997-12-02
PRIOR FILING DATE: 1997-12-02
PRIOR FILING DATE: 1997-12-02
PRIOR APPLICATION NUMBER: 60/067,240
PRIOR APPLICATION NUMBER: 60/067,240
PRIOR APPLICATION NUMBER: 09/073,684
PRIOR APPLICATION NUMBER: 09/073,684
PRIOR FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09198955A Patent No. 6187580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Clostridium thermocellum US-09-198-955A-12
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TYPE: PRT
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APPLICANT:
APPLICANT:
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                           RESULT 15
US-09-136-574A-43
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LENGTH: 493
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                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kongsbak, Lars
TITLE OF INVENTION: NO. 6187580el Pectate Lyases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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sequence 43, Application US/09136574A patent No. 6294366
                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1
                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335 LKVEFYNSNPSDTINSINPQFKVINTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHA-AI 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 IGSNGSYNGITSNVKGTFVKMSSS-TNNADTYLEISETGGTLE 435
                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LGN--SYVDNTSKVTANEVKETASPTSTYDTYLDPSHMRGCLQ 101
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                                                                                      394 IGSNGSYNGITSNVKGTEVKMSSS-TNNADTYLEISETGGTLE
                                                                                                        INFORMATION:
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version
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Schnorr, Kirk
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Glad, Sanne O. S
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                                                                                                                                                                                                                                                                                                                                                                             1998-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.4%; Score 245; DB 4; 51.5%; Pred. No. 8.3e-17; tive 16; Mismatches 30
                                                                                                                                                                                                                                18.4%;
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                                                                                                                                                                                                                 16; Mismatches
                                                                                                                                                                                                                          Score 245; DB 4; ]
Pred. No. 8.3e-17;
6: Mismatches 30;
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TOPOLOGY: 11 near

MOLECULE TYPE: No. 6294366e

SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-136-574A-43
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Search completed: October 27, 2002, 11:12:14 Job time: 14.2642 secs
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Best Local S
                                                                                                                                                                                                                                                                                                                                                Matches
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INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Farrington, Graham K.
                                                                                                                                                                                                                                                      496
                                                                                                                                                                      474 A-----SNVTFNFVK-LSSGVSGADYYL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/136,574A
FILING DATE: 19-Aug-1998
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/932,571
FILING DATE: September 19, 1997
ATTORNEY/ACENT INFORMATION:
NAME: Bak, MATY E.
                                                                                                                                                                                                                                                                                                                                         y Match 11.2%; Score 149.5; DB 4; Length 1426;
Local Similarity 32.9%; Pred. No. 2.4e-06;
hes 50; Conservative 16; Mismatches 35; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPB: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                              59 ALLGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQN 118
                                                                                                                                                                                                                                                                                 1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHA--G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 1997US001/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniels, Roy
Morgan, Hugh W.
Williams, Diane P.
TITLE OF INVENTION: Compositions and Methods for
Treating Cellulose Containing Fabrics Using Truncated
Cellulase Enzyme Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                                                                                           FSRQEVGAATGAVVGGVAGQLF-GKGSGRVSM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Spring House Corporate Center, P.O. Box 457 CITY: Spring House STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson, Paige
Gibbs, Moreland
Bergquist, Peter
                                                                                   -AGQLQPGKDAGDIQV 517
                                                                                                                                                                                                                                                                                                                                            Indels 51; Gaps
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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length:
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1: /SIDS1/gcgdata/gc2: /SIDS1/gcgdata/gc3: /SIDS1/gcgdata/gc3: /SIDS1/gcgdata/gc5: /SIDS1/gcgdata/gc5: /SIDS1/gcgdata/gc5: /SIDS1/gcgdata/gc7: /SIDS1/gcgdata/gc7: /SIDS1/gcgdata/gc7: /SIDS1/gcgdata/gc7:
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Match
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1335
1 MSVEFYNSNKSAQTNSTTPI.....IYGTACPQPDGRWQVISTEK
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:/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
:/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT: *
:/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *
:/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT: *
:/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT: *
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:/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT: *
:/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *
:/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT: *
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:/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT: *
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Copyright (c) 1993 - 2002 Compugen
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256
161
162
162
190
328
341
162
163
382
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IJ
AAB81128
AAB81127
AAG8025
AAB81126
AAE05746
AAE05747
AAE05747
AAE05747
AAR636363
AAE05748
AAE05748
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              C17E2 OspA constru
Optimised OspA pro
Pisciriokettsia sa
OspA antigen amino
Clostridium cellul
Chimeric S peptide
Clostridium cellul
Cellulose binding
Clostridium cellul
Clostridium cellul
                                                                                                                                                                                                                               Description
Gaussia
luciferase
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ALIGNMENTS

RESULT 1 AAB81128

11-JUL-2001 (first entry)

AAB81128;

AAB81128 standard; Protein;

256

B

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Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen; vaccine; OspA; salmonid rickettsial septicaemia; rickettsial disease; SRS; 17E2; fusion construct.
                                                                                                                          Region
                                      17-SEP-1999;
                                                                             CA2281913-A1
                                                                                                                                            Key
Region
                                                                                                                                                                           Synthetic
                                                                                                                                                                                   Piscirickettsia
                                                                                                                                                                                                                                            C17E2 OspA construct with N-terminal fusion partner.
(KAYW/) KAY W W.
                   17-SEP-1999;
                                                         17-MAR-2001.
                   99CA-2281913
                                      99CA-2281913
                                                                                                                                                                                   salmonis.
                                                                                              /label= Undefined_N-terminal_fusion_partner
96..256
/label= C17E2_OspA
/note= "Product of OspA gene optimised for expression
Escherichia coli"
                                                                                                                                                      Location/Qualifiers
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N-PSDB;

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This invention relates to a method for the protection against infection of a poikilothermic fish by the bacterial pathogen, piscirickettsia salmonis. The method comprises administering an immunogenic amount of a salmonis specific antigen termed OspA, or an immunogenic fragment of p. salmonis specific antigen. The method is used for protecting animals, oppA in the form of a vaccine. The method is used for protecting animals, pathogen particularly poikilothermic fish, against the bacterial pathogen p. salmonis. The method is also useful for protecting against salmonid p. salmonis. The method is also useful for protecting against salmonid rickettsial septicaemia (SRS) and other rickettail diseases. The present sequence represents the amino acid sequence of C17E2, a p. salmonis OspA sequence represents the amino acid sequence of C17E2, a p. salmonis OspA undefined N-terminal fusion partner. The fusion protein is used in a undefined to create an anti-OspA antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BURI/) BURIAN J.
(KUZY/) KUZYK M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                       AAB81127 standard; Protein; 161
                                                                                                                                                                Optimised OspA protein 17E2 amino acid sequence.
                                                                                                                                                                                                         11-JUL-2001
                                             synthetic.
                                                                piscirickettsia
                                                                                                                    Poikilothermic vaccine; OspA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-316844/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGNSYVDNTSKVTANEVKETASÞTSTYDTYLDÞSHMRGCLQGSSLITISVELVGCAQNES
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                                                                                                                      fish; piscirickettsia salmonis; rickettsial pathogen; salmonid rickettsial septicaemia; rickettsial disease
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Location/Qualifiers 109..128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                         256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1335; DB 22; pred. No. 1.5e-122; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                         disease.
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(BURI/)
(KUZY/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a method for the protection against infection of a polklichtermic fish by the bacterial pathogen, Piscirickettsia salmonis. The method comprises administering an immunogenic amount of a salmonis specific antigen termed OspA, or an immunogenic fragment of P. salmonis specific antigen termed OspA, or an immunogenic fragment of particularly poikliothermic fish, against the bacterial pathogen particularly poikliothermic fish, against the bacterial pathogen P. salmonis. The method is also useful for protecting against salmonid P. salmonis ospA protecting against salmonid sequence represents optimised P. salmonis OspA protein 17E2. The DNA sequence represents optimised P. salmonis OspA protein 17E2. The DNA sequence represents optimised P. salmonis OspA protein 17E2. The DNA sequence represents optimised P. salmonis OspA protein 18E2 (AAF86247) has been optimised for expression in Ecsherichia coli. An OspA protein with an N-terminal fusion partner is Ecsherichia coli. An OspA protein with an N-terminal fusion partner is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method for protecting poikilothermic fish against salmonid rickettsial septicaemia and other rickettsial diseases comprises administering a vaccine containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 5; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAF86247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                               Piscirickettsia salmonis polypeptide P10.6.
                                                                                                                                                                                    15-JAN-2002
                                                                                                                                                                                                                        AAG78025;
                                                                                                                                                                                                                                                        AAG78025 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
                                                                               septicaemia;
ATCC VR-1361.
                                                                                                                piscirickettsia
                                                                                                                                                                                                                                                                                                                                                                                 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 piscirickettsia
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                                                                                                                                                                                                                                                                                                                                           RROQYCREFQOKAMIAGOKQEIYGTACPOPDGRWQVISTEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                 LGGLIGSKIGQSMDQQDKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGLIGSKIGOSMDQODKIKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQE
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BURIAN J.
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milarity 100.0%;
Conservative 0
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                                                                                                     SRS;
                                                                                                 salmonis; piscirickettsiosis; salmonid rickettsial;
s; surface antigen; vaccine; antibacterial; fish;
                                                    salmonis.
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pred. No. 1.6e-73;
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Query Match Best Local S Matches

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01-JUL-2000;
01-JUL-2000;
29-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a least part of the surface antigen present on Piscirickettsia salmonis for production of a vaccine with antibacterial activity t protect fish against P. salmonis which causes piscirickettsiosis known as salmonid rickettsial septicaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Fig 5; 25pp; English.
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surface antigen present on
protect fish against pisch
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                                                                                                                   Key
Region
                                                                                                                                                                                                                                                                                                                                     OspA antigen
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                                                 CA2281913-A1
                                                                                                                                                                                                                                                                Poikilothermic vaccine; OspA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB81126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB81126 standard;
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    17-MAR-2001
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DB; AAH79040.
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2000GB-0016082.
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                                                                                                                                                                                                                                                                                                                                  amino acid sequence
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                                                                                                                                                                                                                                                                fish; Piscirickettsia salmonid rickettsial s
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                                                                                                                                                                                             salmonis
                                                                                                                      Location/Qualifiers 110..129
                                                                                                /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
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Pred. No. 7.6e-72;
1; Mismatches 1;
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                                                                                                                                                                                                                                                             a salmonis; rickettsial pathogen;
septicaemia; rickettsial disease;
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                                                                                                                                                                                   yarn; fiber; textile; biological crosslinker; mechanical property; Clostridium cellulovorans cellulose binding domain; wet strength; durability; elasticity; CBDclos; cellulose binding protein A; CBP
                           17-MAY-2001
                                                                         WO200134091-A2
                                                                                                                   Clostridium
                                                                                                                                                                                                                                                                Polysaccharide modification;
                                                                                                                                                                     CBD-180
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cellulovorans

polysaccharide binding

domain; PBD; paper;

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Query Match
Best Local (
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N-PSDB;
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vaccine cont
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(BURI/)
Clostridium cellulovorans cellulose binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody
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                                       24-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 158; Conser
                                                                                                                                                                                                                                                                                                                                               ω
                                                                                                                                                                                                                                                                    RGCLQGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL
                                                                                                                                                                                               RQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVISTEK 256
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)B; AAF86246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for protecting poikilothermic fish against salmonid rickettsial aemia and other rickettsial diseases comprises administering a e containing the OspA protein of Piscirickettsia salmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Fig 2B;
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                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AA;
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                                                                                                            Protein;
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Pred. No. 7.6e-72;
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   domain-180 (CBD-180).
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RESULT 6
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18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polysaccharide binding domain (pab) fusion protein. The method is used to alter the structural, chemical, physical, electrical and used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide meterials such as paper, yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD properties such as wet strengths, durability and elasticity. The PBD properties such as its forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker which eliminates the sizing step. The use of a biological crosslinker the fine fibers in a slurry therefore resulting in better recovery of the fibers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.
The method involves treating the polysaccharide structure with a
the method involves treating the polysaccharide structure with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is Clostridium cellulovorans cellulose binding domain (CBD)-180. CBD-180 contains 180 amino acids of C. cellulovora CBD (CBDclos) of cellulose binding protein A (CBP A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
          24-SEP-2001
                                           AAE05749;
                                                                          AAE05749 standard;
                                                                                                                                                                                                                                                        181
                                                                                                                                                         154
                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                2001-457121/49
                                                                                                                                                                                                                                                                                                                                                  LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNES 120
                                                                                                                                                         GTA-PGPD 160
                                                                                                                                                                                                                                                     EKYKAGQYTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY
                                                                                                                                                                                        GTACPQPD 246
                                                                                                                                                                                                                      ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP-
                                                                                                                                                                                                                                                                                                                 RQEVGAATGAVVGGVAGQLEGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nussinovitch A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-IL00708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0164140.
99US-0166389.
             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA,
                                                                             Protein; 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoseyov
                                                                                                                                                                                                                                                                                           FGFASGRATL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 487; DB 22;
Pred. No. 1.4e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                  KKGQFITIQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                   KVTGYIGGAK--VL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                     111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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The present invention relates to methods and compositions for cross-cc linking and/or modifying the properties of polysaccharide materials. CC The method involves treating the polysaccharide structure with a CC polysaccharide binding domain (PBD) fusion protein. The method is CC queed to alter the structural, chemical physical, electrical and CC mechanical properties of polysaccharide materials such as paper, CC yarns, fibers and textiles, using biological crosslinking agents. CC yarns, fibers and textiles, using biological crosslinking agents. CC properties such as wet strengths, durability and elasticity. The PBD creagent is applied in the forming stage in fluting paper manufacture cc reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker cc improves the recyclability of paper products. The pBD reagent maintains can fine fibers in a slurry therefore resulting in better recovery of the fine fibers in a slurry therefore resulting in better recovery of can materials. The pBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polysaccharide modification; polysaccharide binding domain; PBD; paper, fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CBD; chimeric protein; S peptide-cellulose binding domain-S protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimeric protein; S per
Spep-CBD-Sprot; bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric S peptide-cellulose binding domain-S protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200134091-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-2000; 2000WO-IL00708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-457121/49.
N-PSDB; AAD11046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CBDT-) CBD TECHNOLOGIES LTD.
(YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Fig 4b-4g; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Levy I,
                                              Note:
                                                                                                            The present sequ
                                                                                and bovine
                                                                                       The present sequence is (Spep-CBD-Sprot), a fusi
                                                 ID NO:
                                sequence has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nussinovitch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos
                                sequence is stated to be the same as that shown as 10 in the sequence listing of the specification. Hence has 2 additional residues at its C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp.
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99US-0166389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Encoded by TAG"
327..328
/note= "These residues are absent in the sequence as SEQ ID NO: 10 in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "This region is derived 226..326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 30..208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "This region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Unknown
                                                                                                e is S F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shoseyov 0;
                                                                                                       peptide-cellulose
n protein derived
                                                                                                     protein
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                                                                                                            from
                                                                                                                          binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from bovine"
                                                                                                        ding domain-S protein
Clostridium cellulovorans
                                                             However
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Query Match

36.5%;

Score 487;

DΒ

22;

Length 328;

Sequence

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; cellulose binding domain; CBD;
                                                                                                                                                                                                                                                                                                                                                                         08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE05747 standard; Protein; 341 AA.
                                                                                                                                                                                                                                                                                                        (CBDT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                      02-NOV-2000; 2000WO-IL00708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200134091-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE05747;
The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.
                                                                  Example 1.2;
                                                                                                             property
                                                                                                                             Preparation of a polysaccharide containing material having at least desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                    WPI; 2001-457121/49
                                                                                                                                                                                                                                                              Levy I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strength; durability; cross linker protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTA-PGPD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTACPQPD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGNSYVDNTSKVTANFVKETASPTSTYDTYVE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP-----KVTGYIGGAK--VL
                                                                                                                                                                                                                                                                                                      YISSUM RES DEV CO HEI
                                                                                                                                                                                                AAD11044.
                                                                                                                                                                                                                                                              Nussinovitch
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                                                                Fig 2b-2e; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                       99US-0164140.
99US-0166389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "This residue is absent
as SEQ ID NO: 6 in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-
                                                                                                                                                                                                                                                                                                        DEV CO HEBREW UNIV JERUSALEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Encoded by CCATAGGAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -FGFASGRATL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elasticity;
CCP.
                                                                                                                                                                                                                                                              Shoseyov 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.9e-39;
2; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KKGQFITIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the sequence
e listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
                                                                                                                                                     at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
AAR63634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
      Query Match
Best Local Sim
Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The method involves treating the polysaccharide structure with a polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide materials such as paper, yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains the fine fibers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is Clostridium cellulovorans cellulose binding domain (CBD) cross linker protein (CCP).

Note: This sequence is stated to be the same as that shown as SEQ ID NO: 6 in the sequence listing of the specification. However this sequence has an additional residue at its C-terminal.
                                                                                                                                                                                                                                                                                                                                                                     Cellulose binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR63634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR63634 standard; Protein; 162
      Doi RH,
                                                                                                                                                                                                                                          WO9424158-A.
                                                                                                                                                                                                                                                                                                                        Cellulose binding domain; CBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  penetrate paper.
                                            (REGC ) UNIV CALIFORNIA.
(YISS ) YISSUM RES & DEV CO
                                                                                                             14-APR-1993;
                                                                                                                                                     14-APR-1994;
                                                                                                                                                                                                27-OCT-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTA-PGPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACPQPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GRITKSDWSNYTQTNDYSFDASSSTPVVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKVKAGQVTR--WRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEIY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------FGFASGRATL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGNSYVDNTSKVTANFVKETASPTSTYDTYVE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
    Goldstein MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 AA;
                                                                                                                                                                                                                                                                                    cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                     94WO-US04132
                                                                                                           9305-0048164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.5%;
    Shoseyov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 487; DB 22;
Pred. No. 3.1e-39;
2; Mismatches 30;
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    Shpiegl I;
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92

-KVTGYIGGAK--VL

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Length Indels

90;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated cellulose binding domain and fusion proteins - with applications. including drug delivery, affinity separations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                   AAE05745 standard; Protein; 163
                                                                                                                                                                             Polysaccharide modification; polysaccharide binding domain; PBD; parn; fiber; textile; biological crosslinker; mechanical property; Clostridium cellulovorans cellulose binding domain; wet strength; durability; elasticity; CBDclos; cellulose binding protein A; CBP
                                                                                                                                                                                                                                                  Clostridium cellulovorans cellulose binding domain
                                                                                                                                                                                                                                                                                                        AAE05745;
                                                                                                                                                                                                                                                                               24-SEP-2001
                                                                                                                                                     Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                02-NOV-2000; 2000WO-IL00708
                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                         08-NOV-1999;
18-NOV-1999;
                                                                                                                         WO200134091-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 51.7 les 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1994-341767/42.
DB; AAQ72917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGNSYVDNTSKVTANEVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGNSYVDNTSKVTANFVKETASPTSTYDTYVE----
                                                                                                                                                                                                                                                                                                                                                                                                        ----GRITKSDWSNYTQTNDYSFD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 AA;
                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125pp; English.
                           99US-0164140.
99US-0166389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FGFASGRATL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.2%;
51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 483; DB 15;
Pred. No. 2.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KKGQFITIQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                              (CBDclos).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                   paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
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RESULT 10
AAE05748
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Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polysaccharide binding domain (pBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and mechanical properties of polysaccharide meterials such as paper, yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD properties such as wet strengths, durability and elasticity. The PBD properties such as wet strengths, durability and elasticity. The PBD properties such as the forming stage in fluting paper manufacture reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains improves the recyclability of paper products. The PBD reagent maintains raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Levy I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to methods and compositions for cross linking and/or modifying the properties of polysaccharide materials. The method involves treating the polysaccharide structure with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparation of a polysaccharide containing material having at least desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1.1; Page 111-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  penetrate paper.
                                                           Polysaccharide modification; polysaccharide binding domain; PBD; paper; yarn; fiber; textile; biological crosslinker; mechanical property; wet strength; durability; elasticity; protein A-cellulose binding domain;
                                                                                                                                                                                                                        AAE05748 standard; Protein;
                                                                                                                                                                                         AAE05748;
               Clostridium cellulovorans
                                               ProtA-CBD
                                                                                                                            Clostridium cellulovorans
                                                                                                                                                           24-SEP-2001
                                                                                                                                                                                                                                                                                                     118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGNSYVDNTSKVTANEVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVELVGCAQNES 120
                                                                                                                                                                                                                                                                                                                                                                                               RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                LGNSYVDNTSKVTANFVKETASPTSTYDTYVE-
                                                                                                                                                                                                                                                                                                                                  EKVKAGQVTR--WRNPDTGNSYSVE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  esent sequence is Clostridium cellulovorans cellulose binding (CBDclos) of cellulose binding protein A (CBP A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CBD TECHNOLOGIES LTD.
YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nussinovitch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                     -GRITKSDWSNYTQTNDYSFD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                      ----FGFASGRATL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.2%;
51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoseyov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121pp; English
                                                                                                                               protein A-cellulose binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 483; DB 22;
Pred. No. 2.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                             ---KKGQFITIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    least one
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                                                                                                                Matches
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                  mechanical properties of polysaccharide materials such as paper, yarns, fibers and textiles, using biological crosslinking agents. The polysaccharide containing materials have improved mechanical properties such as wet strengths, durability and elasticity. The PBD reagent is applied in the forming stage in fluting paper manufacture which eliminates the sizing step. The use of a biological crosslinker improves the recyclability of paper products. The PBD reagent maintains the filers in a slurry therefore resulting in better recovery of raw materials. The PBD molecules are eluted by strong alkaline conditions which enhances the ability of the alkaline glue used in binding to
                                                                                                                                                                                                  binding domain (ProtA-CBD). This sequence contains a part of CBP A protein and a part of protein A derived from pRTT2T vector sequence Note: This sequence is stated to be the same as that shown as SEQ ID NO: 8 in the sequence listing of the specification. However this sequence has 2 additional residues at its C-terminal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to methods and compositions for cross-
linking and/or modifying the properties of polysaccharide materials.
The method involves treating the polysaccharide structure with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Preparation of a polysaccharide containing material having at least one desired structural, chemical, physical, electrical and/or mechanical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                     polysaccharide binding domain (PBD) fusion protein. The method is used to alter the structural, chemical, physical, electrical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YISS) YISSUM RES DEV CO HE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                          The present sequence is Clostridium cellulovorans Protein A-cellulose
                                                                                                                                                                                                                                                                                           penetrate paper.
330
                                                        270
                           61
                                                     Local
            LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-457121/49
                                                                                                                106;
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nussinovitch
                                                                                                                                                                         428
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 3b-3g; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-IL00708
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99US-0166389.
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427..428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Protein_A
/note- "This region is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Unknown
/note= "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= CBP_A_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEV CO HEBREW UNIV JERUSALEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .426
                                                                                                                            36.2%;
51.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "These residues ID NO: 8 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shoseyov O;
                                                                                                                9
                                                                                                                           Score 483; DB 2
Pred. No. 1e-38;
                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are absent in the sequence sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     derived from pRIT2T vector"
                                                                                                                                          22;
                                                                                                               14;
                                                                                                                                          Length 428;
                                                                                                               Indels
                                                                                                               76;
                                                                                                                                                                                                                                             sequence
                                                                                                             Gaps
                                                      329
                                                                                  60
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RESULT 11
AAY39952
ID AAY39
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В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1998;
15-JUN-1998;
01-OCT-1998;
                                         bioluminescence-generating systems, assays, screening methods, diagnostic method and articles of manufacture. They can be expressed using e.g. bacterial, yeast, fungal, plant, insect or animal cells. The Renilla mulleri, Gaussia and Pleuromamma luciferase or Renilla or Ptilosarcus GrPs can be used in e.g. toys, cosmetics, fountains, personal care items, fairy dust, beverages, soft drinks, foods, textile products, bubble bath, balloons, personal items, dentrifrices, soaps, body paints, bubble bath, ink or paper products. In particular, they can be used in e.g. squirt guns, pellet guns, finger paints, foot bags, greeting cards, slimy play material, clothing, bubble making toys, bath powders, cosmetics, body lotions, gels, body powders, body creams, toothpastes, mouthwashes, soaps, body paints, bubble bath, inks, wrapping paper, gelatins, icings, icos, greeting cards, beer, wine, champagne, soft drinks, ice cubes, frostings, greeting cards, beer, wine, champagne, soft drinks, ice cubes, ice, dry ice or fountains. The nucleic acids can also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PROL-)
(BRYA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaussia luciferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY39952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY39952
                                                                                                                                                                                                                                                                                                                This sequence represents a luciferase of the invention. The invelates to Renilla mulleri, Gaussia and Pleuromamma luciferase
                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                New isolated Renilla mulleri, Gaussia and Pleuromamma luciferase and Renilla and Ptilosarcus green fluorescent protein nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-580443/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bioluminescence-generating system; toy; cosmetic; fairy dust; beverage;
body paint; squirt gun; balloon; slimy play material; soap; toothpaste;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Luciferase;
                               transgenic fish and
                                                                                                                                                                                                                                                                               Renilla and Ptilosarcus green fluorescent protein proteins. The luciferases and GFPs can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ27550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKVKAGQVTR - - WRNPDTGNSYSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROLUME
BRYAN B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        green
                                                                                                                                                                                                                                                                                                                                                                 Page 222-223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0079624.
98US-0089367.
98US-0102939.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fluorescent protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                             plants
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                                                                                                                                                                                                                                                                                                                                                                 233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFP; screening assay;
cosmetic; fairy dust;
                                                                                                                                                                                                                                                                                               protein (GFP) nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KKGQFITIQ--
                                                                                                                                                                                                                                                                                                                              The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis;
                                                                                                                                                                                                                                  The Renilla
                                                                                                                                                                                                                                                                diagnostic
                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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Query Match Best Local Similarity

36 62 . 68;

Score Pred.

480.5; DB :

20;

Length 382;

Sequence

382

AA;

33;

Indels

21;

Gaps

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RESULT 12
AAW90077
ID AAW90
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Matches
           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-1994;
14-APR-1993;
14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. cellulovorans CbpA CBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW90077 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cellulose binding domain; CBD; CbpA; fusion protein; diagimmunoassay; heat-shock protein; cross reactive protein; antigenic fragment; antibody; insulin-dependent diabetes cellulose; chitin; cellulolytic; amorphogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW90077;
                                                                                                                                                                                                                                                                                                                                                                                                             (REGC )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5856201-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                This sequence represents a cellulose binding domain (CBD) derived from the CbpA protein of Clostridium cellulovorans. The sequence is used the construction of a fusion protein which can be used in diagnostic immunoassays, e.g. to detect heat-shock proteins (HSP) and their cross-reactive proteins, antigenic fragments or HSP-specific antibodies (which indicate insulin-dependent diabetes mellitus, or susceptibility to it. The CBD, has very high affinity for cellulose (including to it. The CBD) and chitin (dissociation constant 0.8-1.4 mu M), but crystalline forms) and chitin (dissociation constant 0.8-1.4 mu M), but crystalline forms) and chitin (dissociation constant 0.8-1.4 mu M) but crystalline forms) and chitin (dissociation constant 0.8-1.4 mu M) but crystalline forms are cellulolytic or amorphogenic activities. The CBD binds over has almost no cellulolytic or amorphogenic activities by washing with water.
                                                                                                                                                                                                                                                                                Detection of a specific analyte by reaction with binding agent fused to cellulose binding domain - and subsequent treatment with cellulose and reaction of insoluble product with a label specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                           Claim 3;
                                                                                                                                                                                                                                                                      for the
                                                                                                                                                                                                                                                                                                                                                                                   Doi RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSVEFYNSNKSAQTNSTTPIIKTTNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFSRQ-----EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGA-VLGGLIGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NYTQTNDYSFDASSSTPVVNPKVTGY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107;
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YISSUM RES & DEV
                                                                                                                                                                                                                                                                      analyte
                                                                                                                                                                                                                                                                                                                                           AAV74072
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Goldstein MA,
                                                                                                                                                                                                                                           Fig 1A-B; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                          162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
 Conservative
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93US-0048164.
94WO-US04132.
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A
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                 35.7%;
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 ; Score 477; DB 20; pred. No. 1e-38; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion protein; diagnosis; HSP;
                                                                                                                                                                                                                                                                                                                                                                                        Shpiegl
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                                   20;
          0
                                  Length 162;
          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection;
mellitus;
          0;
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           Gaps
             0
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9

Вþ Q

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SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL 61

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RESULT 13
AAW90081
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        Query Match
Best Local :
Matches
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14-APR-1993;
14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW90081 standard; Protein; 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cellulose binding domain; CBD; CbpA; fusion protein; diagnosis; HSP immunoassay; heat-shock protein; cross reactive protein; detection; antigenic fragment; antibody; insulin-dependent diabetes mellitus; cellulose; chitin; cellulolytic; amorphogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. cellulovorans CBD-KpnI fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW90081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clostridium
                                                                 This sequence represents a fusion protein (CBD-KpnI) composed of the Cb protein cellulose binding domain (CBD) from Clostridium cellulovorans This protein is used in diagnostic immunoassays, e.g. to detect heat-shock proteins (HSP) and their cross-reactive proteins, antigenic fragments or HSP-specific antibodies (which indicate insulin-dependent diabetes mellitus, or susceptibility to it. The CBD has very high affinity for cellulose (including crystalline forms) and chitin (dissociation constant 0.8-1.4 mu M), but has almost no cellulolytic or amorphogenic activities. The CBD binds over a wide pH range and is not released from cellulose by washing with water.
                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5856201-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                   Detection of a specific analyte by reaction with binding agent fused to cellulose binding domain - and subsequent treatment with cellulose and reaction of insoluble product with a label specific
                                                                                                                                                                                                                                                                                                                                   (REGC )
                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-1994;
                                                                                                                                                                                                  Claim 5; Column 55-56; 63pp; English.
                                                                                                                                                                                                                                                                                     WPI; 1999-105130/09
                                                                                                                                                                                                                                                                                                            Doi RH,
                                                                                                                                                                                                                            for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
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                                            Sequence
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                                                                                                                                                                                                                                                                                                                                    UNIV CALIFORNIA.
YISSUM RES & DEV
Similarity 97.0
89; Conservative
                                                                                                                                                                                                                                                                                                            Goldstein MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cellulovorans
                                                154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                       94US-0330394.
93US-0048164.
94WO-US04132.
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                                                AA;
                                                                                                                                                                                                                                                                                                                                      & DEV
            35.4%;
                                                                                                                                                                                                                                                                                                               Shoseyov 0,
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 Pred. No. 3e-3
2; Mismatches
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               472; DB 2
No. 3e-38;
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                                                                                                               Matches
                                                                                                                                                                                                This sequence represents a fusion protein composed of the CbpA protein cellulose binding domain (CBD) from Clostridium cellulovorans and a heat shock protein (HSP) fragment. This protein is used in diagnostic immunoassays, e.g. to detect heat-shock proteins (HSP) and their cross-reactive proteins, antigenic fragments or HSP-specific antibodies (which indicate insulin-dependent diabetes mellitus, or susceptibility to it. The CBD has very high affinity for cellulose (including crystalline forms) and chitin (dissociation constant 0.8-1.4 mu M), but has almost no cellulolytic or amorphogenic activities. The CBD binds over
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-OCT-1994;
14-APR-1993;
14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigenic :
cellulose;
                                                                                                                                                                                                                                                                                                                                                                Detection of a specific analyte by reaction with binding agent fused to cellulose binding domain - and subsequent treatment with cellulose and reaction of insoluble product with a label specific
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulose binding
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                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                             Claim 4; Column 51-52; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellulose binding domain; CBD; CbpA; fusion protein; diagnosis; HSP; Immunoassay; heat-shock protein; cross reactive protein; detection; antigenic fragment; antibody; insulin-dependent diabetes mellitus; cellulose; chitin; cellulolytic; amorphogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW90080 standard; Protein;
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                                                                          SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL 61
                          GNSYVDNTSKVTANFVKETASPTSTYDTYLD 92
             GNSYVDNTSKYTANFYKETASPTSTYDTYVE
                                                             SVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGALL
                                                                                                               . Similarity
89; Conserv
                                                                                                                                                                                                                                                                                                                                                      analyte
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                                                                                                               Conservative
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93US-0048164.
94WO-US04132.
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                                                                                                                                                                                       is
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                                                                                                                                                                                       not released from cellulose by washing with water
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                                                                                                              Score 472; DE Pred. No. 3e-3
2; Mismatches
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AAR95080
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                                                                                                                                                        Query Match
Best Local S
Matches 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellulose binding domain, CBD; hapten; molety; biotin; avidin; streptavidin; affinity chromatography; cell separation; cell immobilisation; protein immobilisation; enzyme immobilisation; multienzyme reactors; signal immunoassays; drug delivery; pesticide
                                                                                                                                                                                                                                                                                                                                                  Modified cellulose-binding partic. biotin, to provide assays, reactors, delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium thermocellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cellulose binding
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                                                                                                                                                                                                                                                                                                                                                                                                                              Bayer EA, Lamed R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellulose; chitin.
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                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TECR ) TECHNION RES & DEV FOUND LTD.
(UYRA-) UNIV RAMOT APPLIED RES & IND DEV
(YEDA ) YEDA RES & DEV CO LTD.
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                        61
 83
                                                   9
                                                                           ب
                                                                                                                                                                                cellulose, or chitin.
             LGN--SYVDNTSKYTANFYKETASPTSTYDTYLDPSHMRGCLQ
                                                                           MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
IGSNGSYNGITSNVKGTFVKMSSS-TNNADTYLEISFTGGTLE
                                                 LKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHA-AI 67
                                                                                                                                                                                                                                                                                                                        12; Page 34-35; 53pp; English
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                        .167
                                                                                                     Conservative
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                                                                                                   Score 245; DB 1
Pred. No. 6e-16;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
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1: Sp_archea:*
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3: Sp_fung1:*
4: Sp_human:*
5: Sp_inverteb:
6: Sp_manmal:*
7: Sp_mhc:*
8: Sp_organel1:
9: Sp_phage:*
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Gapop 10.0 , Gapext 0.5
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                     Q9f9k8 pisciricket
Q9f9k8 rickettsia
Q9f9f2 rickettsia
Q9f9f2 rickettsia
Q9f276 male-killin
Q9k2n6 male-killin
Q9k4w8 male-killin
Q45996 clostridium
Q53154 rickettsia
Q9f9q9 rickettsia
Q9f9q1 rickettsia
Q9f9q1 rickettsia
Q9f9q2 rickettsia
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Q9f9q1 rickettsia
Q9f9q1 rickettsia
Q9f9q1 rickettsia
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155	2316	154	499	499	501	136	508	499	257	182	170	930	199	921	77	1711	1000	996	1751	1426	261	1770	1779	997	321	887	1915
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Q9f6bl edwardsiell Q9rb08 pectobacter	Q9fdj9 bacteroides			bacillus s	083012 bacillus sp	Q92r89 rhizobium m	Q931d0 bacillus su	Q93tj6 bacillus su	Q9a8m8 caulobacter	Q9hxi3 pseudomonas	Q9rfx6 caldibacill	Ω	Q985g4 rhizobium l	a	Q9agc7 rickettsia	P96311 anaerocellu	024820 thermophili	. Q9aqh0 caldicellul	caldicel	icel	caldicel	caldicel	O52374 caldicellul	Q9z4il bacillus sp	6392 clostrid	Q913j8 clostridium	Q9rpl0 acetivibrio

 $\begin{array}{c} 117 \\ 127 \\ 147 \\$

ALIGNMENTS

Q9F9Y88 PRELIMINARY; PRT; 162 AA. Q9F9Y8B; Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) 17 KDA ANTIGEN. QSPA. Piscirickettsia salmonis. Bacteria; proteobacteria; gamma subdivision; Piscirickettsia group; Piscirickettsia. RCBI_TaxID-1238; [1] SEQUENCE FROM N.A. STRAIN-LF-89; "Identification of a genus common Rickettsia! surface antigen in the salmonid pathogen Piscirickettsia salmonis."; SEQUENCE [62P-199] to the EMBL/GenBank/DDBJ databases. EMBL; AF184152; AAG17000.1; SEQUENCE 162 AA; 17661 MW; DDE99E6FD94A527E CRC64; Best Local Similarity 98.8%; Pred. No. 3.6e-59; Matches 158; Conservative 1; Mismatches 1; Indels 9; RGCLOGSSLIIISVFLVGCAQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVL 156 11

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01-JUN-1998 (TrEMBLrel. 06, Lasts
01-WV-1998 (TrEMBLrel. 08, Lasts
17 KDA COMMON-ANTIGEN (FRAGMENT).
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NCBI_TaxID=789;
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OSFSF2

OPFSF2

O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
17 KDA GENUS-COMMON ANTIGEN.
Rickettsia felis (Rickettsia azadi).
Rickettsia felis (Rickettsia azadi):
Rickettsiaceae; Rickettsiaee; Rickettsia.
Rickettsiaceae; Rickettsiaee; Rickettsia.
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                                                                                                                                                                                                                                                                          spotted fever group.";
Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
EMBL; AF195118; AAG28452.1;
- CROUENCE 159 AA; 16497 MW; 34C5B020AF470A1F
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SEQUENCE FROM N.A.

MEDLINE=21217364; PubMed=11321078;

Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,

Bouyer D.H., Stenos J., Foil L.D., Stothard D.R., Azad A.F.,

Zavala-Velazquez J.E., Foil L.D., Stothard D.R., Azad A.F.,
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SKIMIIALAASMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL 63
                                                                  SSLIIISV---FLVGC--AQNESRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
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Pred. No. 1.1e-1
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"Molecular characterization of a novel spotted fever graph species from Ixodes scapularis in Texas";
submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF031534; AAB95267.1; ...
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M. Schulenburg H.J.G.V.D., Majerus M.E.N.; Bertrand D., Hurst G.D.D., Majerus M.E.N.; Bertrand D., Hurst G.D.D., Majerus M.E.N.; Ton the evolution of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Rickettsia (a-Proteobacteria) from transfer of male-killing Ricke
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Best Local S
Matches 52
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Best Local :
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Q9K4W8;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stenos J., Roux V., Walker D., Raoult D.;
"Rickettsia honei sp. nov., the aetiological
spotted fever in Australia.";
Int. J. Syst. Bacteriol. 48:1399-1404(1998).
EMBL; AF027124; AAB81846.1;
EMBL; AF060706; AAD20231.1;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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52; Conserv
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52; Conservative
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the EMBL/GenBank/DDBJ databases
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Pred. No. 3.1e
24; Mismatches
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Pred. No. 3.5e
24; Mismatches
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Best Local :
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01-MAR-2001
01-JUN-2001
SCAFFOLDING
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MEDLINE-20575219; PubMed-11133455;
MEDLINE-20575219; PubMed-11133455;
Schulenburg H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
Bertrand D., Hurst G.D.D., Majerus M.E.N.;
"Incidence of male-killing Rickettsia spp. (alpha-Proteobacteria)
"Incidence of male-killing Rickettsia decempunctata L. (Coleoptera:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; A.
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male-killing Rickettsia from Adalia decempunctata
Bacteria: Proteobacteria; alpha subdivision; Ricket
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=120393;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 35319;
MEDLINE-96218696; PubMed-8636029;
Pages S., Belaich A., Tardif C.,
                                                                                   "Sequence analysis of scaffolding protein CipC and ORFXp, a new cohesin-containing protein in Clostridium cellulolyticum: compariso of various cohesin domains and subcellular localization of ORFXp."; J. Bacteriol. 181:1801-1810(1999).
                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=ATCC 35319; MEDLINE=99173902; I
                                                                                                                                                                                                                                                         Pages S., Belaich A., Tardif C., Reverbel-Leroy C., Gaudin C. Belaich J.P.;
"Interaction between the endoglucanase CelA and the scaffoldi protein CipC of the Clostridium cellulolyticum cellulosome.";
J. Bacteriol. 178:2279-2286(1996).
Reverbel-Leroy C., Belaich J.;
                                SEQUENCE FROM N.A. STRAIN-ATCC 35319;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Clostridium.
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                                                                                                                                                         Belaich J.P.;
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nes 52; Conserv
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PROTEIN PRECURSOR.
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A., Fierobe H.P.,
                  Tardif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular study and overexpression of the Clostridium cellulolyticum celCCF cellulase gene in Escherichia coli."; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases. [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-2000) to the EMBL/GenBank/DDBJ EMBL; U40345; AAC28899.2; -. HSSP; Q06851; INBC.
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Belaich J.P.;
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InterPro; IPR002102; Cohes
InterPro; IPR003880; Phosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00942; CBD_3; 1.
Pfam; PF00963; Cohesin; 8.
ProDom; PD001947; CBD_3; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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                                                                                                                                                                                              group rickettsiae.";
J. Clin. Microbiol. 30:2896-2902(1992)
EMBL; M99391; AAA73386.1; -.
                                                                                                                                                                                                                                                              Baird R.W., Lloyd M., Stenos J., "Characterization and comparison
                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            Rickettsia sp.
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SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
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                                                                   55;
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1546 AA;
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, Last annotation updat
CDS (FRAGMENT).
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                                                                     31;
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Pred. No. 1
                                                                Score 244; DB 2;
Pred. No. 1.7e-12;
1; Mismatches 54
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                                                                                                                                                        F5C35855EDB439D2 CRC64;
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of Australian human
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1999) to the EMBL/GenBank/DDBJ EMBL; AF181036; AAG09427.1; NON_TER 151 151
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Nilsson K., Pahlson C.;
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                                                                                                                                                                                                     Q9F0Q1;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Novel peptide diagnostic reagent and kit for
                                                   Raoult D.;
Raoult D.;
"A new SFG rickettsia isolated from fleas.";
"A new SFG rickettsia isolated from fleas.";
"A new SFG rickettsia isolated from fleas.";
                                                                                                                         Bacteria; Proteobacteria; Rickettsiaceae; Rickettsic NCBI_TaxID=147259;
                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16
01-MAR-2001 (TrEMBLrel. 16
01-KDA PROTEIN (FRAGMENT).
Rickettsia sp. California
                                                                                                                                                                                                                             Q9F0Q1
  Submitted
         SEQUENCE FROM N.A. STRAIN=CALIFORNIA 2; Roux V., Raoult D.;
                                                                                        STRAIN-CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
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                                                                                                     SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                           SKIMITALAASMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
Raoult D.;
1 (DEC-1999)
                                  FROM N.A.
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(TremBLrel. 16, Last seq
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O9L522 PRELIMINARY; PRT; 131 AA.
09L522; O1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
17 KDA SURFACE ANTIGEN (FRAGMENT).
Rickettsia peacockii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             beetle (Adalia bipunctata).";
J. Bacteriol. 176:388-394(1994).
EMBL; U04162; AAA19235.1; -.
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NCBI_TaxID=789;
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Pred. No. 5.6e
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Pred. No. 5.6e-12;
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                                Query Match
Best Local S
Matches 66
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01-JUN-2001
SCAFFOLDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21091941; PubMed-11157215; Simser J.A., Palmer A.T., Munderloh U.G., Kurtti T.J.; Simser J.A. a spotted fever group rickettsia, Rickettsia in a Rocky Mountain wood tick. Dermacentor andersoni, cell appl. Environ. Microbiol. 67:546-552(2001).
EMBL; AF260571; AAF69012.1; -.
                                                                                                                                                                                              Kakiuchi M., Isui A., Suzuki K., Fujino T., Fujino E., Kimura T. Karita S., Sakka K., Ohmiya K.;
"Cloning and DNA sequencing of the genes encoding Clostridium j scaffolding protein CipA and cellulase CelD and identification their gene products as major components of the cellulosome.";
J. Bacteriol. 180:4303-4308(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia. NCBI_TaxID=47589;
                                                                              Prodom; PD001947; CBD_3; 1.

PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_5.

SEQUENCE 1162 AA; 120229 MW; 95F02DDD27ADFBA2
                                                                                                                                                                                                                                                                         MEDLINE=98361925; PubMed=9696784;
                                                                                                                                                                                                                                                                                                                         Clostridium
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Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                      082830;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                Pfam; PF00942; CBD_3; 1. Pfam; PF00963; Cohesin; 6.
                                                                                                                                                                                       EMBL; AB004845; BAA32429.1;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                     InterPro; IPR001956; CBD_3.
InterPro; IPR002102; Cohesin
InterPro; IPR00380; Phosphop
                                                                                                                                                                          HSSP; Q06851; 1NBC
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 KLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK
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1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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                                . Similarity 66; Conserv
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131 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
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                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
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                                         17.5%;
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38.3%;
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                                                                                                                                                                                                                                                                                                                                                                                 Last sequence up
                                Score 233.5; DB 2;
Pred. No. 1.6e-10;
1; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 6.7e-12;
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                                                                               CRC64;
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                                 Indels
                                                      Length
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33 ISVQFNNGSSPTSSSSIYARFKVTNTSGSPINLADLKLRYYFTQDENKQMTFWCDHAGYL

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RESULT 15
Q977Y4
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RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

RA McElling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

RA Noelling J., Breton G., Omelchenko M.V., Molf Y.I.,

RA Glbson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Tatusov R.L., Sobathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

RA Bennett G.N., Koonin E.V., Smith D.R.;

RA Bennett G.N., Koonin E.V., Smith D.R.;

ROBERT G.N., Koonin E.V., Smith D.R.;

RT Genome sequence and comparative analysis of the solvent-producing

RT Genome sequence and comparative analysis of the solvent-producing

RT bacterium Clostridium acetobutylicum.";

RT bacterium Clostridium acetobutylicum.";

RM B. AB007606; AAK78886.1;

DR RMBL; AB007606; CABD_3;

DR InterPro; IPR002102; Cohesin.

DR Pfam; PF00963; Cohesin; 5.

DR Pfam; PF00963; Cohesin; 5.

DR Probom; PD001147; CBD_3; 1.
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Search completed: October 27, 2002, 10:59:56 Job time: 31.7392 secs
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Q977Y4;
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01-OCT-2001 (TremBLrel. 18, Last sequence update)
01-DCC-2001 (TremBLrel. 19, Last annotation update)
01-DEC-2001 (TremBLrel. 19, Last annotation update)
PROBABLY CELLUICOSOMAL SCAFFOLDING PROTEIN, SECRETED,
CELLUICOSE-BINDING AND COHESIN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
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Result
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Maximum Match 100%
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     Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1335
1 MSVEFYNSNKSAQT
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Gapop 10.0 ,
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                                                       \tt MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL
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Conservative

36.5%;

; Score 487; DB 1; I; Pred. No. 6.4e-32; 12; Mismatches 30;

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17 kDa surface antigen precursor.
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STRAIN-MADRID E;
MEDLINE-89359171; PubMed-2768201;
Anderson B.E., Tzianabos T.;
Anderson B.E. aparative sequence analysis of
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J. Ba
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Nature 396:133-140(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                            SEQUENCE
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                                                                                                                                                         PIR; D33971;
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 103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
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159 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q52764;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsiaceae; Rickettsieae; NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95229950; PubMed=7714214;
Furnya Y., Katayama T., Yoshida Y., Kaiho I.;
"Specific amplification of Rickettsia japonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsia japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specimens by PCR.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                           Outer membrane;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                          EMBL; D16515; BAA03965
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                  103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL
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                                                                                                                                                             SKIMILALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGTGQL-VGVGVGALL
                                                                                                                GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
                                                                                                                                     GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN
                                                                  - RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN
                                                                                         KOERROOYCREFQOKAMIAGQKQEIYGTACPQPDGRWQVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surface antigen precursor
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                     pS00013; PROKAR_LIPOPROTEIN; 1.

mbrane; Lipoprotein; Antigen; Signal.

1 19 BY SIMILARITY.
20 159 17 KDA SURFACE ANTIGEN.
20 20 N-ACYL DIGLYCERIDE (PROC
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(Rel.
(Rel.
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             STANDARD;
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35, Last sequence up
35, Last annotation
                                                                                                                                                                                                                                                            16554 MW;
                                                                                                                                                                                                                        21.4%; Score 286; 37.9%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha subdivision;
eae; Rickettsia.
                                                                                                                                                                                                                32;
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                                                                                                                                                                                                                Pred. No. 1.16
2; Mismatches
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                PRT;
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1 CRC64;
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                                                                                                                                                  212
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17 kDa surface antigen precursor.
OMP OR RC1287.
Rickettsia conorii, and
Rickettsia rickettsii.
Bacteria; Proteobacteria; alpha sul
Rickettsiaceae; Rickettsleae; Ricketts
                                                                                                                                                                    EMBL: M28479; AAA26379.1; -.
EMBL: M28480; AAA26376.1; -.
EMBL: AE008675; AAL03825.1; -.
EMBL: M16486; AAA26381.1; -.
EMBL: J03371; -; NOT_ANNOTATED
PIR: A25972; A25972.
PIR: A31836; A31836.
PIR: A33971; B33971.
PRE: B33971; B33971.
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01-AUG-1990
01-MAR-2002
17 kDa surfac
CONFLICT
CONFLICT
SEQUENCE
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SPECIES-R.CONORIL; STRAIN-Malish 7
SPECIES-R.CONORIL; STRAIN-Malish 7
MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiff
Samson D., Roux V., Cossart P., We
                                                               CHAIN
LIPID
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a C between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modification.";
J. Bacteriol. 170:4493-4500(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson B.E., Baumstark B.R., Bellini W.J.; "Expression of the gene encoding the 17-kilodalton Rickettsia rickettsii: transcription and posttrans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-R.ricketts11;
MEDLINE=89008059; PubMed=3139629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-R.rickettsil;
MEDLINE-87222152; Pubmed-3108232;
Anderson B.E., Regnery R.L., Carlone G.M.,
Fu Z.Y., Bellini W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-30 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the 17-kilodalton-antigen rickettsii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                             Outer membrane;
                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mechanisms of evolution in Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 171:5199-5201(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid anchor (Probable).
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(Rel. 15,
(Rel. 41,
  ξ
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                                                                                                                             PROKAR_LIPOPROTEIN;
ipoprotein; Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Renesto-Audiffren P., Fournier P.-E., Cossart P., Weissenbach J., Claverie
  16581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
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eae; Rickettsia.
                  17 KDA SURFACE ANTIGEN.
N-ACYL IN REF. 3).
G -> E (IN REF. 3).
  206A2BBF74FCE169 CRC64;
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                                                                                                                        1.
Signal;
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Best Local Similarity
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01-OCT-1996 (Rel. 1
01-OCT-1996 (Rel. 3
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or send a
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                             gene.";
J. Bacteriol. 171:5199-5201(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=89359171; PubMed=2768201;
Anderson B.E., Tzianabos T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
NCBI_TaxID=785;
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01-AUG-1991
                                                                                                                                                                                                                                          Outer membrane; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rickettsia typhi
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparative
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QTTYGNACRQPDGQWQVVN
                     QEIYGTACPOPDGRWQVIS
                                              TSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY - -
                                                                     KLNOSLEKVKAGOVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQK
                                                                                            NKQGTGTLLGGAGGALLGSQFGHGKGQL-VGVGVGALLGAVLGGQIGASLDEQDRKLLEL
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                                                                                                                                                                                                                                                                              M28481; AAA26377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface antigen precursor
                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                       971; C33971
PS00013; P
                                                                                                                                                                                             159 AA;
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                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19, Created)19, Last sequence update)34, Last annotation updat
                                                                                                                                                                                                                                                      PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                   159
                                                                                                                                                                                           20 N-ACYL DIGLYCERIDE (PROBABLE) 16549 MW; 08973E2648FD8CD8 CRC64;
                                                                                                                                                        20.7%;
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                      253
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                                                                                                                                            27;
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Pred. No. 1.3e-16;
1; Mismatches 53
                                                                                                                                                       Score 276.5; DB 1
Pred. No. 6.3e-16;
                                                                                                                                                                                                                                          OPROTEIN; 1.
Antigen; Signal.
                                                                                                                                                                                                                  17 KDA SURFACE ANTIGEN
                                                                                                                                            Mismatches
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RESULT 6
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
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Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=787;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsia australis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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D1-OCT-1996 (Rel. 34, Last sequence update)

O1-OCT-1996 (Rel. 34, Last annotation updat

O1-OCT-1996 (Rel. 34, Last annotation updat

17 kDa surface antigen precursor (Fragment)
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                                                SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=35792;
                                                                                                                          Bacteria; Proteobacteria; alp
Rickettsiaceae; Rickettsieae;
                                                                                                                                                                                Rickettsia parkeri
                                                                                                                                                                                                                                                                                                                                                             17KD_RICPA
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        Pretzman
                             STRAIN-MACULATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKIMITALAASMLQACNSPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTYRNSN
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        C.I.,
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154
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19
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
          Stothard
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154
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eae; Rickettsia.
          D.R.,
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                                                                                                                                          alpha subdivision;
eae; Rickettsia.
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BY SIMILARITY.
17 KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                     PRT;
             Ralph
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          D.,
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                     Clark J.B.,
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                                                                                                                                                                        Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
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                     Fuerst
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17KD_RICRH
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Best Local S
Matches 57
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p50931;

01-0CT-1996 (Rel. 34, Last sequence update)

01-0CT-1996 (Rel. 34, Last annotation updatu)

17 kDa surface antigen precursor (Fragment)
                                Outer membrane;
SIGNAL 1
CHAIN 20
                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.; submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a li
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=33992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia rhipicephali.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                   PROSITE;
                                                                                                                      EMBL; Ul1020; AAB07706.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSLIIISV---FLVGC--AQNESRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                                                                                                                                                                        anchor (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KOERROQYCREFOOKAMIAGOKOEIYGTACPOPDGR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKIMVIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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Antigen; Signal.
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BY KDA SURFACE ANTIGEN.
N-ACYL DIGLYCERIDE (PROBABLE).
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Pred. No. 1.7e-14;
                       POPPOTEIN; 1.

Antigen; Signal.

BY SIMILARITY.

17 KDA SURFACE ANTIGEN.

N-ACYL DIGLYCERIDE (PROF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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SUBCELLULAR LOCATION: Attached to the outer membrane by a li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anchor (Probable).
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                                                      KOERROQYCREFOOKAMIAGOKQEIYGTACPOPDGR 248
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Clostridium thermore
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01-OCT-1994 (Rel. 30, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Cellulosomal scaffolding protein B (Cellulosomal glycoprotein
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Outer membrane; Lipoprotein; Antigen; Signal.
SIGNAL 1 19 BY SIMILARTY.
CHAIN 20 >154 17 KDA SURFACE ANTIGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stothard D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretz Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane
                                                                        Bacteria; F
Clostridium
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                  SEQUENCE FROM
                                                      NCBI_TaxID=1515;
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                                                                                                                                                                                                                                                                                                                                                                      -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQ
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                                                                                                               thermocellum
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Pred. No. 3.
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Best Local S
Matches 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poole D.M., Morag E., Lamed Gilbert H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEMS Microbiol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; pr00942; CBD_3; 1.
pfam; pr00963; Cohesin;
pfam; pr00404; Dockerin_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00404; Dockerin_1; 2.
ProDom; PD001947; CBD_3; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_1
PROSITE; PS000448; CLOS_CELLULOSOME_R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; x68233; CAA48312.1; -. HSSP; Q06851; 1NBC.
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InterPro; IPR002048; EF-hand.
                                                                                          Q06851;
01-JUN-1994 (
01-NOV-1997 (
01-MAR-2002 (
Cellulosomal
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PRESENT IN CATALYTIC SUBMITS OF THE CELLULOSOME.

SUBCELLULAR LOCATION: CELL SURFACE.

SUBCELLULAR LOCATION: CELL SURFACE.

SIMILARITY: A 24 RESIDUES DOMAIN IS REPEATED TWICE IN THIS ENZYME.
      Clostridium
                                                                                                                                                                                                                                                        CIPA_CLOTM
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(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
1 scaffolding protein A precursor (Cellulosomal n S1/SL) (Cellulose integrating protein A) (Coh
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Pred. No. 1.
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2 X 24 AA APP
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PRO/THR-RICH.
CELLULOSE-BINDING
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InterPro;

; IANU; 23-JUL-97.
;; IAOH; 08-JUL-98.
;; IAOH; 26-SEP-97.
;erPro; IPR001956; CBD_3.
;erPro; IPR002102; Cohesin.
;erPro; IPR002105; Dockerin_

InterPro; [nterPro;

IPR002048;

Dockerin_1. EF-hand.

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J. MOI. BIOL. 273:701-713(1997).

LJ. MOI. BIOL. 273:701-713(1997).

C --- FUNCTION: ACTS AS A SCAFFOLDING PROTEIN IN THE CELLULOSOME.

C --- FUNCTION: ACTS AS A SCAFFOLDING PROTEIN OF THE PROMOTES BINDING OF CELLULOSE TO THE CATALYTIC DOMAINS OF THE PROMOTES BINDING. CELL SURFACE.

C --- SUBCELLULAR LOCATION: CELL SURFACE.

C --- DOMAIN: CONTAINS 9 COPIES OF A DOMAIN (COHESIN) OF ABOUT 15(

C --- DOMAIN: CONTAINS 9 COPIES OF A DOMAIN GOAIN BY THE CATAL RESIDUES THAT BINDS TO THE DOCKERIN DOMAIN BORN BY THE CATAL RESIDUES THAT BINDING LICAND FOR THE ENZYMES. THIS DC COMPONENTS OF THE CELLULOSOME ENZYMES. THIS DC C WELL AS IN OTHER C. THERMOCELLUM CELLULOSOME ENZYMES. THIS DC C MAY FUNCTION AS THE BINDING LICAND FOR THE SL COMPONENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujino T., Beguin P., Aubert J.-P.; roganization of a Clostridium thermocellum gene cluster encoding the "Organization of a Clostridium thermocellum gene cluster encoding cellulosomal scaffolding protein CipA and a protein possibly involved in attachment of the cellulosome to the cell surface."; In attachment of the cellulosome to the cell surface."; J. Bacteriol. 175:1891-1899(1993).
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"Sequencing of a Clostridium thermocellum gene (ci
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MEDLINE-97076134; PubMed-8918451;
Tormo J., Lamed R., Chirino A.J., Morag E., Bayes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A cohesin domain from Clostridium thermocellum: structure provides new insights into cellulosome structure 5:381-390(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frolow F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Crystal structure of a bacterial family-III cellulose-binding domain: a general mechanism for attachment to cellulose."; EMBO J. 15:5739-5751(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tavares G.A., Beguin P., Alzari P.M.; "The crystal structure of a type I cohesin domain at 1.7-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98022914; PubMed=9402065
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                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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L; X67506; CAA478
; S36859; S36859.
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CAA47840.1; -.
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Q1-FEB-1995
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SEQUENCE
                                                                "Gene bequence ....;
Clostridium thermocellum.";
J. Gen. Microbiol. 139:307-316(1993).
I Gen. Microbiol. 139:307-316(1993).
I FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF LICHENIN AND CEREAL
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Pfam; PF00963; Cohesin; 9.
Pfam; PF00404; Dockerin_1; 2.
PF0507B; P500018; EF_HAND; UNKNOWN_1.
PROSITE; PS000448; CLOS_CELLULOSOME_RPT; 2.
PROSITE; PS00448; CLOS_CELLULOSOME_RPT; 2.
                                                                                                                      STRAIN-NCIB 10682;
MEDLINE-93171873; PubMed-8436949;
Hazlewood G.P., Davidson K., Laur
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01-FEB-1995 (Rel. 31, Last
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                                                 GLUCOSIDIC LINKAGES IN CELLULOSE, LICHENIN AND CEREAL BETA-GLUCANS. PRINCIPALLY ACTIVE AGAINST BARLEY BETA-GLUCAN. CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                  PATHWAY: CELLULOSE DEC
                 HYDROLASES).
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SWISS-PROT entry
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Pred. No. 4.1e-12
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Pfam; PF00942; CBD_3; 2.
Pram; PF00759; Glyco_hydro_9; 1.
ProDom; PD001947; CBD_3; 1.
PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9_2; 1.
Cellulose degradation; Hydrolase; Glycosidase;
Jauris S., Ruecknagel K.P., Schwarz W.H., Kratzsch P., Bronnenmeier K., Staudenbauer W.L.;
"Sequence analysis of the Clostridium stercorarium cell a thermoactive cellulase (Avicelase I): identification and cellulose-binding domains.";
Mol. Genet. 233:258-267(1990).
-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-gl
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                                                                                               SEQUENCE FROM N.A.,
STRAIN*NCIB 11745;
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Clostridium
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15-JUL-1998
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entities requires a license agreement (See http://www.isb
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HSSP; P26221; 1TF4.
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                                                                                  MEDLINE=91066838; PubMed=2250652;
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PIR; S12021; S12021
HSSP; P26221; 1TF4
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Probom: PB001947; CBD_3; 1
PROSITE: PS00592; GLYCOSYL_HYDROL_F9_1; 1
PROSITE: PS00698; GLYCOSYL_HYDROL_F9_2; 1
PROSITE: PS00698; GLYCOSYL_HYDROL_F9_2; 1
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InterPro; IPR001701; Glyco_hydro_9.
InterPro; IPR001701; Glyco_hydro_9.
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Pfam; PF00759; Glyco_hydro_9; 1.
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation (Exocellobiohydrolase Exoglucanase II precursor (EC 3.2.1.91) (Exocellobiohydrolase Exoglucanase II) recursor (FC 3.2.1.91)
                                                                                                                                                                                                                               CLOSR
                       SEQUENCE FROM N.A.
STRAIN=NCIB 11754;
Bronnenmeier K., Kundt K.,
                                                                                                                                                                                                                                                                                                                                                                                 : :: :| | | :|| | ::||| :: |:|||:||||| | : | | |||| :: | 898
                                                                                                   Bacteria;
Submitted
         Staudenbauer W.L.
                                                                                                                                                                                                                                                                                944
                                                                        NCBI_TaxID=1510;
                                                                                                                                                                                                                                                                                                                                                       61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGC--LQGSSLIIISVFLVGCAQN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linkages in cellulose.
SIMILARITY: CONTAINS MULTIPLE CELLULOSE-BINDING SITES.
SIMILARITY: BELONGS TO CELLULASE FAMILY E (FAMILY 9 OF GLYCOSYL
                                                                                            ELV.
lostridium stercorarium.
lostridium stercorarium, Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                         1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
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                                                                                                                                                                                                                                                                                                       FSR-----QEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGL 159
                                                                                                                                                                                                                                                                               FSKADWTDYIQTNDYSFSTNTSYG-----SNDRITVYISGVLVSGI 984
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Pred. No. 9.2e-08;
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     EMBL/GenBank/DDBJ databases
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                               Schwarz W.H.,
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Bronnenmeier K., Ruecknagel K.P., Staudenbauer W.L.;
Bronnenmeier K., Ruecknagel K.P., Staudenbauer W.L.;
Bronnenmeier K., Ruecknagel K.P., Staudenbauer W.L.;
Burification and properties of a novel type of
"purification and properties of a novel type of
"thermophile Clostridium stercorarium.";

Bur. J. Biochem. 200:379-385(1991).

Eur. J. Biochem. 200:379-385(1991).

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CHARACTERIZATION.
STRAIN=NCIB 11754;
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ProDom; PD011903; Glyco_hydro_48; 1.
ProDom; PD011903; Glyco_hydro_lase; Glycosidase; Cellulose degradation; Hydrolase; Glycosidase; Cellulose degradation; Hydrolase; Glycosidase; TI.
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Pfam; PF02011; Glyco_hydro_48; 1.
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pir4: *
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D83169
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A27198
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S12021
T31085
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T30433
C97012
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outer membrane l
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cellulase (EC 3
                                                                                                                                                                                                      hypothetical cellulase (EC 17K surface a
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homolog
(EC 3.2.
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PAL cross-reacting	2 164130	155		101.5	5
cellulase (EC 3.2		504	7.7	103	44
outer membrane pr	_			103	43
lipA protein - Rh.				104	42
probable outer men	2 в85771			104.5	41
probable outer men	2 F90922			104.5	40
outer membrane	2 C64921			104.5	39
outer membrane li	2 AG0443			106.5	38
bifunctional ce		186 2		107	37
lipA protein [imp	2 D97478			107	36
probable lipoprot	2 AF0289			107.5	35
lipA protein [imp	2 AD2696			107.5	34
conserved hypothe	В 82837			109	ω
 hypothetical prote 	_			109	32
probable secreted	2 AE0644			109	μ
outer membrane	2 AI0693			109	30

ALIGNMENTS

RESULT 1 A44140

cellulose-binding protein A precursor - Clostridium cellulovorans C;Species: Clostridium cellulovorans C;Dete: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 15 C;Accession: A44140
R;Shoseyov, O; Takagi, M.; Goldstein, M.A.; Doi, R.H. Proc. Natl. Acad. Sci. U.S.A. 89, 3483-3487, 1992
A;Title: primary sequence analysis of Clostridium cellulovorans ce A;Reference number: A44140; MUID:92228810
A;Accession: A44140
A;Rotession: A44140

cellulose binding

pro

27-Jun-1994 #text_change 15-Oct-1999

RESULT D33971 ricket N;Alte C;Spec C;Dace C;Ande R;Ande	Оу	Оy	Qy Db	Qy Db	Qy	Que Bes Mat	A;Crc C;Gen A;Gen
RESULT 2 D33971 rickettslal common antigen precursor - Rickettsla prowazekli rickettslal common antigen precursor - Rickettsla prowazekli rickettslal common antigen precursor - Rickettsla prowazekli C;Species: Rickettsla prowazekli C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 03-Nov-2000 C;Accession: D33971; B71645 C;Accession: B.E.; Tzianabos, T. Bacteriol. 171, 5199-5201, 1989	239 GTACPQPD 246 186 GTA-PGPD 192	181 EKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGOKQEIY 238	121 ROEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLNQSL 180	61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQNFS 120 	1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60 	Query Match 36.5%; Score 487; DB 2; Length 1848; Best Local Similarity 46.8%; Pred. No. 2.8e-32; Matches 116; Conservative 12; Mismatches 30; Indels 90; Gaps 7;	A;Cross-references: GB:M73817; NID:g144748; PIDN:AAA23218.1; PID:g144749 C;Genetics: A;Gene: CbpA

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A;Cross-references: GB:M28482; NID:g152461
A;Note: the sequence in GenBank entry RIRANT17KC, release 109.0, (PID:g152462) omits the R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499
A;Accession: B71645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15258.1; PID:g386135
A;Experimental source: strain Madrid E
C:Genetics:
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A; Residues: 1-159 < AND>
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C;Superfamily: rickettsial common
C;Keywords: surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                 R;Anderson, B.E.; Tzianabos, T.
J. Bacteriol. 171, 5199-5201, 1989
A;Title: Comparative sequence analysis of a
A;Reference number: A33971; MUID:89359171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsial common antigen precursor C;Species: Rickettsia conorii C;Date: 16-Mar-1990 #sequence_revision C;Accession: B33971
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A; Residues: 1-159 <AND>
A; Cross-references: GB:M28479; NID:g152463; PIDN:AAA26379.1; PID:g152464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAVLGGQIGASMDEQDRRLLELTSQRALESAPSGSNIEWRNPDNGNHGYVTPNKTY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RNSAGQYCREYTQTVIIGGKQQKTYGNACRQPDGQWQVVN 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGLIGSKIGQSMDQODK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKIMIIALAASMLQACNGQSGMNKQGTGTLLGGAGGALLGSQFGQGKGQL-VGVGVGALL
                                                                                                                                                                                      SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
                                                                                                                                                   SKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
                       KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                           GGLIGSKIGOSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTVQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61;
     -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN
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                                                                                                                                                                                                                              21.3%; Score 285; DB 2; 37.9%; Pred. No. 1.1e-16; tive 31; Mismatches 53
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Pred. No. 6.3e-17;
2; Mismatches 52
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-RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159

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RESULT 4
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A;Residues: 1-159 <AND>
A;Cross-references: GB:M28480; NID:g152457; PIDN:AAA26376.1; PID:g152458
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A;Title: Comparative sequence analysis of a
A;Reference number: A33971; MUID:89359171
A;Accession: A33971
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J. Bacteriol. 171,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17K surface antigen precursor [imported] - Rickettsia conorii (strain Malish C;Species: Rickettsia conorii C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
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A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: G97860
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A;Cross-references: GB:AE006914; PIDN:AAL03825.1;
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A; Residués: 1-159 <K
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                                                                                                                                               103 SSLIIISV---FLVGC--AQNFSRQEVGAATGAVVGGVAGQLFGKGSGRVSMAIG-GAVL 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSLIIISV---FLVGC--AQNESRQEVGAATGAVVGGVAGQLEGKGSGRVSMAIG-GAVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOERROOYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -RNSTGQYCREYTQTVVIGGKQQKAYGNACRQPDGQWQVVN 159
                                                                                                                      SKIMITALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
                                         GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY--
                                                                             GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
KOERROOYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS
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, 5199-5201, 1989
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Pred. No. 1.1e-16;
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Pred. No. 1.1e-16; ...
Pred. No. 1.1e-16; ...
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                                                                                                                                                                                                                                                 Length 159
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RESULT 8
PC6006
Scaffolding protein CipC precursor - Clostridium cellulolyticum (fragment)
Scaffolding protein CipC precursor - Clostridium cellulolyticum
C;Specles: Clostridium cellulolyticum
C;Specles: 17-Aug-1990 #sequence_revision 16-Aug-1996 #text_change 13-Nov-1998
C;Date: 17-Aug-1990 #sequence_revision 16-Aug-1996 #text_change 13-Nov-1998
C;Accession: PC6006
R;Pages, S.; Belaich, A.; Tardif, C.; Reverbel-Leroy, C.; Gaudin, C.; Belaic
J. Bacteriol. 178, 2279-2286, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Anderson, B.E.; Regnery, R.L.; Carlone, G.M.; Tzianabos, T.; McDade, J.E.; J. Bacteriol. 169, 2385-2390, 1987
A;Title: Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia A;Reference number: A25972; MUID:87222152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A25972

17K antigen precursor - Rickettsia rickettsii

C:Species: Rickettsia rickettsii

C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 20-Aug-1999
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A; Residues: 1-159 < AND>
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A;Residues: 1-159 <AND>
A;Cross-references: GB:M28481; NID:g152459; PIDN:AAA26377.1; PID:g152460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Anderson, B.E.; Tzianabos, T. J. Bacteriol. 171, 5199-5201, 1989
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Best Local :
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                                                                                                                                                                                                                     KQERRQQYCREFQQKAMIAGQKQEIYGTACPQPDGRWQVIS
                                                                                                                                                                                                                                                                         GAVLGGQIGAGMDEQDRRLAELTSQRALETAPSGSNVEWRNPDNGNYGYVTPNKTY----
                                                                                                                                                                                                                                                                                                                                                     SKIMIIALATSMLQACNGPGGMNKQGTGTLLGGAGGALLGSQFGKGKGQL-VGVGVGALL
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                                                                                                                                                                                                 -RNSTGQYCREYTQTVVIGGKQQKAYGDACRQPDEQWQVVN
                                                                                                                                                                                                                                                                                                           GGLIGSKIGQSMDQQDK----IKLNQSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYN 212
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Pred. No. 6.4e-16;
81; Mismatches 54;
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Pred. No. 5.8e-16;
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S36859
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                     submitted to the EMBL Data Library, A; Reference number: S28659
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     A; Reference number: A; Accession: S28659
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Best Local
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A; ACCESSELLE type: DNA
A; Molecule type: DNA
A; Residues: 1-586 < PAG>
A; Cross-references: GB:U40345; NID:g1314291; PID:g1314292
A; Cross-references: ATCC 35319
                                                                                                       A:Molecule type: DNA
A:Residues: 1-1615,1617-1854 <GE2>
A:Cross references: EMBL:L08665
R:Fujino, T.; Beguin, P.; Aubert, J.P.
FEMS Microbiol. Lett. 94, 165-170, 1992
A:Title: Cloning of a Clostridium thermocellum A;Reference number: $25767
A:Accession: $25767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cipA protein - Clostridium thermocellum N;Alternate names: probable cellulosome protein large chain SL C;Species: Clostridium thermocellum C;Species: Clostridium thermocellum C;Date: 11-Jan-195 #sequence_revision 13-Jan-1995 #text_change C;Accession: S36859; S33527; S25767; S28659; T18261 R;Gerngross, U.T.; Demain, A.L.
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F:1-27/Domain: signal sequence #status predicted <SIG>F:1-27/Domain: signal sequence #status predicted <F:28-586/Product: scaffolding protein CipC #status pref:28-187/Domain: cellulose binding #status predicted <F:28-187/Domain: cellulose binding #status predicted <
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                                         A;Molecule type: DNA
A;Residues: 1216-1232,'Y',1234-1241,'T'
A;Cross-references: EMBL:X67406
                                                                                                                                                                                                                                                                                                                                 R;Gerngross, U.T.; Romaniec, M.P.M.; Kobayashi, T. Mol. Microbiol. 8, 325-334, 1993
A;Title: Sequencing of a Clostridium thermocellum A;Reference number: S33527; MUID:93302508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: $36859
A; Accession: $36859
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F;293-439/Domain:
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A; Residues: 1-1854 <GER>
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72; Conserv
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hydrophobic <HYB1:
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Pred.
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August 1992
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                                                                    ,1243-1319,
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No. 5.7e-13;
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predicted <CBD>
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                                                                                                                                                       fragment encoding
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                                                                    ,1321-1615,1617-1854
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                                                                                                                                                                                                                                                                                                                                                          encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
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                                                                                                                                                       polypeptides
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A; Molecule type: DNA
A; Residues: 1216.1232,'Y',1234-1241,'T',1243-1319,'R',1321-1615,1617-1768,'R',1770-1854
A; Residues: 1216.1232,'Y',1234-1241,'T',1243-1319,'R',1321-1615,1617-1768,'R',1770-1854
A; Cross-references: EMBL:X67406
A; Cross-references: EMBL:X67406
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A; Cross-references: EMBL:X6740
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C;Genetics:
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A; Residues: 1821-1854 <FU2>
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A; Accession: T18261
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C;Species: Clostridium josui
C;Date: 22-Oct_1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1162 <KAK>
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A;Accession: T30433
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J. Bacteriol. 180, 4303-4308, 1998
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Best Local S
Matches 53
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probably cellulosomal scaffolding protein
C; Species: Clostridium acetobutylicum
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Best Local S
Matches 66
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Pred. No. 5e-12;
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Pred. No. 2.6e-11;
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C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: C97012 C;Accession: C97012 R; Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibt, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J Bacteriol. 183, 4823-4838, 2001
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
A; Molecule type: DNA; protein
A; Molecule type: CNA;
A; Molecule type: CNA;
A; Molecule type: CNA;
A; Molecule type: CNA;
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VKAGQVTRWRNPDTGNSYSVEPVRTYQR
                                                                                                                           EVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGLIGSKIGOSMDQQDKIKLNQSLEK 182
                                                                                                                                                                                                N----SNVTGNFF-NLSSPKEGADT-----
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Pred. No. 2.4e-10;
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1993
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pred. No. 1.1e-07;
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NCBIP: 125638)
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RESULT 13
$12021

thermoactive cellulase - Clostridium stercorarium

N;Alternate names: avicelase I

C;Specles: Clostridium stercorarium

C;Specles: Clostridium stercorarium

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C;Accession: $12021

C;Accession: $12021

R;Jauris, S.; Ruecknagel, K.p.; Schwarz, W.H.; Kratzsch, P.; Bronnenmeier, K.; Staudenba Mol. Gen. Genet. 223, 258-267, 1990

Mol. Gen. Genet. 223, 258-267, 1990

A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a thermoad A;Title: Sequence analysis of the Clostridium stercorarium celz gene encoding a the celz gene encoding a the celz gene encoding a the celz gene encoding a the celz g
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C;Species: Caldicellulosiruptor sp.
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AF036924; NID:g2760905; PID:g2760909; PIDN:AAB95326.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1779 <
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                    1114 LKVLYKNNETSASTGSIRPWFKIVNGGSSSVDLSRVKIRYWYTVDGDKPQSAVCDWAQIG 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    944 FSKADWTDYIQTNDYSFSTNTSYG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        668
                                                                                                                                                                                                                                                                                                                                  59 ALLGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGC--LQGSSLIIISVFLVGCAQN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xynC
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYXYTSDGTQGQTFWCDHA--G 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHAGAL 60
                                                                                                                                                                         FSRQEVGAATGAVVGGVAGQLF-GKGSGRVSM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GSNNITGTFVK-MAEPKEGADYYLETGFTDGAGYLQPNQSIEVQ-----NR 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQIQMENGNTSDKTNGIMPRYRLTNTGTTPIRLSDVKIRYYYTIDGEKDQNEWCDWSSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <MOR>
                                                                                                                                                                                                                                                                   -SNVTFNFVKLT-SGVSGADYYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -QEVGAATGAVVGGVAGQLFGKGSGRVSMAIGGAVLGGL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.18;
27.68;
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                                                                                                                                   AGQLQPGKDTGDIQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 151.5; DB 2;
Pred. No. 0.00032;
5; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SNDRITVYISGVLVSGI 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
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C;Keyworu.
F;20-320/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: Streptomyces endo-1,4-beta-xylanase A homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F;20-320/Domain: Streptomyces endo-1,4-beta-xylanase A homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Saul, D.J.; Williams, L.C.; Grayling, R.A.; Chamley, L.W
Appl. Environ. Microbiol. 56, 3117-3124, 1990
A;Title: celB, a gene coding for a bifunctional cellulase
A;Reference number: A43802; MUID:91136262
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A; Residues: 1-915 <S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Pathway: cellulose degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: hydrolysis of 1,4-beta-D-glucosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X13602
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                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
                                                                                                                                                                     433
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                                                                                                                                                                                                                                                       411
                                         238
                                                                                   458
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                                                                                                                                                                                                                                                                                                                                        351 IKVLYANKETNSTTNTIRPWLKVVNSGSSSIDLSRVTIRYWYTVDGERAQSAVSDWAQIG 410
  499
                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                                                                                                                                                                                                              1 MSVEFYNSNKSAQTNSITPIIKITNTSDSDLNLNDVKVRYYYTSDGTQGQTFWCDHA--G 58
                                       YGTACPQPDGRWQVISTEK 256
                                                                                                                       QSLEKVKAGQVTRWRNPDTGNSYSVEPVRTYQRYNKQERRQQYCREFQQKAMIAGQKQEI 237
                                                                                                                                                                   ----EIGFKSG-----AGQLQPGKDTGEI----
                                                                                                                                                                                                          FSRQEVGAATGAVVGGVAGQLF-GKGSGRVSMAIGGAVLGGLIGSKIGQSMDQQDKIKLN 177
                                                                                                                                                                                                                                                       A-----SNVTFKFVK-LSSSVSGADYYL-----
                                                                                                                                                                                                                                                                                 ALLGNSYVDNTSKVTANFVKETASPTSTYDTYLDPSHMRGCLQGSSLIIISVFLVGCAQN 118
----PSTNDDWLYVSGNK 512
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                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                 DWSNYNQGNDWSW--LQSMTSYGENEKVTAYI-
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23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 147; DB 2;
Pred. No. 0.00034;
5; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chamley, L.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                            64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 915;
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 100;
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                                                                                                                                                                     ----QIRFN
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